Demography and Social Network Differentiation

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Abstract

Ashton M. Verdery: Demography and Social Network Differentiation
(Under the Direction of Barbara Entwisle)

Nearly all societies in the world 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 focus on understanding what implications such variation

has for social interaction. Though prior literature has explored demographic contributions

to opportunities for interaction between individuals of different ages, it has focused on

social ties between very close kin (such as children and parents), particularly in the

context of multi-generational co-residence. This paper extends this focus by considering

broader kinship links in communities, which are important components of community

integration. To do this, I use a simulation approach that combines the traditions of

demographic micro-simulation and social network generation with techniques of agent-

based modeling. Results are presented concerning how variations in demographic history

manifest as differences in modern social networks. These are validated against a set of

specific cases from Thailand.

Dedication

Dedicated to Daniel F. Verdery.

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Introduction

Evidence of declining social integration in America (McPherson *et al.* 2006; Marsden 1987), and other parts of the developed (Yee 2000) and developing world (de Souza and Grundy 2007) has been of great interest to sociologists. Much of this interest stems from theories suggesting that low social integration has negative implications for individuals' political participation (Putnam 2000), health (e.g., de Souza and Grundy 2007; Berkman *et al.* 2000; Seeman 1996; Moen *et al.* 1989), economic success (Coleman 1988; Granovetter 1985; Woolcock 1998), and other sociologically interesting outcomes. The literature has focused on documenting the decline (e.g., McPherson *et al.* 2006) or discussing its implications (e.g., Putnam 2000), and scores of empirical studies have validated these concerns. Significantly less effort has been put towards explaining these trends.

Why is social integration declining? Contemporary and classical theorists have linked it to the decline in voluntary association (Putnam 2000), others to increasing economic modernization (Durkheim 1893[1933]), and still others to the general processes associated with urbanization (Simmel 1903[1971]). This paper explores the responsiveness of one component of social integration, social network structures

generated by kinship relations, to historical changes surrounding the demographic transition, a pattern of social change that has been observed in nearly every country in the world. Doing so, this paper extends the large literature linking demographic change to 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), but moves the focus from intra-household relationships to broader social networks linking members of communities. Given the importance of kinship networks in the literature and the suggested relation of social networks to demography in both classical and contemporary theory (Durkheim 1893[1933]; Simmel 1903[1971]: 324-339; Blau 1974: 616; Granovetter 1973: 1379; Entwisle 2007), the dearth of prior work on this topic seems strange. This paper fills that gap by addressing how the timing, tempo and extent of mortality and fertility decline influence social network form and differentiation, with specific reference to kin networks.

Societies vary with respect to their experience with mortality and fertility decline. The first section of this paper compares the historical trajectories of demographic transitions throughout 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 fertility and mortality levels. These differences may generate diversity in social network forms, especially those surrounding kinship, but little is known about how much variability in contemporary social network structures is due to these historical factors. To investigate the connection between historical patterns of mortality and fertility decline and contemporary kinship networks, I use simulation as an approach, combining the older

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traditions of demographic micro-simulation and models of social network interaction with newer techniques of agent-based modeling. Such an approach has not previously been used in analyses of the demographic transition or in analyses of social network differentiation; here, I employ the control afforded by this method to manipulate parameters reflecting the timing, tempo and extent of fertility and mortality decline in order to parse the independent contributions of such important sociological features. An important component of this work is that it starts from a set of specific cases which I will attempt to replicate through empirical validation using an unusual set of data from Nang Rong district, Thailand which has frequently been used to study important demographic and sociological phenomena (e.g., Entwisle et al. 1996; Van Wey 2004; Faust et al., 1999; Entwisle et al., 1984).

Demographic Transitions

Almost every society in the world has completed or begun some sort of demographic transition (Guest and Almgren 2003). The demographic transition is "the process of modernization of the reproductive behavior in human populations" (Chesnais 1990: 327). Separating the social phenomenon of the demographic transition from demographic transition theory is challenging, and, indeed, few descriptions of the former are not augmented with arguments concerning the latter (Casterline 2003). Nonetheless, despite the often contentious debates about demographic transition theory (cf. Mason 1997; Coale 1973), the demographic transition itself can be divided descriptively into pre-transitional, transitional, and post-transitional stages (Guest and Almgren 2003).

