

## **Demography and Social Network Differentiation**

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### **Abstract**

Nearly all societies have completed or begun a demographic transition, but their experiences have varied in terms of timing, tempo and extent of mortality and fertility decline. I address what such variation implies for social interaction. Though prior literature has explored demographic contributions to opportunities for interaction between individuals, it has primarily focused on social ties between close kin of different ages in the context of multi-generational co-residence. I extend this work by considering broader kinship links in communities, which are important components of community integration, using the control afforded by simulation methods. Results show that variations in demographic history manifest as differences in modern social networks, suggesting potential modifications to understandings of social solidarity and modernity.

## **Introduction**

Evidence of declining social integration in America (McPherson, Smith-Lovin, and Brashears 2006) and other parts of the developed (Yee 2000) and developing world (de Souza and Grundy 2007) has important sociological implications. Research suggests weak integration negatively impacts individuals' political participation (Putnam 2000), health (Smith and Christakis 2008; Berkman, *et al.* 2000; Moen *et al.* 1989), and economic success (Coleman 1988; Granovetter 1985). Though scholars have documented the decline (McPherson, *et al.* 2006) and discussed its implications (Putnam 2000), the mechanisms which yield weak social integration remain under-specified. Changing social integration concerned early theorists, who typically attributed such changes to economic modernization (Durkheim 1893[1933]) and urbanization (Simmel 1903[1971]). Building on this tradition and more recent theories linking social structure to demographic constraints (Blau 1974: 616; Granovetter 1973: 1379; Entwisle 2007), this article suggests that contemporary social integration is the product of a society's demographic history.

I look specifically at the responsiveness of one type of social integration, operationalized as social network structures generated by kinship relations, to the historical influence of the demographic transition, a pattern of social change experienced in almost all societies. By focusing on broader social networks connecting members of communities, I extend prior work concerning family structure differentiation (Smith and Oeppen 1993; Dykstra and Knipscheer 1995; Ruggles 1986, 1988, 1990, 1994, 1996, 2007; Ruggles and Goeken 1992; Zhao 2001; Post, *et al.* 1997; Ruggles and Heggeness 2008; Kobrin 1976; Soldo 1981) to the level of social integration. Given the importance

of kinship networks in the literature and the suggested relation of social networks to demography in both classical and contemporary theory, this paper address a substantial gap in empirical analyses of the demographic transition. By exploring how the timing, tempo and extent of fertility and mortality decline influence social network form and differentiation with specific reference to kin networks, I relate historical processes to contemporary realities in a way that suggests new directions for social and demographic theory.

The first section of this paper outlines the importance of kinship networks as social structures. Doing so, it highlights classical and contemporary theory which suggests the importance of demography in constraining and patterning social networks, broadly defined, and kinship networks in particular. The second section presents evidence that societies' experiences with mortality and fertility decline have varied. It compares historical trajectories of demographic transitions around the world, focusing on countries' and regions' differentiation in terms of the timing of onset, pace of decline, and difference between pre- and post-transition mortality and fertility levels. I argue that these differences likely generate diversity in network forms, especially those surrounding kinship, but that little is known about how much variability in contemporary network structures owes to these historical factors.

Because of extreme data constraints, little is known about variability in contemporary kinship networks in general, and almost nothing is known about how they may have been influenced by the demographic transition. To investigate the connection between historical patterns of mortality and fertility decline and contemporary kinship networks, I employ the control afforded by simulation methods. I manipulate parameters

reflecting the timing, tempo and extent of fertility and mortality decline in order to parse the independent contributions of such historical conditions. In the third section of the paper, I introduce the agent based model used for simulation and discuss its grounding in a set of specific cases, which are later used to validate the model's plausibility against an unusual dataset from Nang Rong district, Thailand.

The fourth section presents results that suggest the importance of historical demography for kinship networks, that an area's experience with the demographic transition has the capacity to condition features of its current kinship networks. These results also show the potential intransience of contemporary social network differentiation. The unique circumstances which social groups experienced with respect to the demographic transition matter greatly for their current kinship network forms, and it seems likely that such differentiation will persist into the future. Such claims are tested for validity against a real world set of cases (in Nang Rong), and a variety of sensitivity checks are performed. Finally, by relating historical demographic patterns to populations' current social structures and reflecting on the potential theoretical confounding of demographic history with economic modernization, such results call into question classically held assumptions about social solidarity and modernity.

### **Social Networks and Demography**

Kinship networks are important social structures (Schweizer and White 1998) because of their relevance to many aspects of life including employment and economic prospects (Grieco 1987; Zimmer and Aldrich 1987), demographic decision-making (Choldin 1973; Tilly and Brown 1967; Bras and Neven 2007; Entwisle, *et al.* 1996;

Sandberg 2005), health outcomes (Christakis and Fowler 2007, 2008), worldviews (Vaisey and Lizardo 2008; Fowler and Christakis 2008), and revolutions in power and governance (Padgett and Ansell 1993). The affective nature and relative permanence of family-based kin ties makes them a primary unit of social bonding, the so-called strong ties in the social network literature. Beyond direct kin relations, indirect ties through kin act as conduits through which resources, information and obligations might travel. Indirect connections to kin (e.g., a cousin's spouse) are generally more likely to be "weak ties" (Granovetter 1973). Kin predominate information sharing circles throughout the world, as has been shown in the United States (McPherson, *et al.* 2006; Marsden 1987), Kenya (Kohler, Behrman, and Watkins 2001), Mexico (Massey 1990), and Thailand (Entwisle *et al.* 1996). Kinship groups are also a primary locus of resource sharing in the developed (Grundy 2006; Grundy and Henretta 2006) and developing world (Piotrowski 2006; VanWey 2004).

Importantly, kin are products of sociological norms regarding social-symbolic categories and demographic events (Kipp 1984). Though it is broadly acknowledged that societies differ with respect to the former, little thought has been put towards how they may differ with respect to the latter. Demographic events create certain types of people and condition the potential relations between them. Such opportunities are the focus of this paper. The broad opportunities for kin-based interaction created by demography have important implications for the translation of local social processes into global structural forms.

Prior demographic patterns affect social networks by constraining individuals' opportunities for interaction. Classical analyses of social structure<sup>1</sup> paid attention to constraints placed on associational patterns by the spread of people across time, space and social grouping (Durkheim 1893[1933]; Simmel 1903[1971]: 324-339; Marx 1939[1978]: 276-278; Weber 1923[1981]: 352-370, 1904[1958]: 39-40). More recent research has acknowledged that fertility and mortality change might affect social structure and patterns of interaction (Watkins, Mencken and Bongaarts 1987; McNicoll 1986). Such insights remain current; contemporary work has argued that places' network differentiation might be attributable to historical migration patterns (Entwisle 2007; Entwisle *et al.* 2007), a finding supported by evidence that residential segregation is a crucial determinant of friendship association by race among adolescents (Mouw and Entwisle 2006).

Demographic change alters the distribution of people across sociological categories, a fact with important implications for relations between people in these categories (Blau 1977). By looking at how possibilities for interaction covary with patterns of fertility and mortality decline, this paper makes no comment on possible changes in the meaning of different relationships or in likelihoods of activating particular ties. In the homophily literature, this is known as the distinction between “baseline homophily” and “inbreeding homophily” (McPherson *et al.* 2001). While the former is a function of random expectations given relative group sizes (e.g., Blau 1977), the latter

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<sup>1</sup> Throughout this paper, I use the term social structure to mean the set of relations linking individuals or entities.

represents proclivities towards preferential association above the baseline<sup>2</sup> (Goodreau, Kitts and Morris 2009).

For example, age-distribution effects are well studied in the demographic literature, especially at the national level. Chesnais (1990) reports that the demographic transition may manifest in older age populations over 40 times the size of their pre-transition levels in countries such as India, and 100 and 200 times in Mexico and Kenya, respectively. With such a growth in older-age populations, it is more common that middle-aged individuals' parents are alive, which increases the likelihood for interaction between generations, and, at the population level, suggests that parents will be important forces in the lives of those countries' adults. In contrast, Chesnais shows that France, whose demographic transition was the slowest and steadiest in the world, saw only a 10 fold increase in its old age population. Thus, it can be expected that Kenya and Mexico will have experienced greater shifts in their baseline social relations over the past century than France, where middle-aged individuals are only slightly more likely than their parents were to have the opportunity to interact with adults a generation older.

Extrapolating from such age-distribution effects, Ruggles (1986) calls the demographic changes seen in the developed world a necessary condition for the rise of the extended family structure. But demographic influences on the availability of kin matter for reasons beyond the family; as discussed by McPherson *et al.* (2001: 361), "having kin in one's network tends to increase contacts across age categories (through contacts with grandparents, parents or children), educational strata (because of cohort

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<sup>2</sup> McPherson et al. (2001: 419) state that their definition of inbreeding homophily "does not in any sense indicate choice or agency purified of structural factors."

differences in educational stock), and sex (because of the heterosexual nature of marital unions and the sex composition of sibship)”.

Though I argue that demographic contributions to kinship matter beyond immediate families and household co-residence, I do not suggest that such patterns of interaction should be examined on the national scale. This is because the vast majority of interactions (kin-based or otherwise) can be found within a small geographic circle around each respondent. Local, face to face, contact is still thought prominent (Wellman *et al.* 2001; Putnam 2000), though a substantial amount of contact occurs between spatially distant close kin, facilitated by telephonic and electronic communication (e.g., Onnella *et al.* 2007). The focus on neighborhood and village effects in both the developed and developing world underscores the importance of such local interaction in sociological theory and methodology (Entwisle 2007).

Unfortunately, most studies have examined demographic change at the regional or national scale. Still, there is ample evidence of sub-national and even local demographic variation. For example, Entwisle *et al.* (1996) found substantial variation in contraceptive use and fertility patterns between spatially proximate villages in a small district of Northeast Thailand. Axinn and Yabiku (2001) describe similar diversity in the villages of Chitwan Valley, Nepal.

Whether there is a relationship between such documented local variations in demographic determinants and social networks is not fully understood, owing largely to the fact that such variation remains understudied (Entwisle 2007). Though considerable research has explored the ways in which demographic choices are shaped by social structural endowments (Entwisle *et al.* 1996; Godley 2001; Rindfuss, Choe *et al.* 2006;



Massey 1987; Sandberg 2005), little, outside of the household co-residence literature, has explored the possibility that demographic choices also shape those social structures. That is another gap in the literature addressed by this study and the reason for its focus on local demographic settings that capture the contextual network of relations – beyond the immediate ties within the household – amongst individuals.

### **Demographic Transitions**

Almost every society has completed or begun a demographic transition (Guest and Almgren 2003). Despite the often contentious debates about demographic transition theory (Mason 1997; Coale 1973), the demographic transition can be descriptively divided into three stages: pre-transition, transitional, and post-transition. In the pre-transition stage, birth and death rates are both high and in equilibrium, which results in little population growth. In the transitional stage, birth and death rates go from high to low. Death rates, especially those in the first years of life, are generally lower than fertility rates during this stage, a phenomenon which creates often substantial population growth. After the transition, mortality and fertility rates are once more near equilibrium but both low, resulting again in low population growth<sup>3</sup>. Movement through these stages is generally thought of and collectively referred to as the demographic transition. Though experience with the demographic transition has been nearly ubiquitous, societies' exact routes of mortality and fertility decline have varied considerably, both internally and in comparison to other societies.

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<sup>3</sup> Some countries have experienced a “second demographic transition” (Van de Kaa 1987), where fertility rates continue to fall and are below replacement; they are not the focus of this paper.

Most comparative research documenting variations in the demographic transition has focused on fertility transitions (Dyson and Murphy 1985; Mason 1997; Bongaarts and Watkins 1996; Caldwell and Caldwell 2006)<sup>4</sup>. Fertility transitions did not occur simultaneously throughout the world, nor did they proceed at the same speed. To demonstrate the range of variation, table 1 summarizes the general timing and tempo of fertility transitions for 13 world regions<sup>5</sup>. It shows the median year when fertility in each region's countries had declined 10% from pre-transition levels - a change taken to indicate a significant shift in fertility patterns - and the mean number of years countries in that region took to decline from 10% off of pre-transition fertility levels to 40%. With respect to timing, countries in sub-Saharan Africa and the Middle East began their fertility transitions almost 100 years after Europe and the most developed, English-speaking colonial states. With respect to tempo, some countries (e.g., Guadeloupe, Guyana, Singapore, China, and North Korea) took as little as 5 years to proceed from a 10% decline to a 40% decline, while others took 30 or more years (e.g., Belgium, the United Kingdom, Germany, Italy, Iceland, France, and the United States) as can be seen in appendix table A1.

It is well known in the demographic literature that births can only be produced by a specific set of interactions and events - termed proximate determinants. These can be approximated by the average female age at first marriage, the extent of contraceptive use

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4 This singular focus on fertility is unfortunate, but a comparison of national mortality transitions' dates of onset and tempos of change is lacking in the literature. Caldwell and Caldwell (2006: 227) explain that this is because "too many nineteenth and early twentieth-century European mortality statistics were unreliable or nonexistent."

5 This table is adapted from Caldwell and Caldwell (2006). Its regional groupings are argued to be "demographically consistent", meaning that countries in those regions had generally similar experiences with the demographic transition.

and induced abortion, and the duration of post-partum sterility in the population (Bongaarts 1978; Bongaarts 1983). Because of this, examining variation in proximate determinants can help to contextualize variation in demographic transitions currently underway. Toward this end, researchers typically examine changes in the age pattern of fertility (which is linked to changes in age at first marriage) and changes in contraceptive use (Coale and Trussel 1974; Coale and Trussel 1978). Rapid shifts in contraceptive use can be seen in some countries (Nortman 1977). For instance, in the Thai population, use rose from 15% in 1969 to 33% in 1975; in Mexico it jumped from 30% to 40% between 1977 and 1978 (Tsui 1985). Such changes suggest heterogeneity of tempo. There was also heterogeneity of timing, as can be seen by levels of contraceptive adoption by the time of the World Fertility Surveys (WFS) in the 1970s. By then, 34% of Latin Americans surveyed had begun using contraceptives compared to 21% of Asians, 20% of Middle Easterners, and only 5% of Africans (Tsui 1985: 122). Variation throughout the world has also been found in non-contraceptive (and non-abortive) restraints on fertility. This variation has been attributed to cultural norms influencing age of first sexual intercourse, periods of marital separation, and length of interbirth intervals (Leridon and Ferry 1985; Rindfuss and Morgan 1983).

Mortality transitions, like fertility transitions, have also varied in terms of timing of onset and tempo of decline, though generally less is known about them (see note 3 above; Mason 1997; Hirschman 1994; Heueveline 2001). Infant and child mortality rates are the best studied components of the mortality transition owing to their influence on measures of life expectancy, their responsiveness to social change, and the long-standing availability of comparative data about them from the WFS (Preston 1985b). These

examples from sub-Saharan Africa give a sense of the diversity in the progression of the mortality transition. The estimated probability of dying before the age of 5 decreased 0.111 in the 34 years between 1949 and 1983; in contrast, in Burkina Faso, there was a decline of 0.209 in the 33 years between 1948 and 1981. Just as with fertility declines, the developed world experienced mortality declines much sooner than the developing world. For instance, age patterns of infant mortality were almost identical in 1976 Colombia and 1931-1935 Scotland (Preston 1985b). However, mortality declines in the developing world happened more quickly and at significantly lower levels of development (Preston 1985a; Davis 1956; Caldwell 1986).

Different lag periods between onsets of fertility and mortality decline account for much of the global variance in experience with the demographic transition. Bongaarts and Watkins (1996) show that countries experienced fertility transitions at different levels of development and with differences in infant mortality rates and life expectancy at birth. Such variation can be seen in this short list: Singapore, Hong Kong and Jamaica began their fertility transitions with infant mortality rates of 37, 41, and 43 per 1,000 and life expectancies of 63, 65, and 67 respectively, while Turkey, Egypt and India began theirs with infant mortality rates of 176, 166, and 131 per 1,000 and life expectancies of 49, 50 and 50 respectively.

Most research on the impacts of the demographic transition has considered its implications for economic development (e.g., Zhang, Zhang and Lee 2001; Chesnais 1990; Coale and Hoover 1958), a topic outside the scope of this paper. Much of the rest has focused on its implications for social interactions between individuals (e.g., Ruggles 1986, 1988, 1994, 1996, 2007). This focus highlights important theoretical contributions,

yet research on the topic has concentrated almost exclusively on intra-household relations, specifically weighing the relative contributions of demography and economic development to declining intergenerational co-residence and interactions between individuals of different ages (Smith and Oeppen 1993; Dykstra and Knipscheer 1995; Ruggles 1986, 1988, 1990, 1994, 1996, 2007; Ruggles and Goeken 1992; Post, *et al.* 1997; Ruggles and Heggeness 2008; Kobrin 1976; Soldo 1981). Though extra-household kinship links in communities have predictive capacity for sociologically meaningful phenomena (e.g., Entwisle, *et al.* 2007; Entwisle, *et al.* 2009; Entwisle, *et al.* 1996; Fowler and Christakis 2008; Christakis and Fowler 2008), the processes generating differences in such networks have not received much attention in the literature, most likely due to lack of available data (Entwisle 2007). I suggest that the demographic transition has played a vital role.

### **Simulation Approach**

To explore demographic contributions to social structure, this paper uses an agent-based model simulating the demographic behavior of individuals in a kinship system.<sup>6</sup> This is an ideal method to study demographic contributions to social network differentiation, because it allows for controlled parameter manipulation that can isolate how changes in historical demographic patterns play out as lagged changes in social structure (see Epstein (2006: 1-46) for a discussion of the theoretical underpinnings of

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<sup>6</sup> This program was developed using Matlab (2007) in conjunction with Peter J. Mucha, Katherine Faust, Barbara Entwisle and Ronald R. Rindfuss. I intend to make the code for this program and the programs which generates the analyses and parameters discussed in this paper available online after publication of the first-paper to result from this work pending the agreement of all interested parties.

social simulation; see Macy and Willer (2002) for a review of its applications). Testing bottom-up hypotheses about social structure that are informed by a demographic model of entrance and exit from the population about is an important contribution of this paper. Also, given the paucity of comparative data on kinship structures and the inexact understandings of comparative demographic transitions in the literature, this method overcomes many of the problems endemic to classical survey analyses in the face of limited data; indeed, it may be the only feasible means of examining such hypotheses.

The approach I use improves on prior models of social network interaction (e.g., Robins *et al.* 2005) and demographic micro-simulation (e.g., Smith and Oeppen 1993). Simulation models of social networks typically test how prohibitions or predilections towards association between certain individuals, governed by their attributes and relational positions in the network, produce different types of network structures. An example is the work of Behrman, Moody and Stovel (2004) who found that a taboo against four-cycles (e.g., a male dating an ex-girlfriend's ex-boyfriend's ex-girlfriend) yields romantic networks quite similar to those found among heterosexual adolescents. The networks created by such a prohibition were found to be more similar to the empirical dating networks than any that could be generated accounting for the (non-structural) attributes of the individuals involved.

The model I employ differs from most simulation analyses of social networks in that it emphasizes how individuals' entrances and exits from the population contribute to social structure. As outlined in the review above, this is a key demographic insight. In this sense, it is more like a demographic micro-simulation of the kind employed in the household co-residence literature. However, demographic micro-simulations have

received a significant amount of criticism as they typically do not allow agent interaction, model correlated traits across the life-course and within families, or allow for changing vital rates (see critiques in Ruggles 1993; see Wachter, Blackwell and Hammel 1997 for an approach that overcomes many of these problems)<sup>7</sup>. All of these problems are addressed by the agent based microsimulation approach used.

### **Setting of the Model**

I set my analysis in the villages of Nang Rong, Thailand, a location that is ideal for a study of this kind owing to its varied demographic history and present differentiation of village-level kinship networks. In addition, the unique demographic and social network data collected in Nang Rong (Nang Rong Projects 2008) help inform the operation of the model and allow for its empirical validation. Nang Rong is one of more than 700 districts in Thailand. Located in the Northeastern part of the country, it is approximately the size of a typical county in the Eastern United States (1,300 km<sup>2</sup>). It is a rural, primarily rice-growing region.

Nang Rong was a frontier area for new settlement until the early 1970s (Entwisle *et al.* 2008; Entwisle *et al.* 2009). Because the area was largely uninhabited until 1900, most villages are new (Faust *et al.* 1999), although a few were settled hundreds of years ago when the region was part of Cambodia. As such, most villages in the district were

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<sup>7</sup> These criticisms have led authors to largely abandon such simulation techniques in favor of using genealogical data gleaned from parish registers and other sources (e.g., Plakans 1984; Ruggles 2007). The use of such data has made vital contributions, but those data are typically not available for the developing world (outside of China see Zhao 1994) and may never be. Further, such data are very sensitive to issues of accuracy and incompleteness owing to under-registration of individuals and vital events (see Post *et al.* 1997 for an extensive review of these problems; Quinlan and Hagen 2008; Henry 1956).

initially characterized by large numbers of in-migrants and high levels of natural increase. These demographic patterns persisted until the 1960s, when, as with the rest of Thailand (Knodel *et al.* 1987), fertility rates in Nang Rong began to fall. Despite the drop in fertility and despite the closing of the frontier and a general reversal of migration streams in the 1970s (Entwisle *et al.* 2007; Entwisle *et al.* 2009), the population of the region's small villages continued to grow until the 1990s. These are, of course, general trends in the region, there was likely local variation.

The villages of Nang Rong remain relatively small. In 2000 their populations ranged from 333 to 1,260 individuals with a median of 665; including migrants not residing in the village at the time of the 2000 data collection, these numbers were 475 to 1,600 with a median of 873. Though prior research has shown that village residents tend to know one another, it has also found substantial variation from one village to the next in the patterning of economic and kin ties and that such information meaningfully predicts information flows (Entwisle *et al.* 2007).

Because I seek to maximize the validity of my model, I have attempted to mimic demographic patterns assumed present in the Nang Rong villages. Because villages have been the setting of prior work on social networks in developing countries, and because explorations of variation in local social integration are lacking in the literature, I have limited all analyses to events that take place within the village. Doing so focuses on the village as an important context for social life. It also circumscribes the network boundaries (Laumann *et al.* 1983; Laumann *et al.* 1992). As an example of these restrictions on network boundaries, consider the case of a person who enters the village through marriage or as a single person through in-migration. When this happens, my



simulation model treats them as coming without kinship ties that are relevant to the population of interest. Who lives in a village thus depends on fertility, mortality and migration patterns experienced by that village, patterns which in turn dictate the number, nature and structure of that village's kin ties, at least to the extent that kinship is measured objectively. More details of the model's operation can be found in Appendix B.

### **Demographic Scenarios**

Thailand's experience with the demographic transition is generally described as follows. The mortality transition began around 1950 and progressed rapidly. From 1947 to 1960 life expectancy at birth increased by about 11 years, with gains in mortality mostly leveled off by the year 1980 (Chamratrithirong and Pejaranonda 1986). The fertility transition began soon after the mortality transition, in approximately 1960. Marital fertility in Thailand fell by about 40% in the decade between 1969 and 1979, with a 10% decline having been registered prior to 1969 (Knodel, Havanon, and Pramualratana 1984; Caldwell and Caldwell 2006). However, there may have been considerable local variation in these trends. In particular, Nang Rong and the rural Northeast region where it is located are likely to have begun their demographic transitions somewhat later than the rest of Thailand (Knodel, Havanon, and Pramualratana 1984), although the larger, more developed towns of the district may have had experiences similar to the rest of the country.

To simplify my analysis of the demographic transition's contributions to kinship network structure, I simulate nine combinations of fertility and mortality scenarios. Scenarios were chosen to mimic the general demographic history of Nang Rong, but they

also strive for sufficient abstraction to hint at what other changes might imply for network differentiation. By considering variations in terms of timing of onset, tempo and extent of fertility and mortality decline, some of the variation in regional demographic transition patterns seen in table 1 (and table A1 in the appendix) is explored.

The panels of figure 1 depict the variation in demographic transitions explored. Each row of panels contains the same fertility scenario while each column contains the same mortality scenario. The x-axes of all panels order years 1940-2000, the period during which Thailand experienced the demographic transition<sup>8</sup>. The row-column combinations of panels show the general fertility and mortality trends over that period in each scenario using the total fertility rate<sup>9</sup> (read on the right y-axis) and female life expectancy<sup>10</sup> (read on the left). In a quick summary, mortality scenario one is an early onset, quick transition; mortality scenario two is an early onset, slow transition; mortality scenario three is a late onset, median transition; fertility scenario one is an early onset, gradual transition; fertility scenario two is a late onset, slow initial decline then quickened tempo; and fertility scenario three is a late onset, rapid transition.

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<sup>8</sup> Note that the model begins in 1900 but that levels of fertility and mortality used in all scenarios remain constant from 1900 to 1940 at the level shown in 1940.

<sup>9</sup> The total fertility rates shown are only approximations to make the figure more familiar to non-demographers, as the underlying parameter concerns marital fertility. To convert the age-specific marital fertility rates into a total fertility rate, I multiplied each age-specific rate by the proportion of the population that considers some form of marriage and summed. This is analogous to the conversion of marital fertility rates to total fertility rates given in Preston et al. (2006), but accounts for the uncertainty regarding the true proportion of women at each age who are married. A further complication of the precision of the fertility rates is that individuals have person-specific shifts from the global mean in the likelihood of giving birth in each year, as described in appendix B. Thus, the fertility rates presented ought to be viewed as a description of the underlying data generating process rather than exact rates that will be experienced in the population.

<sup>10</sup> Changes in male life expectancy follow the same pattern but do not proceed as high, as has been the case empirically (Preston 1980).

The combination of mortality scenario three with fertility scenario three (the bottom right panel of figure 1) is the one that appears to most closely conform to the experiences of Thailand and will be considered the baseline model. In the other scenarios, I consider how things might be different had the demographic transition proceeded differently, or if there was local variation around the national mean expressed as the baseline scenario.

I begin by asking how the gap between the timing of onset of mortality decline and the timing of onset of fertility decline influences social network structure. This gap is crucial to the growth of the population and constitutes a substantial difference between demographic transitions in developed and developing countries. I examine the influence of this gap in the combinations of fertility and mortality decline (see appendix B for a description of the calculation of fertility and mortality parameters). For instance, combining mortality scenario 1, where life expectancy begins to rise in 1940 and all gains are completed by 1960, with fertility scenario 1, where a drop corresponding to 10% of the pre-transition total fertility rate takes place between 1950 and 1960 yields a gap between the timing of onsets of fertility and mortality decline of 10 years<sup>11</sup>. In contrast, combining mortality scenario three with either fertility scenario two or three, where the initial 10% decline from pre-transition levels does not begin until 1960, yields a gap of 20 years. The gap between the timing of onset of fertility and mortality decline is longest in the combination of fertility scenario two and mortality scenario one, while it is shortest in the combination of fertility scenario one and mortality scenario three.

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11 Preston (1985b) notes that mortality declines in the developing world slowed in the in the 1960s and 1970s.

In general, I expect that longer gaps between the beginning of fertility and mortality decline will create more cohesive social structures, while shorter gaps will create less social cohesion in terms of kinship networks. Such a hypothesis comes from the well-known influence of long-periods of rapid population growth on the age-distribution of the population and individuals' average number of siblings. Simply, the cohort born during the period when mortality has fallen more quickly than fertility will have more siblings than previous cohorts because more infants will survive. They will also have more siblings than later cohorts born when women have fewer children. At least as long as that cohort remains alive, the length of this period influences the number of people with such sibling counts and thus increases the likelihood that individuals have greater numbers of kin. Such a finding will speak to concerns about whether the declining social cohesion observed in developed countries is a certain future for developing countries experiencing demographic transitions, as developing countries experienced a significantly longer gap between the onsets of fertility and mortality decline than developed ones.

The timing of onset of mortality and fertility decline is also interesting because it shapes the age distribution of the population (Coale 1972). As is well-known in the demographic literature, when fertility temporarily exceeds mortality it creates a larger than usual cohort. This means that for the length of time this occurs, which is explored above, there will be a bubble in the age-structure, called the baby-boom in the developed world and sometimes referred to as the demographic dividend (Bloom, Canning and Sevilla 2003). Such a bubble reverberates through the demographic profile of a population for many years (cf. Chesnais 1990), and the length of time that has passed

since its creation will have profound influences on the population at a given later date. The length of time since it was created, which is dictated by the onset of the demographic transition, will control whether the plurality of the population has larger numbers of children, siblings, or parents.