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Generally, societies progress from stage 1, where birth and death rates are both high and in equilibrium with little population growth, to stage 2, where death rates, especially those in the first years of life, are lower than fertility rates, allowing significant room for population growth. From there, societies progress to stage 3, where mortality and fertility rates are again near equilibrium but both low, resulting again in low population growth. Movement through these stages is generally thought of and collectively referred to as the demographic transition. The numerous debates surrounding this pattern are not the focus of this paper; instead, I focus on variation between societies in terms of their experiences regarding the timing, tempo and extent of mortality and fertility decline.

Societies throughout the world have exhibited substantial variation in their experiences with mortality and fertility declines. The majority of research focus has been on fertility transitions (cf. Dyson and Murphy 1985; Mason 1997; Bongaarts and Watkins 1996; Caldwell and Caldwell 2006), though some efforts have been made to understand mortality transitions (e.g., Caldwell 2006; Preston 1980; Preston 1985a). Table 1 summarizes the general timing and tempo of fertility transitions for 13 world regions (Caldwell and Caldwell 2006)[1]. For large regions of the world, the table shows the year in which the median country from that region's fertility had declined 10% from its pre-transition levels, a change that is taken to indicate a significant shift in fertility patterns,

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1 The regions in the table are argued to be "demographically consistent" by Caldwell and Caldwell (2006), meaning that countries in those regions had generally similar experiences with the demographic transition in terms of timing of onset and tempo of fertility and mortality decline. This singular focus on fertility is unfortunate, but a comparison of dates of onset and tempo of change national mortality transitions 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."

and the mean number of years that countries in that region took to decline from 10% to 40%.

As shown in table 1, there is great variation in the timing and tempo of fertility transitions. The fertility transition did not happen simultaneously throughout the world. Indeed, the countries of sub-Saharan Africa and the Middle East began their fertility transition almost 100 years after Europe and the most developed, English-speaking colonial states. As shown in the more complete table A1 in the appendix, some countries (Guadeloupe, Guyana, Singapore Hong Kong, China and North Korea) took as little as 5 years to proceed from a 10% decline to a 40% decline, while a considerable number of others took 30 or more years (Belgium, England and Wales, the Netherlands, Germany, Scotland, Italy, Iceland, France, Ireland and the United States).

It is well known in the demographic literature that fertility is the product of a specific set of interactions and events, termed proximate determinants, which can be approximated by the average female age at first marriage, the extent of contraceptive use and induced abortion, and the duration of post-partum sterility in the population (Bongaarts 1978; Bongaarts 1983). When looking at changes in fertility patterns over time, researchers typically explore changes in the age pattern of fertility (which is linked to the changes in the age at first marriage) and changes in contraceptive use (Coale and Trussel 1974; Coale and Trussel 1978). Tsui (1985), among others (e.g., Nortman 1977), looked at changes in contraceptive use. She found stunning changes in contraceptive use over short periods of time (see Tsui 1985: 118). For instance, contraceptive prevalence in the population rose from 15% in 1969 to 33% in 1975 in Thailand; in Mexico it rose from 30% to 40% in just one year between 1977 and 1978. In the developing world, there was

considerable heterogeneity in the prevalence of contraceptive adoption by the time of the

World Fertility Surveys (WFS) – 34% of Latin Americans surveyed had adopted

contraceptive use, compared to 21% of Asians and 20% of Middle Easterners but only

5% of Africans (see Tsui 1985: 122). Leridon and Ferry (1985), among others (e.g.,

Rindfuss and Morgan 1983), focused on the role of non-contraceptive (and non-abortive)

restraints on fertility noting the role of cultural norms in influencing the age of onset of

sexual intercourse, periods of marital separation, length of interbirth intervals, and the

end of exposure to the risk of pregnancy. Again, substantial variation throughout the

world and substantial changes over the course of the 20th century were some of the key

findings from these analyses.