Variation in the tempo of fertility and mortality declines – the speed with which rates fall in isolation and combination – is another worthwhile comparison. In my scenarios, such comparison is achieved by contrasting within the mortality and fertility scenarios and by varying combinations of these contrasts. For instance, in mortality scenario one, life expectancy rises over a period of 20 years, in mortality scenario two, life expectancy rises over a period of 40 years, while in mortality scenario three life expectancy rises over a period of 30 years. Similar contrasts can be found in the fertility scenarios. Such a comparison is again interesting because of differences between the developed and developing regions of the world. Recalling table 1, broad regions of the world ranged from 12 to 26 years to complete their fertility transitions, with those which began later (i.e., those outside of Europe) generally completing at a faster rate than those which began earlier (cf. Preston 1985a). And, as can be seen in the appendix table A1, variation between individual countries is more extensive than between regions. Whether such differences will generate different kinship structures is an important consideration; I hypothesize that they will.

In addition to considerations of the timing of onset, tempo and extent of fertility and mortality decline, I explore the contribution of initial village conditions to social network structure. At the start of the period being modeled in 1900, most of the Nang Rong villages were comprised of young, sparsely kin-linked in-migrants who had moved

to settle the frontier, while a few others had been settled for centuries. In keeping with the rural Thai setting, I use two stylized initial conditions that roughly correspond to those known to have existed in the region: an established village and a newly founded village. With such stratification, I ask to what extent is contemporary kin network differentiation influenced by the network differentiation of the past.

This question has a great deal of substantive importance for those interested in local demographic and social network variation. In developing countries, urbanization and intra-rural migration account for a sizeable share of migration (Bilsborrow 2002). Such large-scale movement of the population results in the establishment of new cities, towns and neighborhoods and, consequently, brings large groups of unconnected individuals into close proximity – even though migrants tend to cluster in residential enclaves (Shao, Walsh, Entwisle and Rindfuss 2008). Given this, whether places which have experienced such a rapid influx of migrants can be expected to fundamentally differ from those which have not is a worthwhile consideration. When this phenomenon occurred in the developed world, it was of great concern to early sociologists (e.g., Park, Burgess and McKenzie 1925; Durkheim 1893[1933]; Simmel 1903[1971]). Between places which inherit a history of settlement and those which have developed recently, there is also likely to be substantial heterogeneity in terms of age-structure and kinship network cohesion. Because of this, exploring the impacts of variations in initial conditions is crucial to understanding the demographic transition at a local scale.

In the scenarios meant to represent those villages which had been settled for long periods of time, the initial conditions are chosen from a 150 year old established village with approximately 70 living members distributed according to age and sex ratios of high

fertility, high mortality populations and characterized by extensive (within-village) kinship links<sup>12</sup>. In the scenarios meant to represent the frontier villages of the district that were uninhabited prior to approximately 1900, the initial conditions are chosen from a group of 70 recent in-migrants who are predominantly young (ages 15-50) and childless with approximately 50% of the women linked to spouses. In all of their combinations with the fertility and mortality scenarios, introducing these two sets of initial conditions yields a total of 18 scenarios.

These scenarios and their associated parameters are chosen to reflect the experience of a frontier region governed by crude presumptions of the temporal evolution of Nang Rong villages, but they also encapsulate a diversity of demographic transitions. In combination, the 18 scenarios outlined allow for the independent and simultaneous examination of the ways in which the timing of fertility and mortality onset, the gap between them, the speed with which they progress, and the initial conditions from which they are path dependent affect the social structure of the population.

A thorough treatment of the underlying operation of the model, including the rules governing demographic behavior and all additional behavioral parameters (such as those relating to migration and marriage) are discussed in appendix B.

### **Measuring Kinship as Social Structure**

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<sup>12</sup> This initial village is “grown” by simulation. Tracking the village for longer than 150 years is computationally challenging owing to the number of individuals that live and die. In addition, I know of no work attempting to quantify demographic patterns that far back in rural Thailand, so choosing accurate input parameters is a challenge. Finally, links between individuals connected by large chains of indirect kin are not considered as outcomes in this paper, thus growing the village for longer than this is largely irrelevant.

There are two key concerns in measuring kinship. First, it is preferable that any measure must be cross-culturally valid (White and Moody 2003). Measuring kinship objectively is important because kin are partially determined by social-symbolic categories distinctive to each society, making cross-cultural comparisons difficult, if not meaningless. Second, it is important to understand both the immediate relations of individuals and the broader social network that the compounding of direct links generates. Previous analyses have used both measures: while some have relied on counts of specific types of kin (e.g., Ruggles 1993; Zhao 2001), others have focused on structural properties of the kinship system treated as a complete social network (e.g., Entwisle *et al.* 2007; Entwisle *et al.* 2009). To operationalize kinship structure objectively and integrate both direct and indirect kin links, the work proposed uses network analytic methods (Wasserman and Faust 1994). It treats kinship structures in both ways, as aggregations of direct relations and as broader systems of direct and indirect relations.

I consider three features of kinship networks: average numbers of direct kin, average numbers of indirect kin, and the extent of community connectivity through kinship. To create these measures I define a socio-matrix ( $\mathbf{A}$ ) for the population of individuals who have ever lived in the village. Every row ( $\mathbf{A}_i$ ) of this matrix represents one individual, as does that row's corresponding column ( $\mathbf{A}_j | i=j$ ). Each cell ( $\mathbf{A}_{ij}$ ) of this matrix represents a potential kinship tie between the individual represented by the row (the ego) and the individual represented by the column (the alter). Its  $ij$ th (and  $ji$ th) cell is assigned a value of one if the ego is a child or parent of the alter, or if the two have ever been spouses; otherwise, it is assigned a value of zero. Simple arithmetic operations were



performed on this matrix to calculate the various features of interest (algorithms available upon request; cf. Batagelj and Mrvar 2008; Batagelj 2009)<sup>13</sup>.

My analysis focuses on mean numbers of directly tied kin in the population because of the attention paid to this metric by the literature on demographic change and social structure (e.g., Smith and Oeppen 1993; Dykstra and Knipscheer 1995; Ruggles 1986, 1988, 1990, 1994, 1996, 2007; Ruggles and Goeken 1992; Zhao 2001; Post *et al.* 1997; Ruggles and Heggeness 2008; Kobrin 1976; Soldo 1981). Close kin are typically operationalized as living first-degree kinship connections, plus siblings (who are technically second degree kin<sup>14</sup>), and I follow this definition. As outlined above, the relations between such kin are important because they often provide or receive direct social support and can condition the broader connectivity to the village kinship system that someone may enjoy. I hypothesize that the speed of the demographic transition will negatively correlate with numbers of such kin.

I also examine counts of indirectly tied kin as a second means of understanding changes in social structure. Though weak ties should not be misconstrued with indirect relations, it is a reasonable assumption that indirectly related kin are typically more likely “weakly” tied than directly related kin. Granovetter (1973) himself specified indirect

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13 All measures are presented on a subset of the adjacency matrix consisting of the living and resident population, but they are calculated on the matrix of all individuals who have ever lived in the village because restricting the analysis to those currently living creates missing social network data that has been shown to strongly affect social network measures of kinship (Verdery *et al.* 2009).

14 First degree kin are those reached through child, parent or spousal ties (see Keyfitz and Caswell 2005; White and Moody 2003). Higher order degrees are the defined by the smallest power to which the first degree adjacency matrix must be taken to find the kinship connection of interest. Thus examples of second degree kin include siblings (parent’s children) and grandparents (parent’s parents) while aunts and uncles (parent’s parent’s children) would be third degree kin and cousins (parent’s parent’s children’s children) would be fourth degree.

relations as a potential source of weak ties. Weak ties have long been theorized as crucially important features of social networks in the literature (Granovetter 1973). As such, indirect kin – cousins, grandparents, aunts, uncles and beyond – are likely important for passing information from distant parts of the social network (Entwisle *et al.* 2009). To understand how varying experiences with the demographic transition relate to counts of indirect kin, I examine individuals' mean number of second- through fourth-degree kin.

Another important concept in the literature on kinship relations is the extent to which information and resources might transfer through the population, the network's potential for "contagion"<sup>15</sup> and community connectivity. Regarding kinship, similar concepts have been shown useful for understanding the diffusion of innovations (e.g., Rogers 2003), migration (e.g., Entwisle *et al.* 2009), fertility (Entwisle *et al.* 1996), and other topics. Additionally, community connectivity has been singled out for its dependence on demographic history, especially that owing to migration (Entwisle 2007). I measure it by considering the percentage of the population reachable in (shortest) kinship paths of four or fewer degrees.

As two of the three substantive measures - counts of direct and indirect kin - are arguably related to the size of the currently living population, I also consider differences in that metric. Considering such differences contextualizes the simulation results within more formal metrics of demographic analysis, and allows a simple test of the nominal

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<sup>15</sup> I follow Leenders (2002) and use the term contagion to describe any network effect including those due to transmission, emulation, or other social process that may operate directly or indirectly through the relations in the network.

validity of the models when the results conform to what would be expected from the demographic scenarios.

### **Simulation Results**

In this section, I present simulation results from the agent based model under the 18 combinations of fertility and mortality scenarios and initial conditions that capture a variety of experiences with the demographic transition. As 1,000 simulations with different sequences of random numbers were run for each scenario, there is considerable variability of estimates. Thus, for each scenario, table 2 presents the quartiles across simulations of the features of kinship networks I consider. Results are measured in the year 2000 and grouped according to kinship network feature, with combinations of fertility, mortality and initial conditions outlined. As this paper considers whether differences in kinship network structures relate to the demographic transition, I evaluate the models using two criteria. First, I consider substantial differences between models as those where the interquartile ranges do not overlap. Second, I consider distinguishable differences between the models as those where the interquartile range of one model does not overlap the median of another.

This form of differentiation between the models relies on the notion that many of the processes explored are inherently stochastic. Thus, the distribution of observed features of kinship networks found for any scenario is taken to be the range of likely outcomes given stochastic variability around the data generating process. By considering two scenarios as substantially different when the interquartile ranges of their observed distributions do not overlap, I am assuming that the differences in the data generating

processes between the two scenarios - in this case their relative experience with the demographic transition - yields different results that are outside the realm of what would be expected at random.

The gap between the timing of onset of mortality and fertility declines helped motivate my choices of demographic scenarios. To explore its contribution, I consider the simulation results holding fertility scenario constant. Recalling from figure 1 that the mortality transition began early in scenarios one and two and late in scenario three, we would expect to see the influence of this gap in comparing these scenarios. As the tempo of change in mortality scenarios two and three were rather similar, this is the best comparison to isolate the influence of a gap in the timing of onset of mortality decline.

For population currently alive, for numbers of close kin, for numbers of indirect kin, and for village connectivity, there is not a single substantial difference related to the length of time between mortality declines and fertility declines. Indeed, for all of the dependent variables, in all of the fertility scenarios, whether the simulation began from a new village or an established one, there is not a single instance where the influence of this gap exceeds the influence of the stochastic randomness introduced. That is, while the values for the early onset scenario (two) are consistently larger than those for the later onset scenario (three), there is not a single instance where the median of the simulation runs for early onset is greater than the third quartile of simulation runs for late onset. Generally, the average individual living in an early onset scenario had more close and indirect kin than the average individual living in a later onset scenario, and the average village was more connected. Yet these are not large differences; the average individual who lived in a newly established village in which the mortality transition began early had

almost 0.1 more close kin and around 0.7 more indirect kin than someone who lived in a new village with a late mortality transition onset. That the late onset scenario, with its more contemporary onset of mortality decline, did not generate significant differences from the earlier onset scenario also suggests that the duration of time that has passed since the demographic transition began significantly influences the structure of kinship networks.

However, holding fertility scenario constant, there are several instances of distinguishable and substantial differences between mortality scenario one (early onset, rapid tempo) and mortality scenarios two (early onset, gradual tempo) and three (late onset, median tempo). Recalling that life expectancy rises over a period of 20 years in mortality scenario one, over a period of 40 years in mortality scenario two, and over a period of 30 years in mortality scenario three, such differences between scenarios could be attributed to the differential tempo of the increase in life-expectancy. Were the tempo of life-expectancy increase responsible for differences in kinship structure between the mortality scenarios outlined, we would expect that, within fertility scenarios, the rapid tempo scenario (one) would be more similar to the median tempo scenario (three) than to the gradual tempo scenario (two) because of the length of time it took life expectancy to rise from its initial low to its resultant high. However, the results do not conform to this expectation, as the estimates are generally more similar between the rapid tempo scenario and the gradual tempo scenario than they are between other combinations. Such a finding suggests that the tempo of mortality increase is not the principle mechanism generating differences in kinship structure.

Instead, it seems that the length of time that a society experiences both high fertility and low mortality - its exposure to population growth - is the driver of differences between kinship structures. This is a more complex interpretation, relating to the interaction of the timing of onset and the tempo of increase in life-expectancy. Continuing the comparison within fertility scenarios, mortality scenario one reaches its maximum life expectancy most rapidly and has the highest life expectancy during all of the transition years. Mortality scenario two, though it reaches its maximum life expectancy at the same time as mortality scenario three, begins its onset earlier than mortality scenario three, thereby exposing the population living through it to a longer period of low mortality probabilities. In other words, within fertility scenarios, those mortality scenarios wherein life-expectancy and fertility are simultaneously high for longer periods of time generate larger numbers of people alive, close kin and indirect kin and greater levels of village connectivity. That mortality scenario two and three are generally more similar in terms of life-expectancy at any point during the period between approximately 1955 and 1980 - a good portion of the mortality transition - than they are to mortality scenario one drives home this point. This is the only consistent finding with regard to mortality, and it explains the majority of the differences between mortality scenarios.

Thus far I have looked at the influence of the gap between the three demographic transitions in terms of their timing of onset, their tempo of decline, and the length of time that mortality and fertility are simultaneously high *in terms of mortality*, that is, holding fertility scenario constant. However, it is equally important to compare results *in terms of fertility*. In so doing, one of the most consistent findings to emerge from this paper

becomes apparent: variation in fertility scenarios generate substantially larger kinship network differentiation than variation in mortality scenarios.

Evaluating the relative timing of onset of fertility transitions within mortality scenarios, figure 1 shows that the fertility decline began early in fertility scenario one and later in fertility scenarios two and three. Thus, were timing of onset of fertility decline driving differences in kinship networks, we would expect fertility scenarios two and three to be more similar to each other than either is to fertility scenario one. Such a result is found: the early onset scenario (one) generates substantially smaller numbers of close kin than either of the later onset scenarios (two and three) in almost all fertility scenarios, and the same general pattern holds for indirect kin. These differences are large: comparing fertility scenarios one and two, the average individual living in a new village had about 0.8 more close kin and three more indirect kin than the average individual living in a village where the fertility transition began earlier. Village connectivity exhibits the same general trends, but they are more muted. New villages where the fertility transition began later were about an additional 0.15% more connected than villages where it began earlier. Interestingly, differences between numbers of living population members also exhibit the same pattern, though, as with connectivity, none of the differences are substantial. Unlike from the mortality perspective, it appears that the gap between the timing of onset of the mortality transition and the timing of onset of fertility transition is a substantial influence on close and indirect kin. However, as was seen when looking from the mortality perspective, such a gap does not appear to generate substantial differences between village connectivity and population size.

Were the tempo of fertility decline the most significant force influencing kinship structure, figure 1 suggests that fertility scenarios one and two will be more similar to each other than they are to fertility scenario three, holding mortality scenario constant. For close kin this does not seem to be the case. Indeed there is a larger difference between the two gradual tempo scenarios (one and two), with fertility scenario two consistently generating the largest numbers of kin and fertility scenario one generating the smallest such numbers, than there is between scenarios one and three. Examining indirect kin makes this point even more clear, as, in all cases, fertility scenario one generates substantially smaller numbers of indirect kin than fertility scenario two, but only distinguishably smaller numbers of such kin than fertility scenario three. The general point is further highlighted in an exploration of connectivity and population sizes - distinguishable differences exist in all of the contrasts between fertility scenarios one and two, but in only one of the six potential contrasts between fertility scenarios one and three. Though substantial differences were found between scenarios that began from a new village, the evidence is less strong when considering those which began from an established village. For close kin, there are substantial differences between fertility scenarios one and two and noticeable differences between fertility scenarios one and three, but the general trend of diminishing differences for indirect kin and for connectivity and population size persists. Indeed, there is not a single distinguishable difference between the fertility scenarios in terms of connectivity or population size when they begin from an established village.

As it did between the mortality scenarios, considering exposure to population growth draws attention to the main dimension of stratification between the fertility



scenarios. When the population experiences a gradual decline in fertility with a late onset (as in fertility scenario two), the simulated village is exposed to the longest period of high fertility. In contrast, when the decline in fertility begins early and proceeds more rapidly (as in fertility scenario one), there is a short period of population growth. Thus, the consistent finding that, holding mortality scenarios constant, fertility scenario one yields kinship structures least similar to fertility scenario two confirms this finding. And, of course, being exposed to longer periods of high fertility generates larger population sizes as the results show. That such contrasts are more apparent considering first degree kin and siblings than they are in the estimates of indirect kin or village connectivity, and that they are more prevalent in the new village scenarios than the old village scenarios is again seen.

Finally, the demographic scenarios considered in this paper also acknowledged the influence of initial conditions, a potentially key feature of local variation in demographic processes. I modeled the same combinations of fertility and mortality scenarios from an initial village which displayed the kinship networks and population structure of a newly founded place and from an initial village which had been simulated for 150 years prior to the start of the model, thus reflecting the kinship networks and population structure of a place which had been established for a long time and experienced demographic conditions thought to characterize historic Northeast Thailand. In evaluating the influence of these initial conditions, I pay attention to the differences between simulations beginning from the new and established village within the same fertility and mortality combinations.

Comparing results obtained from the same sets of fertility and mortality scenarios when they originated from new or established villages brings to light another consistent finding. In no instance, for any of the features of kinship networks considered, are the new village scenarios substantially different from the old village scenarios. In other words, there is overlap in the results owing to random processes generating the data, suggesting that such differences exert a greater influence over the results than the initial conditions from which the model began. However, a secondary trend comes to light. In many cases, the interquartile range of estimates obtained in the established village scenarios encompass the interquartile range of estimates obtained from the new village scenarios. I attribute this finding to the longer periods during which the established villages were subjected to both high fertility and high mortality. Such conditions yield highly variable estimates, as the population may crash or grow rapidly prior to the initiation of the demographic transition. Another interpretation is simply that the longer history allows for random fluctuations to make a larger difference.

As a whole, results indicate that even slightly differing demographic transition experiences matter for kinship network structures, but that this is more true for some features of kinship networks than others. That extremely variable estimates are obtained when populations are exposed to long periods of high fertility and mortality is another interesting finding. Considering these findings in broader context, they suggest that societies' divergent experiences with the demographic transition can be expected to generate different kinship networks. Furthermore, it can be expected that places which have not yet or only recently begun the demographic transition will have substantial heterogeneity in kinship network structures in the present and near future, owing to long

periods of exposure to uncertain demographic conditions. In this vein, fertility scenario two yields the largest interquartile ranges of all fertility scenarios, while fertility scenario one yields the smallest. Indeed, that the mortality scenarios are not as consistently delineated into which yields the largest and smallest interquartile ranges of estimates is consistent with the conclusion that variation in fertility decline matters more for kinship structure than variation in mortality decline.

### **Validating the Model**

Simulation methods are met with skepticism if they cannot generate, given proper parameter specifications, outcomes that are theoretically expected and encompass the range of those observed in a real world setting. Theoretically, given my scenarios, demographers would expect that the quickest move to low mortality (as in mortality scenario one) and the slowest move to low fertility (as in fertility scenario two) would generate the largest populations. My results certainly conform to this expectation.

Empirically evaluating the model's validity is trickier, but to do so I use the diversity of kinship relations in the 51 villages of Nang Rong (Rindfuss *et al.* 2004; Entwisle *et al.* 2009). I assess the extent to which distributions of kinship counts and connectivity generated by simulation fall within the distributions represented by the 51 Nang Rong villages through exploratory analysis and by comparing the quartiles of the kin count distributions. Table 3 presents summary statistics of the distributions of counts of close and indirect kin and kinship connectivity across the 51 villages of the Nang Rong dataset as measured in year 2000, corresponding approximately to the simulation results from year 100. As was presented in table 2 for the simulated villages, the results in table

3 are restricted to living individuals who were ever residents of Nang Rong villages (and thus include both in- and out-migrants).

As can be seen, the models generate counts of close and indirect kin and connectivity that are plausible representations of the diversity found in Nang Rong. Though the model-generated kinship structures do not perfectly overlap with the distribution of kinship structures found in Nang Rong as the empirical case tends to indicate greater levels of indirect kin and connectivity, it is important to note that such simple and stylized models can generate kinship structures that are within the range of those found in the empirical case. Such plausibility of estimates speaks to the importance of considering local variation in experience with the demographic transition. It is important to notice that the interquartile ranges found in table 3, for all variables, are much greater than those found within any fertility-mortality-initial conditions scenario combination in the simulated data. One potential interpretation of this is that the Nang Rong villages had much more variability in their experiences with migration, which, as per the design of the analyses in this paper, was held constant in all scenarios. Such variability has been suggested by Entwisle and colleagues (Entwisle 2007; Entwisle et al. 2007), but exploring its influence is outside of the scope of this paper, especially given that such networks have been argued to influence migration (Massey et al. 1993). A second reason is that the villages experienced heterogeneity in fertility and mortality transitions. A third reason relates to the differential timing of settlement of the Nang Rong villages; as stated above, some were settled centuries ago while others were settled as recently as the last 75 years.

Notably, the range of key features of kinship networks found in Nang Rong overlap a number of the demographic transition scenarios used as data-generating models. That the breadth of kinship structures found within one district in rural Thailand could be generated by such a variety of experiences with the demographic transition further underscores a broader point of this paper, that variation in demographic history across both small and large areas of the globe will have important implications for the present structure of those societies, at least in terms of social network differentiation. To the extent that kinship network differentiation has meaningful impacts on social processes (as suggested by the numerous articles reviewed above), demographic history may contribute importantly to explaining variation in all sorts of social processes.

### **Sensitivities**

Having established that the features of kinship networks obtained through simulation are within the range of possibility of those seen in a real world example, I now consider my results' sensitivity to other modeling decisions which have not hitherto been the focus of this paper. I first consider the lag between the timing of the demographic transition and the evidence of differentiation in kinship networks that such transitions create. I then ask whether heritability of fertility preferences drives the results by turning off the parameter reflecting such heritability. Finally, I assess how the model's results change when migration not due to exogamous marriage is disallowed. Though these three considerations do not cover the entire range of possible alternative models and thus cannot offer exhaustive tests of its validity, they do cover a range of alternatives that

substantially differ from those presented above and that are of theoretical and substantive interest to sociologists and demographers.

To generalize the results of this model from rural Thailand to other places in the world is beyond the scope of this paper. However, some traction on the issue can be gained by exploring the relative timing of the demographic transition and measurement of kinship network differentiation. Figures 2, 3, and 4 present the median results for all 18 scenarios for close kin, indirect kin, and village connectivity, respectively, on an annual basis for years 40-100. To make evident the relative contributions of fertility and mortality, those figures are organized as follows. Lines depicting results from fertility scenario one are black, lines depicting results from fertility scenario two are blue, and lines depicting results from fertility scenario three are red. The mortality scenarios are denoted by markers on the lines: mortality scenario one has no markers, mortality scenario two has circular markers, and mortality scenario three has triangular markers. The results are stratified into those scenarios emanating from a new village and those scenarios emanating from an established village.

A quick glance demonstrates that color (fertility) organizes the results better than marker type (mortality) for counts of kin, while the opposite is true for village connectivity. This conforms to the general discussion above concerning the relative importance of fertility and mortality. To get a sense of the influence of the lag between changes in demographic patterns and measurement of the results, it is important to look at the trajectory of the results over time. Looking at counts of close and indirect kin, it appears that the differentiation in kinship networks discussed above is not fully realized until approximately year 90. Prior to year 75 the mortality transition seems to exhibit a

larger influence, as would be expected owing to its earlier onset. Connectivity, on the other hand, reaches its maximum level of differentiation around year 80, when the mortality transition has completed in all scenarios. Interestingly, differentiation between scenarios in terms of connectivity appears to be decreasing, while it remains relatively persistent for counts of kin. It is important to note that during the demographic transition, when fertility and mortality are changing, there is still a great deal of differentiation between demographic scenarios; noticeable gaps between models generally emerge between years 50 and 65, which is compelling as vital rates were the same in all scenarios as recently as 10-25 years prior. The conclusion to be drawn from this is that the demographic transition impacts kinship networks relatively rapidly.

Another important question related to the lag between the demographic transition and the differentiation of kinship networks is whether the present differentiation of kinship networks might owe to the relatively short period since the demographic transition took place. Recall that my scenarios are set in Thailand which began its demographic transition about 50 years after several parts of the developed world. To explore this issue, I project the model from the year 2000, when the demographic transition has ended and all parameters are equal in all scenarios, into the future using transformations of the United Nations' median variant life-expectancy and age-specific fertility rate projections for Thailand (United Nations 2008a; United Nations 2008b). The goal of this exercise is not to speculate about how future demographic influences will impact social network forms; rather, it is a strict test of whether what we currently observe in terms of kinship network differentiation can be expected to persist over a long

time. I evaluate this influence on the models by examining differences in features of kinship networks in year 150 compared to year 100.

Table 4 presents the quartiles of the simulation results in year 150 as table 2 did in year 100. Two interesting features of this table are immediately evident. First, even after 50 additional years during which there is no differentiation in terms of fertility and mortality levels, or indeed in any part of the model, significant differences between the scenarios persist. Keeping in mind that all scenarios were subjected to the exact same parameters - probabilities of giving birth and dying drawn from the United Nations' median variant projections for Thailand - from years 100 to 150, this is a very strict test. Second, there are great differences between features of kinship networks in years 100 and 150; indeed, the average person has about 3 fewer close kin in year 150 than the average person did in year 100. The differences are so marked that the average person had about the same number of close kin in year 100 as the average person had in indirect kin in year 150.

Though the medians of all network features have changed dramatically over the 50 simulated years between 2000 and 2050, different scenario combinations - principally those stemming from differences in fertility scenarios - produce results outside of the realm expected at random. Indeed, in terms of differences between the models, the same general trends observed in year 2000 are present in year 2050, even under such a strict test. This suggests that differences in kinship network structures owing to the location-specific experience with the demographic transition are likely to persist over a long period of time and to be found in post-transitional societies which completed their demographic transitions long ago. Further, comparing whether timing of transition onset,



tempo of transition or duration of exposure to population growth best explains differences between models, it appears that, as was found in year 2000, exposure to growth is the most important element. Again, differences between scenarios suggest that fertility transitions conditions such kinship network differentiation more fully than mortality transitions.

Examining the model's sensitivity to the parameter reflecting heritability of fertility preferences demonstrates its robustness to this analytic choice. I compare the extent to which key features of kinship networks in the baseline scenario (fertility three mortality three beginning from a new village) differ when individuals inherit no fertility preferences from their parents. These considerations are presented in table 5 for years 50, 100 and 150, with results for the baseline scenario included for ease of comparison. As would be expected given that high fertility parents give birth to greater numbers of children with high fertility preferences, the model without preference exhibits slightly smaller numbers on all kinship network features of interest. However, in no instance is the scenario without fertility preferences substantially different than the scenario with them, suggesting that the model is not terribly sensitive - at least over the time frame considered and with respect to the features of kinship networks analyzed - to introduced correlations between mothers and daughters in terms of numbers of children.

Finally, I explore the model's sensitivity to elimination of migration not due to exogamous marriage. The results show differential sensitivities of features of kinship networks to assumptions about migration. Though the model lacking migration consistently exhibits substantially smaller populations and much greater levels of connectivity than the model including it, the same is generally not true for close or

indirect kin. Though numbers of close and indirect kin are distinguishable between the model excluding migration and the one including it, that greater differences were not found is surprising given the importance attributed to migration in the literature (e.g., Entwisle 2007). However, the type of migration considered in this paper – migration for purposes other than marriage – is a very particular type of migration, and my results may not be directly comparable to those theoretically posited. Comparing this finding between years 100 and 150, it seems that migration matters more the longer in the past the demographic transition occurred.