Mortality transitions, like fertility transitions, have also varied, though less is

known about their comparative timing and tempo (see note 1 above, Mason 1997;

Hirschman 1994; Heueveline 2001). Infant and child mortality rates have received a

significant focus, especially due to the comparative data made available by the WFS

(Preston 1985b). As an example of diversity in the progression of the mortality transition,

consider these examples from sub-Saharan Africa. 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. As

with fertility declines, the developed world experienced mortality declines much sooner

than those in the developing world, though mortality declines in the developing world

have happened more quickly and at significantly lower levels of development (Preston

1985a; Davis 1956; Caldwell 1986).

Not only have mortality declines in the developing world begun later than those in the developed world, there has also been a much smaller lag period between onsets of mortality and fertility decline. This lag period accounts for a large part of the variance in experience with the demographic transition throughout the world. Bongaarts and Watkins (1996) show that countries experienced their fertility transitions at vastly different levels of development and with large differences in infant mortality rates and life expectancy at birth. Indeed, the variation can be seen in this small 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.

Previous considerations of the impacts of the timing and tempo of the demographic transition can be grouped into two categories. The majority of work has considered the demographic transition's implications for economic development (e.g., Zhang, Zhang and Lee 2001; Chesnais 1990; Coale and Hoover 1958), while some work has focused on the implications for social interactions between individuals of different ages (e.g., Ruggles 1986, 1988, 1994, 1996, 2007). The former work is outside the scope of this paper, given the complementary relationship between demographic change and economic development. The latter however, points the way to important theoretical contributions to be made by considering the demographic transition's implications for social interactions.

Unfortunately, despite the wealth of literature on the topic of demographic contributions to the opportunities for interaction between individuals of different ages,

the majority of the focus has been within the household (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). The primary consideration in this literature has been a debate about the relative contributions of demography and economic development to the phenomenon of declining intergenerational co-residence, and the evidence seems in favor of economic development (e.g., Ruggles 2007). However, these analyses have focused largely on whether historical demographic realities were a limiting influence on household co-residence patterns, particularly multi-generational families. I extend this concept outside of the household, as kinship network links in communities have been shown important predictors of community integration (Entwisle *et al.* 2007). Understandings of the processes which create differences between places in terms of such extra-household networks are entirely lacking, and as a start, I consider the role of the demographic transition.

Social Networks and Demography

Kinship networks, defined more broadly than household co-residence, are important social structures (Schweizer and White 1998). They have been shown relevant 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 structures

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(Padgett and Ansell 1993). The affective nature and relative permanence of family ties makes them a primary unit of social bonding, the so-called strong ties in the social network literature (Granovetter 1973). Beyond direct kin relations, indirect connections to kin (in social network terms, ties which are more likely to be "weak" (Granovetter 1973) such as a cousin's spouse) can be thought of as conduits through which resources, information and obligations might pass. Throughout the world, kin predominate information sharing circles, as has been shown in the United States (McPherson *et al.* 2006; Marsden 1987), Kenya (Kohler *et al.* 2001), Mexico (Massey 1990), and Thailand (Entwisle *et al.* 1996). Kinship groups also act as a primary locus of resource sharing in the developed (Grundy 2006; Grundy and Henretta 2006) and developing world (Piotrowski 2006; VanWey 2004). Kinship networks are, in short, vital units of sociological analysis.

The broad opportunities for kin interaction created by demography have important implications for the translation of local social processes into global structural forms. Indeed, a key insight of the demographic literature is that the availability of certain types of people – for instance, reproductive aged women – are critical determinants of sociologically important phenomena. Such an insight, the importance of accounting for the risk of an event occurring by accounting for the underlying population distribution, has greatly enhanced understandings of numerous demographic phenomena. This idea is not lacking in the social network literature, though it is not always explicitly acknowledged (Blau 1974; Robins *et al.* 2005). Classical analyses of social structure[2] paid great attention to the constraints that the spread of people across time, space and

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2 Here I use the term social structure to mean the set of relations linking individuals or entities.

social grouping placed on associational patterns (Durkheim 1893[1933]; Simmel 1903[1971]: 324-339; Marx 1939[1978]: 276-278; Weber 1923[1981]: 352-370, 1904[1958]: 39-40).