### **Discussion and Conclusion**

In *The Metropolis and Mental Life*, Georg Simmel (1903[1971]) posited that individuals who live in cities were fundamentally different than those who live in rural areas. This paper builds on his ideas by showing that demographic antecedents of urbanization – the surplus of births over deaths stemming from the demographic transition – fundamentally alter the social embeddedness of individuals in kinship networks. Of course, demographic history is only one of the many factors that changed social organization so dramatically during the early industrial era, and only one factor contributing to urbanization. But, by considering how the demographic transition altered social relations in rural areas which send migrants, rather than the urban areas which tend to receive them, this paper has shown that social organization has changed more broadly; a result which calls into question the single minded focus on the social lives of individuals in urban areas.

This work also builds on the classic sociological concepts of organic and mechanical solidarity (Durkheim 1893[1933]). Whereas Durkheim posited that social organization changed fundamentally from a system wherein individuals were homogenous and extensively linked by kinship – mechanical solidarity – to a system where individuals were increasingly differentiated and linked by other forms of social contact – organic solidarity. He held that these changes owed to the specialization of employment and economic development, an increased division of labor. Considering the results of this paper in that light, the results in this paper suggest that Durkheim’s understanding of the shift from mechanical to organic solidarity may be confounded with demographic changes, an argument presupposed by Simmel (1903[1971]). This is not to say that broad scale economic development did not contribute to changes in social organization, nor that they were somehow less important than demographic factors, it is only to note that they likely occurred simultaneously. Indeed, as the literature has not untangled whether economic development leads to demographic changes or whether the relationship is in the other direction, consideration of this topic is purely speculative.

Another contribution of this paper is its focus on the broader networks of relations amongst kin, rather than on the more measurable variable, domestic co-residence. Prior analyses of kinship networks and demography in the simulation tradition have primarily focused on prediction and attempting to resolve debates over the numbers of kin individuals have (cf. Ruggles 1993; Wachter, Blackwell and Hammel 1997). I have taken a different tack in this paper, using the simulation method to ask whether differences in experience with the demographic transition can generate different kinship network structures. The results obtained are complex, but they all point to one conclusion:

demographic history matters for current social structures. Of course, kinship networks are but one type of network, and, though it is likely that demographic changes impacted other types of social interactions, a rigorous exploration of that topic is well outside the scope of this paper.

I considered the independent role of fertility and mortality transitions in determining these processes, finding evidence that fertility transitions matter more for the aspects of social structure related to kinship than mortality transitions - at least in the range associated with demographic transitions. I also considered the staying power of social network differentiation that was determined by demographic processes, finding that such features can be expected to persist over a long time. Further, I found little evidence in the simulations that social structures related to counts of available kin were likely to be different when the migration regime differs dramatically; however, as hypothesized by Entwisle (2007), community connectivity appears to be influenced by migration. Finally, I found that initial conditions matter less than experience with the demographic transition in determining kinship structures, though a secondary trend suggests that longer periods of demographic uncertainty leads to greater variability in terms of kinship network structures.

The results in this paper cannot definitively answer how much change in kinship networks can be attributed to the demographic transition, yet they overwhelmingly point to the idea that the transition, no matter how it proceeded, has had substantial impacts on kinship networks. It appears that fertility matters more than mortality and that exposure to longer periods of population growth matters more than either the timing of onset of the tempo of fertility and mortality decline. Many of these findings conform to classical

theories of demography, and they suggest that demographic considerations should be taken into account in explanations of social structural differentiation, an argument long espoused in the literature on demography and social networks as reviewed above.

The focus on one particular case - the historical evolution of Nang Rong villages - is both a strength and a limitation of this work. On the one hand, focusing the model so specifically allows me to isolate the influences of slightly different experiences with the demographic transition. But, on the other hand, it leaves open the question of whether such results would be found elsewhere. For instance, one might ask whether such variability is likely to be present in societies long past the demographic transition, such as by comparing the United States and France. However, to this end, the results concerning persistent kinship network differentiation long into the future (nearly 100 years after the onset of the demographic transition) suggest that such findings would be obtained.

Recalling table 1, which showed the median dates of fertility decline and the tempo of that decline also gives some context to the results found in this paper. The fertility transition took between 11 and 26 years to decline from 10% off of the baseline to 40% in broad regions of the world, and the results presented in this paper considered a range of about 15-25 years. In addition, the results presented in this paper considered fertility declines that happened 100 years ago, about the length of time that has passed since the fertility decline in Europe and "English speaking 'Europe Overseas'", as well as fertility declines which began only recently (as seen in sub-Saharan Africa). This is not to say that the trends in Thailand are similar to those experienced elsewhere in the world, only that the range of variability considered in this paper, though grounded in the

experience of Thailand, is extensive and covers much of the variability seen around the globe.

Figures 2-4 and table 4 suggested that, while we might still expect differences in kinship structures owing to the demographic transition for such regions - differences in counts of kin for Europe and differences in connectivity for sub-Saharan Africa - the largest differences should be found in those countries where the fertility transition occurred in the 1950s to 1970s, including most of Asia, Latin America and the Caribbean. These differences would be due to differences in the timing of onset, tempo of change, and exposure to population growth between countries in these regions. Generally, the differentiation in kinship networks owing to variation in demographic experiences is a mid-range phenomenon that increases shortly after the demographic transition and, though it persists for a long period of time, begins decreasing after about 50 years after the onset of the demographic transition.

Another weakness related to focusing on the case of Nang Rong is that rural Thailand is primarily a sending population in terms of migrants. There are many examples of sending populations in the world, as places which have recently experienced the demographic transition have also typically experienced a concomitant increase in population size, which leads the “excess” population to move out. What the implications of such changes might be for a receiving population are beyond the scope of this paper. However, some intuition can be gained. The sensitivity check that explored removing the migration parameters showed that community connectivity is significantly higher when there is no migration in or out. This implies that for receiving areas, connectivity will also be lower as the amount of migration is larger. Of course, this depends on the extent to

which those moving to the receiving area are kin linked, and the extent to which ethnic (or migration determined) homogamy prevails.

Though this paper was not attempting to show that the findings of increasing social network isolation are due to demography, it has made suggestions in that regard. Indeed, one of the largest differences between the simulation results for 2000 and 2050 are the dramatically smaller numbers of available kin and lower levels of community connectivity. Looking to table 4, the collapse in kinship networks occurred after year 100, or about 30 and 50 years after the onset of the demographic transition. Such a result contextualizes the findings of McPherson et al. (2006) and others, and, given the literature's focus on kin-based social support for elderly individuals (e.g., de Souza and Grundy 2007; Berkman *et al.* 2000), suggests that the long-term viability of such support is indeed worth worrying about.

Considering the vast array of demographic transitions throughout the world, the findings in this paper suggest that available kinship networks will differ by country and, potentially, by sub-national region or even more local contexts owing to differential experiences with the demographic transition. To that end, the results presented in this paper call into question the viability of considering aggregated measures of kinship structures, a result echoed in Entwisle et al. (2007) and espoused in the community effects literature (cf. Entwisle 2007). Attention to local variability is an important avenue for future research; this paper contributes to the literature by suggesting that we look to historical demography to explain some of that variation.

Finally, the most important contribution of this paper is its demonstration that demography matters. Looking outside of household co-residence is important to

understand the breadth of social structural changes that have occurred as the demographic transition has shaped societies. Considering that demographic history reverberates through the life-course of a society, it is important to consider the ways in which present demographic policies and events may influence future social structures and, in turn, individual experiences in terms of political participation, health, economic success and other outcomes of interest to sociologists. For instance, what will be the impact of the dramatic reversal in life-expectancies owing to the HIV/AIDS epidemic in sub-Saharan Africa? What are the implications of the long running levels of below replacement fertility seen in Eastern Europe? For kinship structures, this paper has offered one step in the direction of considering such implications, but important work must be done translating these kinship structures into outcomes of interest to sociologists. The broad point that demographic transitions matter for social structures suggests that attention to these demographic trends is more than merited.

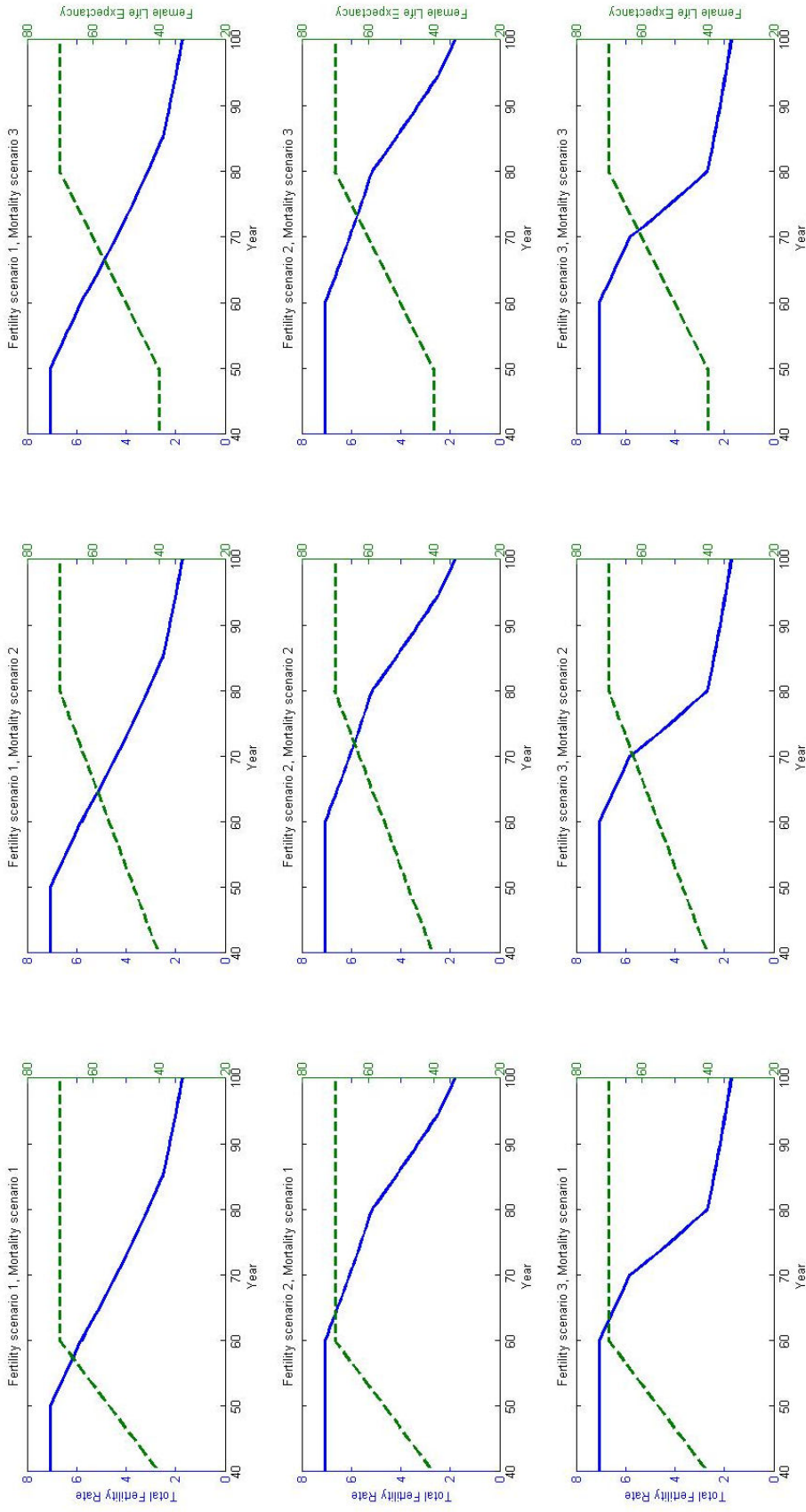


**Table 1. Patterns of fertility declines in regions of the world.**

<u>Region</u>	<u>Median Date of Onset of Decline (10% Decline)</u>	<u>Average period from 10 to 40% decline (Years)</u>
English speaking "Europe Overseas"	1878	20
Europe	1910	26
Spanish speaking "Europe Overseas"	NA	22.5
Early Industrial Asia	1930-35	15
Ex-USSR Asia	1950-70	15
Caribbean	1965-70	12
Other Oceanic	1970-75	11
South America	1970-75	12
Central America	1975-80	12.5
Mainstream Asia	1975-80	12
North Africa	1980	15
Middle East	1980-85	15
Sub-Saharan Africa	>1990-95	20

**Notes: Reproduced from Caldwell and Caldwell (2006: 226); the regional groupings are argued within that text. Also see table A1 in the appendix. NA denotes not available.**

**Figure 1. Combinations of fertility and mortality scenarios used in the analysis.**



**Table 2. Medians and interquartile ranges of features of kinship networks in year 100.**

			<u>New Village</u>			<u>Established Village</u>		
			<u>Mort. 1</u>	<u>Mort. 2</u>	<u>Mort. 3</u>	<u>Mort. 1</u>	<u>Mort. 2</u>	<u>Mort. 3</u>
<b>Population Alive</b>	<b>Fert. 1</b>	<b>25th Pct.</b>	684	618	587	295	285	239
		<b>Median</b>	800	722	676	618	543	493
		<b>75th Pct.</b>	912	828	771	1,105	966	884
	<b>Fert. 2</b>	<b>25th Pct.</b>	887	799	733	416	367	321
		<b>Median</b>	1,031	931	863	813	710	646
		<b>75th Pct.</b>	1,184	1,070	984	1,395	1,242	1,161
	<b>Fert. 3</b>	<b>25th Pct.</b>	762	690	635	360	325	288
		<b>Median</b>	882	794	730	715	620	589
		<b>75th Pct.</b>	1,007	916	844	1,192	1,080	989
<b>Close Kin</b>	<b>Fert. 1</b>	<b>25th Pct.</b>	4.30	4.13	4.02	4.16	3.98	3.84
		<b>Median</b>	4.44	4.27	4.16	4.43	4.24	4.09
		<b>75th Pct.</b>	4.58	4.40	4.30	4.63	4.43	4.30
	<b>Fert. 2</b>	<b>25th Pct.</b>	5.10	4.91	4.82	4.99	4.77	4.65
		<b>Median</b>	5.24	5.06	4.97	5.24	5.04	4.89
		<b>75th Pct.</b>	5.38	5.21	5.10	5.43	5.25	5.12
	<b>Fert. 3</b>	<b>25th Pct.</b>	4.61	4.41	4.29	4.49	4.25	4.17
		<b>Median</b>	4.75	4.57	4.45	4.72	4.52	4.42
		<b>75th Pct.</b>	4.91	4.71	4.61	4.93	4.72	4.61
<b>Indirect Kin</b>	<b>Fert. 1</b>	<b>25th Pct.</b>	10.05	9.23	8.57	8.26	7.53	7.00
		<b>Median</b>	11.14	10.21	9.61	10.82	9.59	8.83
		<b>75th Pct.</b>	12.20	11.11	10.45	12.75	11.33	10.63
	<b>Fert. 2</b>	<b>25th Pct.</b>	13.20	11.91	11.25	11.26	10.14	9.29
		<b>Median</b>	14.37	13.08	12.36	13.78	12.47	11.52
		<b>75th Pct.</b>	15.49	14.21	13.54	16.36	14.66	13.82
	<b>Fert. 3</b>	<b>25th Pct.</b>	11.52	10.49	9.77	9.87	8.75	8.29
		<b>Median</b>	12.69	11.66	10.86	12.03	10.95	10.29
		<b>75th Pct.</b>	13.91	12.70	11.87	14.32	13.07	12.21
<b>Connectivity</b>	<b>Fert. 1</b>	<b>25th Pct.</b>	1.23	1.12	1.03	0.78	0.70	0.65
		<b>Median</b>	1.34	1.21	1.13	1.05	0.94	0.84
		<b>75th Pct.</b>	1.45	1.33	1.24	1.45	1.25	1.15
	<b>Fert. 2</b>	<b>25th Pct.</b>	1.38	1.27	1.20	0.94	0.84	0.80
		<b>Median</b>	1.50	1.38	1.31	1.25	1.14	1.06
		<b>75th Pct.</b>	1.64	1.51	1.44	1.77	1.60	1.49
	<b>Fert. 3</b>	<b>25th Pct.</b>	1.33	1.21	1.13	0.88	0.77	0.71
		<b>Median</b>	1.45	1.31	1.24	1.13	1.04	0.95
		<b>75th Pct.</b>	1.57	1.43	1.35	1.56	1.42	1.31

**Note: Connectivity multiplied by 100.**

**Table 3. Summary statistics of kinship counts and connectivity found in Nang Rong.**

	Close Kin	Indirect Kin	Connectivity
Minimum	4.17	8.17	0.84
25th Percentile	4.72	12.77	1.47
Median	4.96	14.06	1.86
75th Percentile	5.38	17.59	2.18
Maximum	6.42	29.38	3.62

**Note: Connectivity multiplied by 100. Nang Rong data from year 2000.**

**Table 4. Medians and interquartile ranges of features of kinship networks in year 150.**

			<u>New Village</u>			<u>Established Village</u>		
			<u>Mort. 1</u>	<u>Mort. 2</u>	<u>Mort. 3</u>	<u>Mort. 1</u>	<u>Mort. 2</u>	<u>Mort. 3</u>
<b>Population Alive</b>	<b>Fert. 1</b>	<b>25th Pct.</b>	430	384	359	181	178	149
		<b>Median</b>	501	448	421	390	340	311
		<b>75th Pct.</b>	582	518	485	701	601	551
	<b>Fert. 2</b>	<b>25th Pct.</b>	632	562	515	290	259	230
		<b>Median</b>	735	657	612	579	510	453
		<b>75th Pct.</b>	851	761	704	992	879	820
	<b>Fert. 3</b>	<b>25th Pct.</b>	483	433	400	233	203	183
		<b>Median</b>	564	506	466	461	389	368
		<b>75th Pct.</b>	648	587	543	762	681	622
<b>Close Kin</b>	<b>Fert. 1</b>	<b>25th Pct.</b>	1.53	1.50	1.48	1.45	1.42	1.40
		<b>Median</b>	1.61	1.59	1.56	1.58	1.56	1.54
		<b>75th Pct.</b>	1.69	1.67	1.63	1.69	1.67	1.65
	<b>Fert. 2</b>	<b>25th Pct.</b>	1.96	1.91	1.90	1.88	1.84	1.81
		<b>Median</b>	2.04	2.01	1.99	2.02	2.00	1.97
		<b>75th Pct.</b>	2.13	2.09	2.08	2.14	2.13	2.10
	<b>Fert. 3</b>	<b>25th Pct.</b>	1.59	1.55	1.53	1.50	1.48	1.44
		<b>Median</b>	1.66	1.63	1.62	1.63	1.60	1.59
		<b>75th Pct.</b>	1.74	1.71	1.70	1.74	1.70	1.69
<b>Indirect Kin</b>	<b>Fert. 1</b>	<b>25th Pct.</b>	2.65	2.46	2.29	2.13	2.00	1.86
		<b>Median</b>	2.97	2.76	2.59	2.79	2.57	2.43
		<b>75th Pct.</b>	3.31	3.07	2.92	3.37	3.13	2.97
	<b>Fert. 2</b>	<b>25th Pct.</b>	4.41	4.01	3.84	3.69	3.36	3.19
		<b>Median</b>	4.84	4.47	4.24	4.62	4.25	3.99
		<b>75th Pct.</b>	5.24	4.87	4.69	5.51	5.04	4.78
	<b>Fert. 3</b>	<b>25th Pct.</b>	3.07	2.83	2.70	2.53	2.32	2.17
		<b>Median</b>	3.46	3.16	3.06	3.26	2.94	2.84
		<b>75th Pct.</b>	3.79	3.50	3.36	3.83	3.55	3.38
<b>Connectivity</b>	<b>Fert. 1</b>	<b>25th Pct.</b>	0.16	0.15	0.14	0.11	0.10	0.09
		<b>Median</b>	0.18	0.17	0.16	0.14	0.13	0.12
		<b>75th Pct.</b>	0.20	0.19	0.18	0.20	0.18	0.17
	<b>Fert. 2</b>	<b>25th Pct.</b>	0.24	0.23	0.22	0.17	0.16	0.16
		<b>Median</b>	0.27	0.25	0.24	0.23	0.22	0.21
		<b>75th Pct.</b>	0.30	0.28	0.27	0.33	0.31	0.29
	<b>Fert. 3</b>	<b>25th Pct.</b>	0.18	0.17	0.16	0.12	0.11	0.11
		<b>Median</b>	0.20	0.18	0.18	0.16	0.15	0.14
		<b>75th Pct.</b>	0.22	0.21	0.20	0.22	0.21	0.19

**Note: Connectivity multiplied by 100.**

Table 5. Sensitivity of results to models without migration outside of marriage and without fertility preferences in years 50, 100 and 150 of the simulation.

Kinship feature	Statistic	Year 50			Year 100			Year 150		
		Base	No Mig	No Pref	Base	No Mig	No Pref	Base	No Mig	No Pref
Population Alive	25th Pct.	253	201	254	635	399	632	400	191	394
	Median	284	223	286	730	466	730	466	228	460
	75th Pct.	318	248	316	844	537	832	543	266	532
Close Kin	25th Pct.	4.19	4.75	4.19	4.29	4.57	4.26	1.53	1.77	1.51
	Median	4.44	5.02	4.42	4.45	4.76	4.41	1.62	1.89	1.59
	75th Pct.	4.69	5.28	4.65	4.61	4.95	4.54	1.70	2.00	1.67
Indirect Kin	25th Pct.	4.48	6.05	4.50	9.77	11.06	9.66	2.70	3.34	2.58
	Median	5.26	7.08	5.25	10.86	12.31	10.63	3.06	3.84	2.89
	75th Pct.	6.12	8.22	6.20	11.87	13.67	11.70	3.36	4.30	3.20
Connectivity	25th Pct.	1.37	1.99	1.35	1.13	1.65	1.11	0.16	0.23	0.16
	Median	1.53	2.25	1.54	1.24	1.79	1.22	0.18	0.26	0.17
	75th Pct.	1.73	2.53	1.74	1.35	1.97	1.33	0.20	0.29	0.19

Note: Connectivity multiplied by 100. Base stands for the baseline fertility three, mortality three scenario combination beginning from a new village. Mig stands for model with no migration except for the purpose of exogamous marriage. Pref stands for model with no fertility preferences.

Figure 2. Trends in close kin over time by fertility and mortality scenario and initial village.

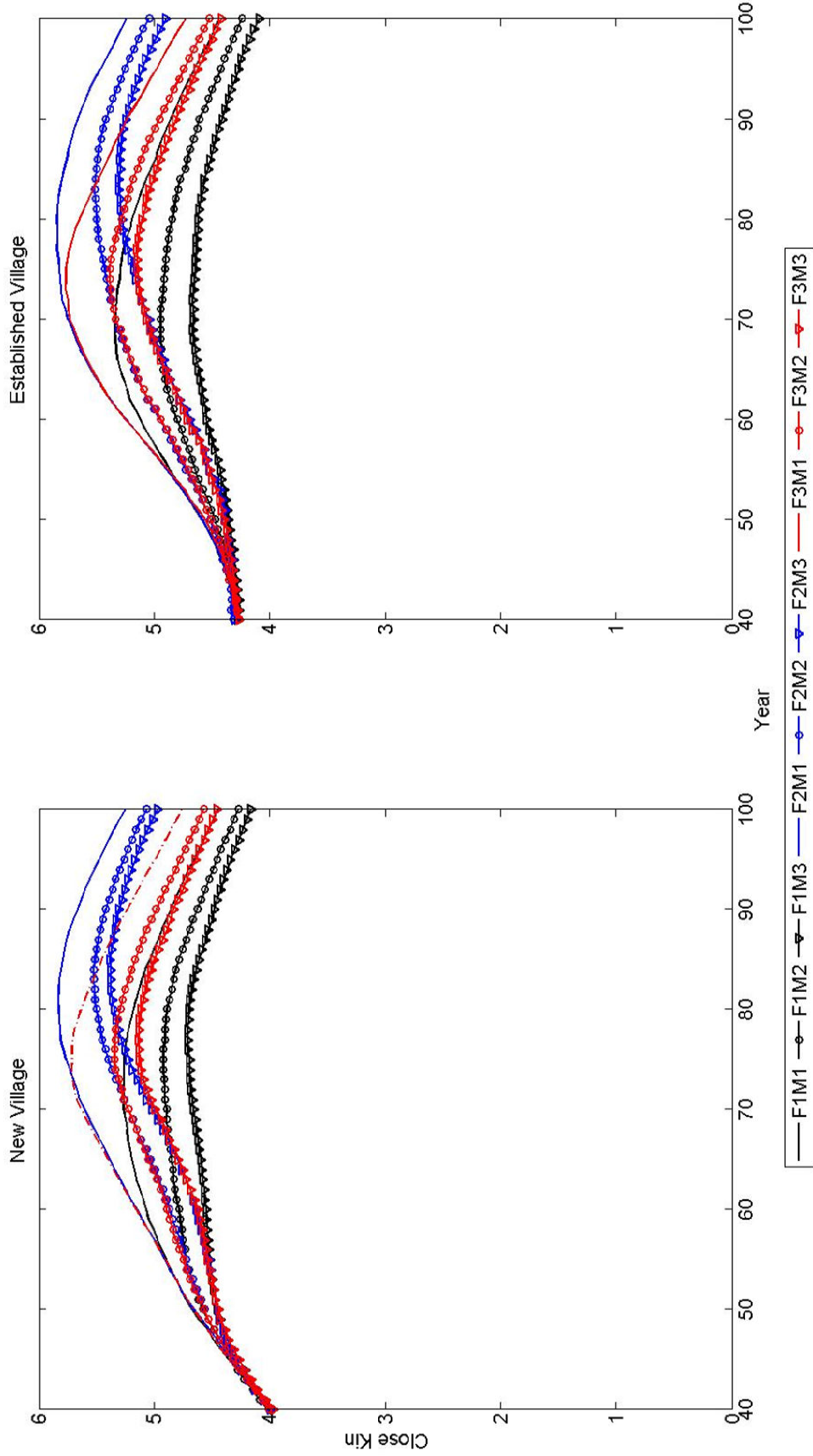


Figure 3. Trends in indirect kin over time by fertility and mortality scenario and initial village.