These early insights did not disappear. For instance, Blau (1974: 616) posited that structural parameters were the basis of observed social structures, indeed that social structure could be defined as "population distributions among social positions along various lines – positions that affect people's role relations and social interactions." Likewise, Granovetter (1973: 1379) thought that "demography, coalition structure and mobility are just a few of the variables which would be important in developing a micro-macro linkage" in the explanation of social network differentiation. More recent research has acknowledged the ways that fertility and mortality change might affect social structure and patterns of interaction (Watkins, Mencken and Bongaarts 1987; McNicoll 1986). Contemporary work has argued that social network differentiation might be attributable to historical migration patterns (Entwisle 2007; Entwisle *et al.* 2007).

Prior demographic patterns affect social networks by constraining individuals' opportunities for interaction. This paper thus explores how the possibilities for interaction covary with patterns of fertility and mortality decline; it makes no comment on the possible changes in the meaning of different relationships or changes in the likelihood of activating the ties that are possible. The idea is well put in articles concerning homophily and racial segregation. In the literature on homophily – the tendency for individuals with similar attributes to be associated – careful distinctions are made between "baseline homophily" and "inbreeding homophily" (McPherson *et al.* 2001), with the former being a function of random expectations given relative group sizes (see also Blau 1977) and the

latter of proclivities towards preferential association above a randomly expected baseline[3] (Goodreau, Kitts and Morris 2009). The distribution of populations across space is another dimension of baseline homophily that is less frequently considered in the social networks literature, yet it has been shown crucially important for estimates of friendship segregation by race among adolescents (Mouw and Entwisle 2006).

Demographic change alters the distribution of people across sociological categories, which will have important implications for relations between people in these different categories. Such age-distribution effects are well studied in the demographic literature, especially at the national level. For instance, 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; given the principles of baseline homophily, such an increase will clearly affect the likelihood that a middle aged individual's parents, aunts and uncles are alive and an important force in their lives. In contrast, France, whose demographic transition was the slowest and steadiest in the world, saw only a 10 fold increase in their old age population. Such differences between countries are stunning, and the opportunities for interactions which they influence are critically important. Likewise, Ruggles (1986) attributes the demographic change seen in the developed world as a necessary condition for the rise of the extended family structure. Indeed, 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),

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3 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."

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

When we consider where such interactions occur, it becomes apparent that looking at the national level is not ideal. Though a substantial amount of contact occurs between spatially distant close kin ties in the developed world, facilitated by telephonic and electronic communication (e.g., Onnella *et al.* 2007), such types of contact are not universal. The vast majority of individuals whose inputs are sociologically important remain within a small geographic circle of each respondent; the majority of social network findings conform to this notion of spatial proximity. Indeed, even in the developed world, local, face to face, contact is still thought prominent (Wellman *et al.* 2001; Putnam 2000); indeed, the focus on neighborhood and village effects in both the developed and developing world speaks to the importance of local face to face interaction (Entwisle 2007).

In addition to being an important locus for examining social networks, there is ample evidence of substantial sub-national and even local variation in demographic determinants. However, the majority of studies examining demographic change have done so at the regional or national scale. As an example of the possibility for local variation in demographic determinants, there Entwisle *et al.* (1996) found substantial variation in contraceptive use and fertility patterns between 51 spatially proximate villages in Nang Rong district of Northeast Thailand (Entwisle *et al.* 1996). To further underscore the point, social networks were also found to differ between the villages (Entwisle *et al.* 2007), and they were found to have important implications for migration (Entwisle *et al.* 2009). Axinn and Yabiku (2001) found a similar diversity regarding

contraceptive use and community integration in the villages of the Chitwan Valley of 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 variations remains understudied (Entwisle 2007). Though considerable research efforts have 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 research, outside of the household co-residence literature discussed above, has explored the possibility that demographic choices also shape those social structures. That is another recommendation for 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.