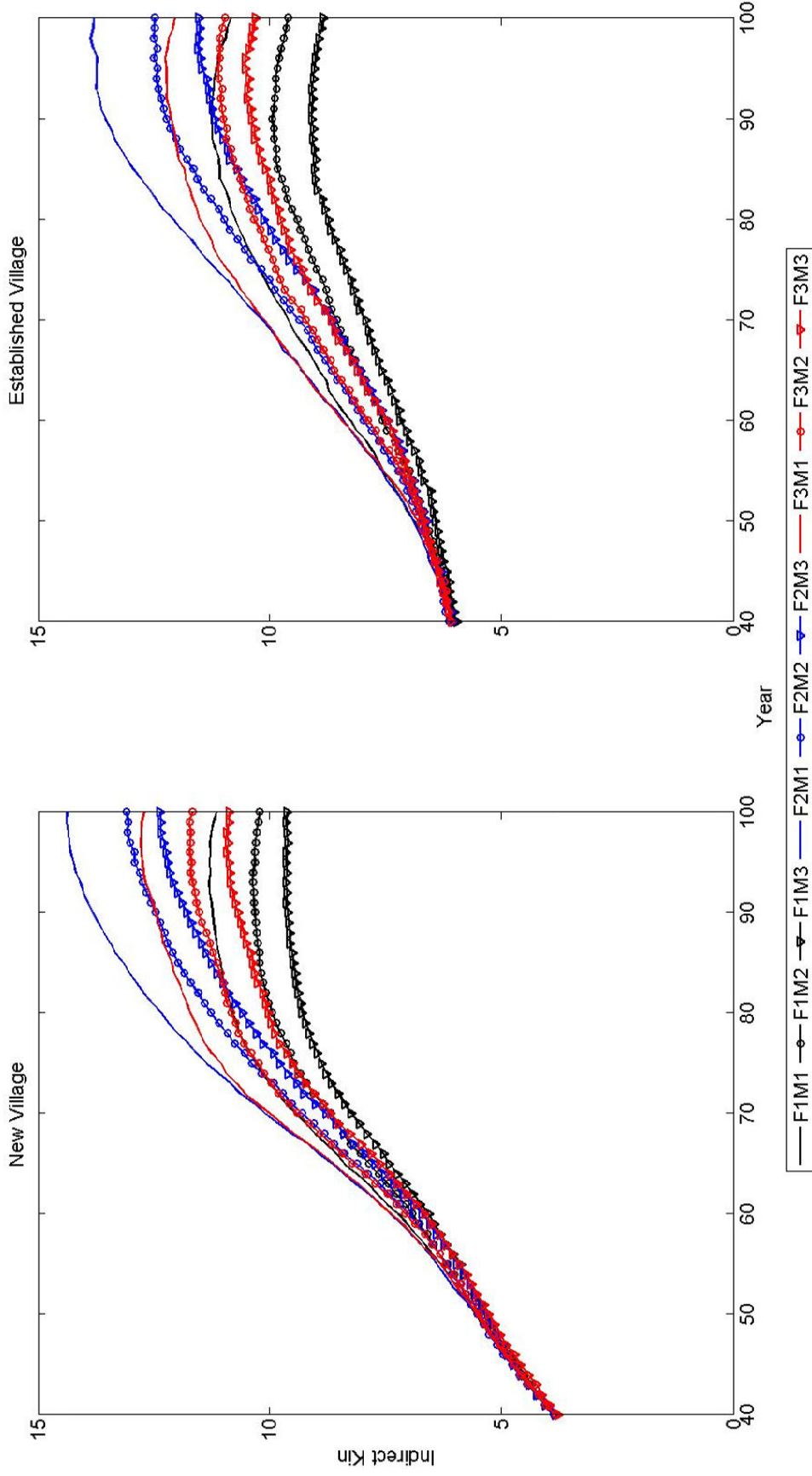
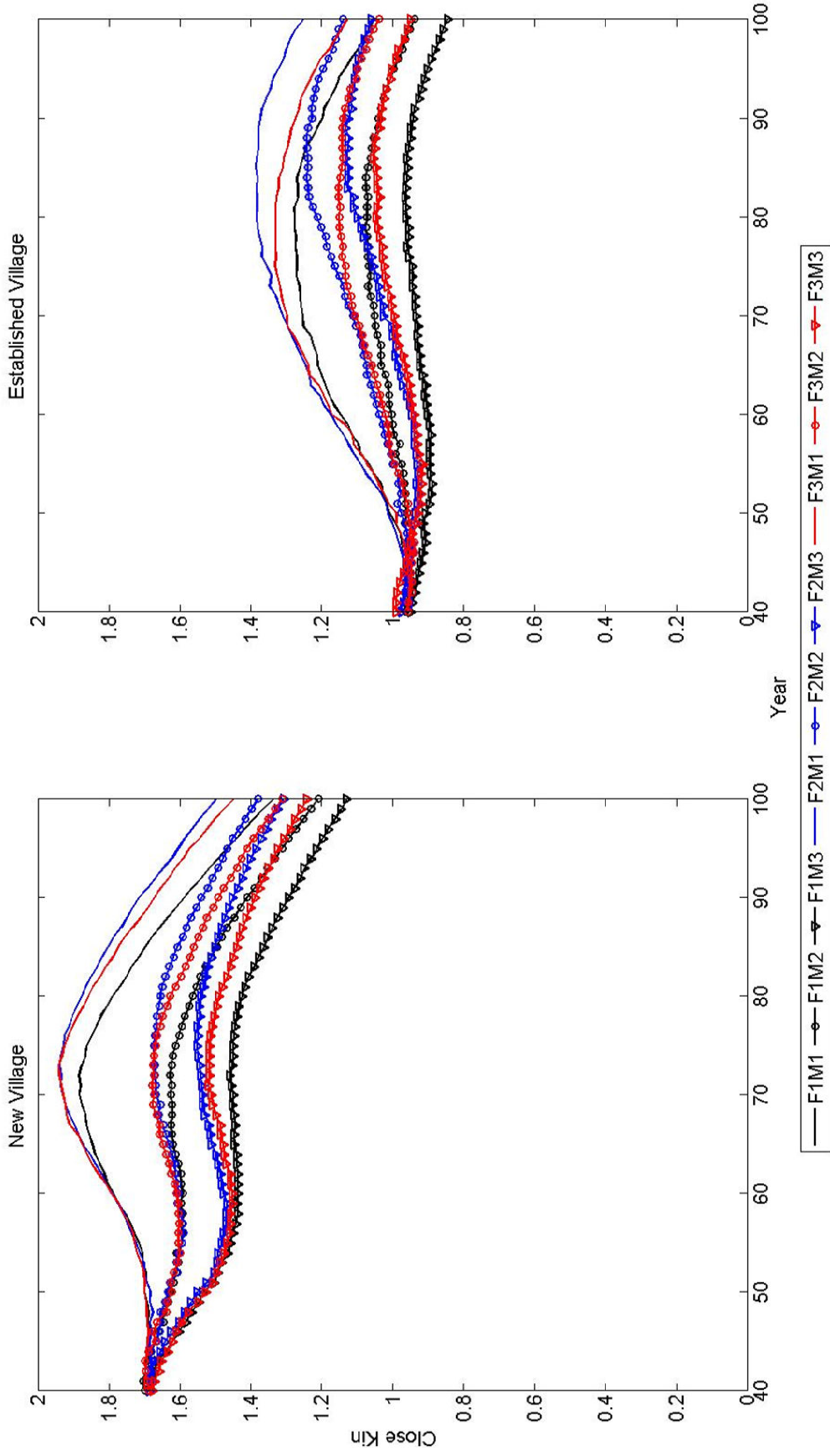




Figure 4. Trends in connectivity over time by fertility and mortality scenario beginning from a new village.



Note: Results multiplied by 100.

**Appendix A: Supplementary tables and figures**

**Table A1. Fertility Transitions in Select Countries.**

<u>Region/ country</u>	<u>Total fertility</u> <u>(If)</u>	<u>25% (If)</u>	<u>40%</u> <u>(If)</u>	<u>Years 10% to</u> <u>40%</u>
English speaking "Europe Overseas"				
Australia	1881	1891	1901	20
New Zealand	1881	1886	1891	10
United States	<1880	1891	1901	>31
Europe				
France	1800	1836	1894	94
Iceland	1870	1920	1926	56
Belgium	1890	1910	1920	30
England and Wales	1891	1901	1921	30
Scotland	1891	1911	1931	40
Ireland	1891	1936	1985	94
Netherlands	1899	1920	1930	31
Germany	1900	1910	1933	33
Finland	1910	1920	1930	20
Spain	1930	1930	1940	10
Sweden	1910	1915	1925	15
Switzerland	1910	1910	1920	10
Denmark	1911	1921	1930	19
Italy	1911	1931	1951	40
Norway	1920	1920	1930	10
Greece	1928	1928	1951	23
Romania	1930	1930	1956	26
Yugoslavia	1931	1931	1960	29
Spanish speaking "Europe Overseas"				
Uruguay	1905	1910	1930	25
Argentina	1910	1910	1930	20
Chile	1965	1970	1975	10
Early Industrial Asia				
Japan	1930	1945	1945	15
Ex-USSR Asia				
Azerbaijan	1965	1975	1980	15
Turkmenistan	1975	1980	1990	15
Uzbekistan	1975	1980	1990	15
Caribbean				
Martinique	1965	1970	1975	10
Trinidad and Tobago	1965	1970	1985	20
Dominican Republic	1970	1975	1980	10
Guadeloupe	1970	1975	1975	5
Jamaica	1970	1975	1985	15

**Table A1 continued.**

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Other Oceanic					
Fiji	1960	1965	1970		10
New Caledonia	1960	1970	1975		15
Mauritius	1965	1970	1975		10
Reunion	1965	1975	1975		10
Guam	1965	1970	1975		10
French Polynesia	1970	1975	1980		10
Samoa	1970	1980	1985		15
South America					
Brazil	1965	1970	1975		10
Venezuela	1965	1970	1980		15
Columbia	1970	1970	1980		10
Ecuador	1970	1980	1985		15
Guyana	1970	1970	1975		5
Peru	1970	1980	1985		15
Surinam	1970	1975	1980		10
Central America					
Costa Rica	1965	1970	1975		10
El Salvador	1970	1980	1990		20
Panama	1970	1975	1980		10
Mexico	1975	1975	1985		10
Mainstream Asia					
Sri Lanka	1960	1970	1980		20
South Korea	1960	1965	1975		15
Singapore	1960	1965	1965		5
Brunei	1965	1975	1980		15
Hong Kong	1965	1970	1970		5
Malaysia	1965	1970	1975		10
Philippines	1965	1975	1985		20
Turkey	1960	1970	1980		20
China	1970	1975	1975		5
North Korea	1970	1975	1975		5
Cambodia	1970	1975	1985		15
Indonesia	1970	1970	1985		15
Thailand	1970	1975	1980		10
Mongolia	1980	1990	1990		10

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**Table A1 continued.**

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North Africa				
Egypt	1970	1975	1990	20
Tunisia	1970	1980	1985	15
Morocco	1975	1980	1990	15
Algeria	1980	1985	1990	10
Bahrain	1970	1975	1985	15
Lebanon	1970	1975	1990	20
Kuwait	1975	1980	1985	10
Sub-Saharan Africa				
South Africa	1970	1980	1990	20

**Note: Reproduced from Caldwell and Caldwell (2006), the regional groupings are argued in that text.**

## **Appendix B: Technical Methods of Simulating Demography and Kinship**

The agent based microsimulation model used in this paper tracks demographic events and kinship structures in villages that attempt to mimic those of Nang Rong, Thailand. As discussed in the text, this model shares the key features of all agent based models: it starts with a heterogeneous pool of individuals who may interact with each other and by doing so influence the actions of others. The model employed in this paper achieves this by starting with a group of individuals of varying ages, genders, kinship connectivity, and propensities towards higher or lower fertility. These individuals then interact by marrying each other (or those outside of the village) and giving birth to further residents, who may, in turn, marry others in the village. At all points, these individuals are subject to the risk of dying or permanently out-migrating from the village, and new individuals may enter the population by in-migrating. The parent-to-child transmission of fertility preferences constitutes a key feature by which agents in the model influence the behavior of other agents, in this case that of their children.

In this technical appendix I describe the operation of the model. I begin by introducing the order of demographic operations, the sequence of demographic events which individuals experience each year and over the course of their lives. After this I justify and define the means by which individual shifts in fertility preferences are transmitted. Finally, I describe the specific calculation of the demographic parameters which inform the model in this order: fertility, mortality, marriage, and migration.

### *Order of Demographic Operations*

All agent based models begin with a heterogenous set of autonomous actors (Macy and Willer 2002). In this paper, this set is conceived as an initial village, analogous to the villages of Nang Rong district, Thailand, where the model is set. As described in the text, two types of initial villages were considered – a new village and an established village. The simulation begins from either of these two populations in year 0, corresponding to the calendar year 1900.

In the first year of the simulation, eligible residents are subjected to the following sequence of demographic events. First, individuals are subjected to the risk of migrating out of the village, and, if they leave, they do so immediately. Second, individuals decide whether to not attempt to marry that year, to marry someone from outside of the village and immediately settle with their spouse in a different village, to marry someone from outside of the village and settle with their new spouse in the village, or to attempt to marry an eligible partner within the village. Third, if they are a woman who was married in the previous year, they are subjected to the risk of giving birth to a child. Fourth, everyone is subjected to the risk of dying. Finally, at the conclusion of these operations, in-migrants, who may or may not be linked by kinship, move into the village.

After the model begins in 1900, there are three ways to enter the village. Someone may enter the village by marrying a village resident and deciding to reside in their spouse's village, they may be born to a village resident, or they may in-migrate. There are three ways to exit the village. A village resident may out-migrate, they may marry someone from a different village and decide to settle in their spouse's home, or they may die. In the pages that follow I detail these manners of entrance and exit from the population, but first I concentrate on one of the interactions that occurs within the village,

specifically the transmission of fertility preferences from parents to children and from village residents to their exogamous spouses who settle in the village.

### *Fertility Preferences*

A second key feature of agent based models is the heterogeneity of agents and the ability for agent traits to be passed, imitated, or inherited locally through the interactions that agents experience with each other (Macy and Willer 2002). The model employed allows for a similar possibility through a focus on the heritability of numbers of children. Without accounting for intra-individual and intergenerational stability in fertility decisions, estimates of family structure have been shown to be biased in the literature (Ruggles 1993), and it can be expected that broader networks of kin relations will have a similar experience.

In general, because it is broadly acknowledged that mothers and daughters have correlated fertility levels (Pearson and Lee 1899; Huestis and Maxwell 1932; Berent 1953; Kantner and Potter 1954; Duncan *et al.* 1965; Hendershot 1969; Johnson and Stokes 1976; Anderton *et al.* 1987; Pullum and Wolf 1991), and because there may be reasons – ranging from stable individual preferences to biological capacities in terms of fecundity<sup>16</sup> – for which individuals are consistently subjected to higher (or lower) risks of childbirth, I endow the initial agents, both male and female, each with a log odds shift that, for women, will constitute their deviation from the global probability in the likelihood that they give birth in a given year of exposure (note that a similar process was described in Wachter, Blackwell and Hammel 1997). Individual agents' heterogeneity in

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<sup>16</sup> Henceforth, I refer to this as fertility preferences, but the term is used for simplicity and is intended to capture the broad suite of reasons that individuals may experience consistently higher or lower fertility.

terms of fertility preferences is also treated as heritable<sup>17</sup>. For this reason, both male and female agents are assigned preferences, though only those of the woman matter for her likelihood of childbirth. Initial agents and those who migrate into the village receive a random shift from 0. Children born and spouses who marry into the village receive the average of their parents' or spouses preferences, respectively, plus random error.

Random shifts are constructed from each individual's predetermined fertility probability – either zero or the average of one's parents' or spouse's probabilities – by equation B1:

$$(B1). p_i^* = \frac{1}{1 + e^{-s + \ln(-1 + \frac{2}{p_i})}},$$

where  $p_i^*$  is the shifted likelihood of person  $i$ ,  $s$  is the random shift (0.1 in all scenarios), and  $p_i$  is individual  $i$ 's predetermined fertility probability. Notably, individuals only receive a shift when they enter the village.

### *Fertility Parameters*

The dominant means by which individuals may enter the population is by being born to a village resident. This section describes how resident women are subjected to the risk of giving birth. Female village residents who were married and whose spouse was resident in the village in the previous year are subjected to the risk of giving birth determined by the combination of their age and the year of the model.

To derive the age-specific fertility probabilities, I used the Coale and Trussel (1974; 1978) model marital fertility schedules. These schedules operate through two key

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<sup>17</sup> I use the term heritable to convey the idea that such traits may be passed from generation to generation, ignoring whether the mechanism of their transmission is genetic, socio-cultural or both.



parameters (M and m) which define, respectively, the population's inherent deviation from natural fertility and its extent of contraceptive use.

From years 1-100, the annual M and m parameters are specific to each scenario. In fertility scenario 1, M is 0.85 from years 1 to 50. It then suffers a linear decline from years 51 to 60 to a level of 0.70, this corresponds to an initial drop in fertility, which is typically used to diagnose the onset of a fertility transition. From years 61 to 85 it linearly declines from 0.70 to 0.35; this captures some of the broader decline in fertility discussed in the text. Finally, from years 86-100, M linearly decline from 0.35 to 0.25. In fertility scenario one m, the parameter reflecting contraceptive use, is 0 until year 60. From years 61 to 100 m linearly increases from 0 to 0.575.

In fertility scenario 2, M is 0.85 until year 60, wherein from years 61 to 80 it declines linearly to 0.70. After this, from years 81-95, M linearly declines from 0.70 to 0.35. In years 96-100 it linearly declines from 0.35 to 0.25. In this scenario, m does the same thing it does in fertility scenario 1, remaining constant at 0 until year 60 then linearly rising to 0.575 by year 100.

In fertility scenario 3, M remains constant at 0.85 until year 60. After this it declines to 0.70 over the decade between years 61 and 70. From there it declines rapidly to 0.35 in the years 71 to 80. Finally, its decline slows between the years 81 and 100 when it reaches 0.25. In fertility scenario 3, unlike the others, the contraceptive revolution occurs later and more rapidly; m remains constant at 0 until year 70, and from years 71 to 100 it rises to 0.575.

Notably, all three fertility scenarios are governed by the same parameters until year 50 and have the same ending parameters in year 100. The difference between them

occurs in their trajectory between these points, their fertility transitions. From years 101-150, the fertility parameters were chosen to reflect the age-specific fertility put forth in the median variant of the United Nations' prospects for Thailand (United Nations 2008a). They were not defined according to the model marital fertility schedules of Coale and Trussel, but were instead put directly into the model. The UN data come in five year age brackets for five year periods. This data was translated into single age and single year intervals by two sets of linear interpolations. Notably, all fertility scenarios experience the same exact fertility parameters from years 101 to 150.

### *Mortality Parameters*

In the agent-based model employed in this paper, death is the chief means of exiting the population. In each year, each individual is subjected to the period specific risk of dying specific to their age and sex. These parameters were defined using the  $nQ_x$  column of the United Nations' model life tables (United Nations 1995; see also Coale, Demeny and Vaughan 1983; Coale and Guo 1989). These model mortality schedules are indexed by the life-expectancy at birth in the population. In keeping with the recommendations of Siegel, Swanson and Shryock (2004), I use the "Latin American" model as this approximates Thai mortality schedules<sup>18</sup>. The specific life expectancy parameters used in each scenario can be seen in figure 2.

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<sup>18</sup> Notably, the United Nations' model life tables leave age 85 as an open category for probabilities of dying, which means that all individuals above age 85 are subjected to a 100% probability of dying while they are in that age group. Lacking specific annual probabilities of dying above that age, I substitute the probability of death extrapolated from the category average in prior years; after repeated exposure to this, very few individuals live to be 100 years old.

As with fertility, the age-sex-period specific risks of dying are unique to each scenario between the years 1 and 100. As these are graphed in figure 1 in the main text, I do not discuss them here. However, unlike the fertility scenarios where the United Nations' median variant projections yielded age-specific fertility rates, the most consistently available mortality data concerns life expectancy at birth. I used this data (United Nations 2008b), as inputs to the model mortality schedules discussed above to define the age-period specific mortality rates. Note that the five year brackets of the United Nations' data was handled by linear interpolation and rounding. As with fertility, the mortality data between years 101 and 150 are the same for all scenarios.

### *Marriage Parameters*

Complexity is a common theme in demographic models of marriage (cf. Todd, Billari and Simao 2005). Wachter, Blackwell and Hammel (1997) distinguish demographic simulations as either considering a closed model, where all marriage occurs within the modeled population, or an open model, where all marriage occurs to outsiders who move into the simulation. Clearly, this choice will have important implications for the shape of the kinship network, and neither approach is an ideal representation of demographic realities.

Here, the parameters regarding marriage attempt to reflect the marriage market of a small community. To do so, I consider a mixed model wherein some individuals marry others from within the village and other individuals marry people from outside of the vilalge. Marriage parameters are motivated by Coale and McNeil's (1972) work on model marriage schedules. Coale and McNeil argue that a schedule which records first

marital frequencies takes the same basic shape in all populations. Their model demonstrates that a convolution of a normal distribution of age of entry into marriageability and three other delays (time to meeting a potential spouse, time from meeting to engagement, and time from engagement to marriage), each of exponentially less importance, describes the first marriage patterns of many populations.

Though this schedule works to describe population averages, it is challenging to imagine how it would be applied to an individualized model (cf. Todd *et al.* 2005 for one attempt which yielded results largely in keeping with Coale and McNeil's model; see White 1999 for an entirely different model). Thus, the solution used in this paper retains the spirit of that work, but has slight differences. As with Coale and McNeil's model, individuals cannot marry until they have reached an "age of entry into marriageability". This threshold, similar to the first and most important delay in the Coale and McNeil model, is assumed to be normally distributed with a right skew. It was constructed using a cumulative distribution of ages from 15-25. In other words, no one is eligible to consider marriage until age 15, but everyone is considering it by age 25. Note that women lose their eligibility to marry after age 50 and men do so after age 70.

Once an individual has reached the point at which he or she begins to consider marriage, that individual then chooses between one of four options: not getting married that year, marrying someone from outside of the village and settling in a different village, marrying someone from outside of the village and settling within the village, or attempting to marry someone within the village. If they choose the second option – exogamous marriage with post-nuptial residence outside of the village – then they leave the village in that year. If they choose the third option – exogamous marriage with post-

nuptial residence in the village – then their spouse moves into the village. By default, male spouses who move into the village are two years older than their wives and female spouses who move into the village are two years older than their husbands. As discussed above, spouses who move into the village receive the fertility preferences of their partner plus random noise.

It is the fourth option that is most complex, but which is also a crucial form of interaction within the village and a key reason that this agent based model of demographic interaction differs from prior micro-simulation models elaborated in the main text. Each year, males and females who have opted to attempt to marry someone from within the village – that is, to marry endogamously – are arrayed into two lists, which are randomly permuted to avoid ordering effects. Females proceed sequentially, in the randomly permuted order, to consider each male in the randomly permuted male list. If it is possible for them to marry that individual – that is, if they are not close kin – they consider marrying that person. Each eligible within village pair is subjected to a 10% risk of marrying. If they do not marry, then the woman proceeds to the next eligible man on the list and considers marrying him, and so on until she is married, at which point the next woman begins to consider men.

Whenever a particular pair marries, both are removed from the pool of eligible individuals. Thus, it is quite possible that a woman at the bottom of the list in a given year will not have any eligible men that she might marry, or that men may remain on the list after all women have married others. This is akin to the second, exponentially less important, delay of the Coale and McNeil model of marriage. Though, roughly in keeping with the experience of rural Thailand, the model makes no allowances for divorce,

individuals who were previously married may reenter the pool of individuals who are eligible to marry if their spouse dies and they are below the threshold ages. In this case, they are treated in the same way as anyone else in that pool.

The marriage parameters for the model were defined in keeping with the experience of Thailand and after testing to ensure that the likelihood of an eligible endogamous pair becoming married was large enough to maintain the population over time<sup>19</sup>. Through observation of data regarding marriage in Thailand, it was determined the age pattern of marriage and the proportions married varied little over time. As a result, the parameters regarding age of entry into marriageability, the proportions of those eligible to consider various types of marriage, and the likelihood of endogamous success were held constant over time. The proportions considering each type of marriage were held constant: 50% decide not to get married each year, 10% decide to marry exogamously and leave the village, 10% decide to marry exogamously and remain in the village, and the remaining 30% decide to attempt to marry someone from within the village. Men and women share the same parameters for all of these things.

### *Migration Parameters*

Nang Rong, as a frontier area, moved from being a net receiver of migrants in the early 20<sup>th</sup> century to a net exporter by the latter part of the century. Thus, each scenario, in keeping with the experience of Nang Rong, moves from a state of low out-migration and high in-migration to a state of high out-migration and low in-migration. However, translating this basic historical pattern into manipulatable and interpretable parameters is

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<sup>19</sup> An effort was made to keep it small as it does not need to be large. If there are 10 eligible men, a woman is near certain to marry one of them with a 10% success rate.

a challenge. The most readily available means of doing so is through the use of crude rates of migration, but, as with all crude rates, these are problematic for describing the amount of migration that can be expected because they ignore the age structure of the population at risk of migrating. Thus, in order to use these crude rates in this model, I translate them into expected age-specific rates of migration using the age-distribution of migration in Nang Rong between 1994 and 2000. In this section I describe these translations, first for in-migration and then for out-migration.

The in-migration component of the model is controlled by two parameters, a) the proportion of the population within the village which enters (akin to the crude-rate of in-migration, the most readily available means of characterizing in-migration given that the population at risk of moving into the village is unknown) and b) the extent to which those migrating into the village are kin.

This is done in two steps. First, I use the age distribution of migration, given by equation B2:

$$(B2) R_{\alpha} = \frac{N_{\alpha}}{P_{\alpha}},$$

where  $N_{\alpha}$  is the number of migrants of a given age and sex,  $P_{\alpha}$  is the number of individuals of a given age and sex in the population, and  $R_{\alpha}$  is the age-sex specific rate of migration. This equation is then broken down so it can be used in the simulation. I achieve this by noting that the number of migrants of at a given age and sex is determined by equation B3:

$$(B3) N_{\alpha} = P \times M \times N_{\alpha},$$

where  $P$  is the total population,  $M$  is the proportion of the population that are migrants (the parameter which I later manipulate), and  $N_{\alpha}$  is the proportion of the migrants that are

of a given age and sex. Substituting (2) into (1) yields a situation that, with the assumption that  $N_a$  is the same in the simulated population and Nang Rong<sup>20</sup>, allows for the calculation of an age-sex specific rate of in-migration in the simulation using a controllable parameter ( $M$ ) and the information from the population being simulated. In equation form this looks like B4:

$$(B4) R_a = \frac{P \times M \times N_a}{P_a},$$

where  $P$  denotes the size of the population of interest in a given year of the simulation,  $N_a$  is the relevant proportion of migrants of a given age and sex in the observed population (Nang Rong),  $P_a$  is the proportion of the simulated population that is a given age and sex in that year of the simulation, and  $M$  is the parameter governing the sex-specific proportion of the population that will be set to move in during that year of the simulation.

The in-migration component of the model is also influenced by a parameter ( $K$ ) which governs the extent to which those who migrate into the village are kin-linked to one another. Specifically, once the age-sex specific number of migrants who move into the simulated village in a given year has been defined, all opposite sex-pairs of in-migrants over the age of 15 are subject to the risk of marriage defined by  $K$ . The model then attempts to assign all children below the age of 12 to one set of parents, if this cannot be done they are assigned to a random mother or father, in the unlikely event that

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20 That is, assuming that the age-distribution of migrants are the same in both populations, which is reasonable as the migrants who have come to Nang Rong over the past century are likely similar in their age and sex distribution to those who left Nang Rong for somewhere outside of Buriram province between 1994 and 2000. Those are the individuals whose age and sex distribution are used to determine the ages and sexes of the immigrants.



neither of these can be done it is assumed that the children are hosted by distant kin or friends of the family<sup>21</sup>. The parameter  $K$  is set to 50% for all years.

Like the in-migration component, the out-migration component of the model is governed by a parameter which controls the proportion of the at-risk population (unmarried individuals who were born in the village<sup>22</sup>) who leave. However, the two components use this parameter very differently. For the out-migration component, the proportion leaving is multiplied by the population of the village and rounded to select an approximate number of individuals who will leave. So to introduce an element of stochasticity into the out-migration component, this approximate number is then translated into the actual numbers who leave by drawing from a Poisson distribution with a mean given by the approximate number. From here, out-migrants are selected randomly from the population of unmarried and childless individuals; thus, the age-sex distribution of out-migrants will be proportional to the age-sex distribution of unmarried and childless individuals in the simulated village in that year. There is no parameter in the out-migration model describing the connectivity of those who leave, but, because they must be unmarried individuals, they will have neither spouses nor children.

Finally, in keeping with Kingsley Davis's demographic theory of multi-phasic response (cf. Davis 1963; Friedlander 1969), I ensure that the population of the simulated village neither crashes to zero nor expands to an overly large level by imposing swells of migration when the village population grows too small or too large. Thus, when the

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21 Note that these childrens' kin links to their distant kin are not included in the model. However, given that the age distribution of migrants typically includes very few children, it is extremely unlikely that children will not be assigned to parents.

22 In Nang Rong, few married individuals leave the village for the purposes of migration. Though migration for the purposes of marriage is substantial (Čhampāklāi [Jampaklay] 2005, 2006), this type of migration is defined in the marriage model described above. The model keeps no track of individuals who temporarily migrate into the village only to later leave.

population declines to fewer than 5 individuals, a random number of people drawn from a Poisson distribution with a mean of 15 moves in. In contrast, if the population grows to more than 1,500 individuals, I define the number of emigrants as 250. Though these restrictions keep the model running in cases where the population becomes unsustainable, an examination of the model outputs shows that they were very rarely exercised, and only in years prior to 1900 during the growth of the initial village.

Thus far I have described how the migration model is defined by analogs of the crude rates of in- and out-migration, I now turn to a description of the trajectories of these rates used over the course of the model, which are the same in all scenarios. As discussed above, the villages of Nang Rong proceeded from a state of high in-migration and low out-migration to a state of high out-migration and low in-migration. In the model, this switch occurs in the following fashion. For out-migration, a very small 0.01% of the population leaves each year from 1900 to 1970. Between 1970 and 1980 this transitions to 3%, and remains there from 1980 until 2000. From 2000 to the conclusion of the model, out-migration declines to 0.25%. For in-migration, the trends are roughly reversed but reflect the different time scale of when in-migration tapered off in the region. In each of the years between 1 and 45 in-migrants whose total is equivalent to 0.50% of the population enter the village. Between 1945 and 1955, the proportion entering the village transitions to 0.25% and remains at that level until the end of the simulation.

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