Simulation Approach

This paper uses an agent-based model that simulates the demographic behavior of individuals in a kinship system[4] and data from the Nang Rong projects (Nang Rong Projects 2008). Such a method is ideal for the study of 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

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4 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.

changes in social structure (see Epstein 2006:1-46 for a discussion of the theoretical underpinnings of social simulation; see Macy and Willer (2002) for a review of its applications). This is an important contribution as it allows for the testing of bottom-up hypotheses about social structural generation (e.g., Robins *et al.* 2005) that are informed by a demographic model of entrance and exit from the population. It has the potential to treat kinship structure as an endogenous dependent variable that may, in turn, influence demographic patterns, something not feasible in classical survey analysis.

Such a simulation approach 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 test how prohibitions or predilections towards friendship or association with different individuals, governed by the attributes of those individuals and those individuals' relational positioning, create different types of network structures. One example is the work of Behrman, Moody and Stovel (2004) where the authors found that heterosexual adolescent dating networks were primarily determined by prohibitions on four cycles (a male dating an ex-girlfirend's ex-boyfriend's ex-girlfriend), rather than by the attributes of the individuals involved. The models of social network interaction chiefly suffer in their failure to control the entrance and exits of individuals from the population, a key demographic insight. In contrast methods of demographic micro-simulation focus on the entrances and exits from the population, but have other problems (see critiques in Ruggles 1993; Wachter, Blackwell and Hammel 1997) such as their inabilities to allow agent interaction, to model the

heritability of traits, and to allow for changing vital rates over time[5]. All of these

problems are addressed by the agent based microsimulation approach used. Owing to

these issues, this paper uses an agent based microsimulation approach that combines

social network simulation with demographic micro-simulation.

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 its present

differentiation of village kinship networks. In addition, the unique demographic and

social network data 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^2). 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). Though a few villages have been settled for hundreds of years since

the region was part of Cambodia, the vast majority are new settlement, the area being

largely uninhabited until 1900 (Faust *et al.* 1999). As such, the villages were initially

characterized by large numbers of in-migrants and high levels of natural increase. Such

rates of natural increase persisted until the 1960s, when, as with the rest of Thailand

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5 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).

(Knodel *et al.* 1987), fertility rates began to fall. Despite the drop in fertility and despite the closing of the frontier and a general reversal of the migration streams in the 1970s (Entwisle *et al.* 2007; Entwisle *et al.* 2009), the population of the 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, ranging from 19 to 475 households with an average of about 100 households in 1994 (Faust *et al.* 1999). In terms of individuals, villages ranged from 333 to 1,260 residents with a median of 640 in 2000; including migrants not currently residing in the village, these numbers are 475 to 1,600 with a median of 873. Even though village residents tend to know one another, earlier research on Nang Rong has shown that there is substantial variation from one village to the next in the patterning of economic and kin ties and that such information meaningfully correlates with 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 locus of prior work on social networks in developing countries, and because explorations of variation in local level social integration are lacking, I have limited all analyses to events that take place within the village. Doing so circumscribes the network boundaries (Laumann *et al.* 1983; Laumann *et al.* 1992), and focuses on the village as an important local context for social life. Who lives in the village depends on fertility, mortality and migration patterns, which will in turn dictate the number, nature and structure of kin ties within the village. As an example of these restrictions on the 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, they are treated as coming without kinship ties (that is, they do not have any ties that are relevant to the population of interest). In the pages that follow, I describe other characteristics of the model and simulation scenarios to be used before describing the measures by which the model will be evaluated.

Demographic Scenarios

Thailand's experience with the demographic transition is generally described as follows. The mortality transition began around 1950; in the period 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; indeed, 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, the rural Northeast region where Nang Rong is located is likely to have begun its demographic transition somewhat later (Knodel, Havanon, and Pramualratana 1984), though it may be that the larger, more developed towns of the district had similar experiences to the rest of the country.

To simplify the analyses of the study proposed, parameters of interest are classified into three fertility and three mortality scenarios and stratified by two initial conditions to yield a total of 18 combinations. These parameters are intended to mimic demographic likelihoods assumed present in Nang Rong villages, but they also strive for

sufficient generality to hint at the effects of more broad changes for general differentiation in social network form. 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) will be explored.

To do this, I begin with three fertility trends and three mortality trends in combination for a total of nine scenarios based on changing rates. The panels of figure 1 depict each of these combinations, by showing the total fertility rate and female life expectancy for each scenario (changes in male life expectancy follow the same pattern but do not proceed as high, as has been the case empirically (Preston 1980)). In it, the fertility scenarios are held constant across the rows while the mortality scenarios are constant down the columns. Total fertility rate is read on the left axis of each figure while female life expectancy is read on the right axis[6]. In a quick summary, recalling that all combinations of fertility and mortality scenarios are tested, 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

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6 Note that the fertility and mortality scenarios remain constant from years 1900 to 1940 at the level shown in 1940. Also note that the total fertility rates shown are only approximations to make the figure more familiar to 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.

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. 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, where both begin at the same time.

Thus, 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.

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. This is achieved by

exploring 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[7]. 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. In general, I expect that longer gaps between the beginning of fertility and

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

mortality decline will create more cohesive social structures, while shorter gaps will create less social cohesion in terms of kinship networks. Such a finding will speak to the concerns about whether the declining social cohesion observed in developed countries is a certain future for developing countries experiencing the demographic transition, as developing countries experienced a significantly longer gap between the onsets of fertility and mortality decline than developed countries.

The timing of onset of mortality and fertility decline is also interesting because it creates the shape of 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. The length of time since it was created, which is dictated by the onset of the demographic transition, will control whether it means that the plurality of the population has larger numbers of children, siblings, or parents than other cohorts.

Variation in the tempo of fertility and mortality declines – the speed with which the rates fall in isolation and combination – is another worthwhile comparison. In my scenarios, such a comparison can be 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 contrast, 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 transition, with those which began later (i.e., those outside of Europe) generally completing at a faster rate than those which began earlier; as can be seen in the appendix table A1, the variation between individual countries is even more extensive than that between regions. Whether these differences can be expected to generate different kinship structures is an important consideration; I hypothesize that they will.

In keeping with rural Thai setting, at the start of the model in 1900, several of the Nang Rong villages were comprised of young, sparsely kin-linked in-migrants who had moved to settle the frontier, while others had been settled for centuries. 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. By introducing two stylized initial conditions roughly corresponding to those known to have existed in the region, 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 level demographic and social network variation. In developing countries, urbanization and intra-rural migration account for a large share of migration (Bilsborrow 2002). Such large-scale movement of the population results in the establishment of new cities, towns and neighborhoods and, consequently, large groups of unconnected

individuals in close proximity. 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.

The hypothetical villages which I simulate will start from one of two initial conditions. In one model 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 70 living members distributed according to age and sex ratios of high fertility, high mortality populations and characterized by extensive (within-village) kinship links[8]. In the other model that is 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.

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8 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.

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.

Understanding Social Structure

In measuring kinship structures, 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 an entire social network (e.g., Entwisle *et al.* 2007; Entwisle *et al.* 2009). The work proposed thus uses network analytic methods (Wasserman and Faust 1994) to operationalize social structure in both ways, as an aggregation of direct relations and as a broader system created by direct and indirect relations.

Three features of kinship structure are considered in order to understand its covariance with demographic change: average numbers of close kin, average numbers of

indirect kin, and the extent of community connectivity through kinship. These outcomes reflect an interest in social structure at the level of the kinship system and will be discussed in conjunction with a description of their method of calculation. 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). At the end of each simulation run, three adjacency matrices were constructed for the population of all individuals who have ever lived in the village by assigning a matrix cell (a potential kinship tie) a value of one if the individual represented by the row (called the ego) of the matrix is the spouse, child or parent of the individual represented by the column of the matrix (called the alter) and a value of 0 otherwise. The spousal matrix is symmetric (non-directional) and unweighted, while the child-to-parent and parent-to-child matrices are directional and unweighted transposes of each other. From here, matrix multiplication and addition was used to calculate the various features of interest (algorithms available upon request).

As much of the literature looking at demographic change and social structure has focused on the counts of close kin for the average individual living in the population (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), I begin my analyses with that focus. Counts of close kin are typically operationalized as the number of living first-degree kinship

connections, plus siblings (who are technically second degree kin[9]). Numbers of first-degree kin and siblings are an important metric because they are a key means of direct social support (Shanas 1979; Marks and McLanahan 1973) and condition the broader connectivity in the kinship system that someone will enjoy. Further, as I hypothesize that the speed of the demographic transition will be negatively correlated with numbers of such kin, this is an important metric for contextualizing the findings of McPherson *et al.* (2006) regarding the declining numbers of close confidants of Americans.

As a second means of understanding changes in social structure, I examine counts of more distant kin. Such kin – cousins, grandparents, aunts, uncles and beyond – are important for passing information from distant parts of the social network (Entwisle *et al.* 2009). Weak ties have long been theorized as crucially important features of social networks in the literature (Granovetter 1973). Though weak ties should not be construed with indirect relations, it is a reasonable assumption that indirectly related kin are more likely "weakly" tied than directly related kin; further, Granovetter (1973) specifies that indirect relations are a potential source of weak ties. As a means of understanding how varying experiences with the demographic transition relate to differences in counts of indirect kin, I examine the mean number of kin individuals have in the second through fourth degrees.

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

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9 First degree kin are child, parent and spousal ties (see Keyfitz and Caswell 2005; White and Moody 2003). Higher order degrees are the defined by the 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.

potential for "contagion"[10]. Such a concept has been shown useful to understanding the diffusion of innovations (e.g., Rogers 2003), migration (e.g., Entwisle *et al.* 2009), fertility (Entwisle *et al.* 1996), and other sociologically interesting topics. I measure this by considering the percentage of the population reachable in (shortest) kinship paths of four or fewer degrees. This measure was singled out as one which is likely to be particularly dependent on demographic history, especially that owing to migration (Entwisle 2007).

As two of the three substantive measures - counts of close kin and counts of 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 increases the face-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. To aid in interpretation of the results, table 2 breaks down the fertility and mortality scenarios into whether they had a late or an early onset and whether they had a rapid or gradual tempo. The classifications in table 2 are meant as a heuristic only, as the real classifications are more complex; for

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10 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.

instance, it is clear from figure 1 that the rise in life-expectancy in mortality scenario three is somewhere between the rise in life expectancy in the other two scenarios.

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 3 presents the quartiles across the simulations of the features of kinship networks discussed in the last section as measured in the simulation year 2000. Within the table, results are grouped according to kinship network feature, with combinations of fertility, mortality and initial conditions outlined. As the aim of this paper is to show meaningful differences in kinship network structures related 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 was a key feature that motivated my choices of demographic scenarios. To explore this, I consider the simulation results holding fertility scenario constant. Recalling from table 2 (and 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

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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 does significantly influence 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

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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 level of life expectancy most rapidly and during any of the transition years has the highest life expectancy. 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, 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 regards to mortality, and it explains the majority of the differences between the 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 the results *in terms of fertility*. Indeed, in so doing, one of the most consistent findings to emerge from this paper becomes apparent: that differences in the fertility scenarios generate substantially larger differences in the features of kinship networks than differences in mortality scenarios.

Evaluating the relative timing of onset of fertility transitions within mortality scenarios, table 2 highlights 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 scenario two and three to be more similar to each other than they 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, table 2 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 key feature of local variation in demographic processes. To do this, 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 Thailand. In evaluating the influence of these initial conditions, I pay attention to the differences between the simulations beginning from the new and established village within the same fertility and mortality combinations.

Comparing the results obtained from the same sets of fertility and mortality scenarios when they originated from the new or the established village 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. That is, there is overlap in the results that owes to the 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, the results indicate that even slightly differing experiences with the demographic transition matter a great deal 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 high mortality is another interesting finding. Considering these findings in broader context, they suggest that the wildly differing experiences with the demographic transition in different parts of the world can be expected to generate different kinship networks. Furthermore, it can be expected that places which have not yet, or only very recently, begun the demographic transition will have substantial heterogeneity in kinship network structures in the present and near future, owing to the long period 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

Though the simulation approach used presents an analytical tool for evaluating demographic contributions to social network differentiation, simulation methods are met with skepticism if they cannot generate, given the proper parameter specifications, network forms that encompass the range of those observed in a real world setting. In order to validate the model, I make use of the diversity of kinship relations in the 51 villages of Nang Rong (Rindfuss *et al.* 2004; Entwisle *et al.* 2009). Such diversity is a key strength of the Nang Rong data, whose detailed accounts of kinship and demographic history can be analyzed for overlap with the demographic scenarios used.

To do this, I assess the extent to which the distribution of kinship counts and connectivity generated in the simulations fall within the distributions represented by the 51 Nang Rong villages. Through exploratory analysis and by comparing the quartiles of the kin count distributions, I compare the distributions found in the simulations and those in Nang Rong, focusing on whether the simulations encompass the range of kin distributions found in Nang Rong. Table 4 presents such summary statistics for the distribution (across the 51 villages) of counts of close and indirect kin and kinship connectivity found in Nang Rong villages in 2000, corresponding approximately to the simulation results from year 100. As was presented in table 3 for the simulated villages,

the results in table 4 are restricted to living individuals who were ever residents of Nang Rong villages (and thus include 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 experience of Nang Rong villages 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 4, 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 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 the kinship networks obtained through simulation are within the range of possibility of those seen in Nang Rong, in this section I consider the sensitivity of my simulation results to other aspects of the model 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 evolves from different transitions. I then ask whether turning off the parameter reflecting the heritability of fertility preferences substantially alters the results. 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 whether variable experiences with the demographic transition creates differentiation in kinship network form, they do cover a range of alternatives that substantially differ from those presented above and that are of theoretical and substantive interest to 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 how the relative timing of the demographic transition and the timing of the 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 indicated by the 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 subdivided into those scenarios emanating from a new village and those scenarios emanating from an established village.

It is apparent 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

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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 the demographic scenarios; noticeable gaps between the models generally occur between years 50 and 65, which is compelling as all scenarios experienced the same vital rates 10-25 years prior. The conclusion to be drawn from this is that the demographic transition makes a large impact on kinship networks relatively early.

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 lag since the demographic transition took place. To explore this issue, I project the model from the year 2000, when 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 an attempt to quantify whether what we currently observe in terms of kinship network differentiation is likely to persist over a long time. I evaluate this influence of time on the models by examining differences in features of kinship networks in year 150 compared to year 100.

Table 5 presents the quartiles of the simulation results in year 150 as table 3 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, it is remarkable that such differences persist between the scenarios. Second, the features of the kinship networks are greatly different 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 though all models experienced an additional 50 years of simulation with the same fertility and mortality parameters. Such a result 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 likely to be found in post-transitional societies which completed their demographic transition long ago. Further, comparing whether the timing of transition onset, the tempo of transition or the duration of exposure to population growth best explains the differences between models, it appears that, as was found in year 2000, exposure to growth best explains the differentiation of kinship structures. Again, the

differences between the scenarios suggest that it is the fertility transition which conditions such kinship network differentiation rather than the mortality transition.

Examining the model's sensitivity to the parameter reflecting heritability of fertility preferences demonstrates the robustness of the model to this analytic choice. Here, I compare the extent to which the 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 6 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 model without fertility preferences substantially different than the model 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.

Here, I explore the model's sensitivity to the elimination of migration not due to exogamous marriage. The results in this regard are interesting and show the differential sensitivities of features of kinship networks to the 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 the numbers of close and indirect kin are distinguishable between the model excluding migration and the one including it, that

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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 the 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. The work presented in this paper builds on this idea by showing that the 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 of the factors that contributed to urbanization. But, by considering how the demographic transition altered social relations in the rural areas which send migrants, rather than the urban areas which 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 netwoks 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 5 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 5, 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.

Region	Median Date of Onset of Decline (10% Decline)	Average period from 10 to 40% decline (Years)
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.
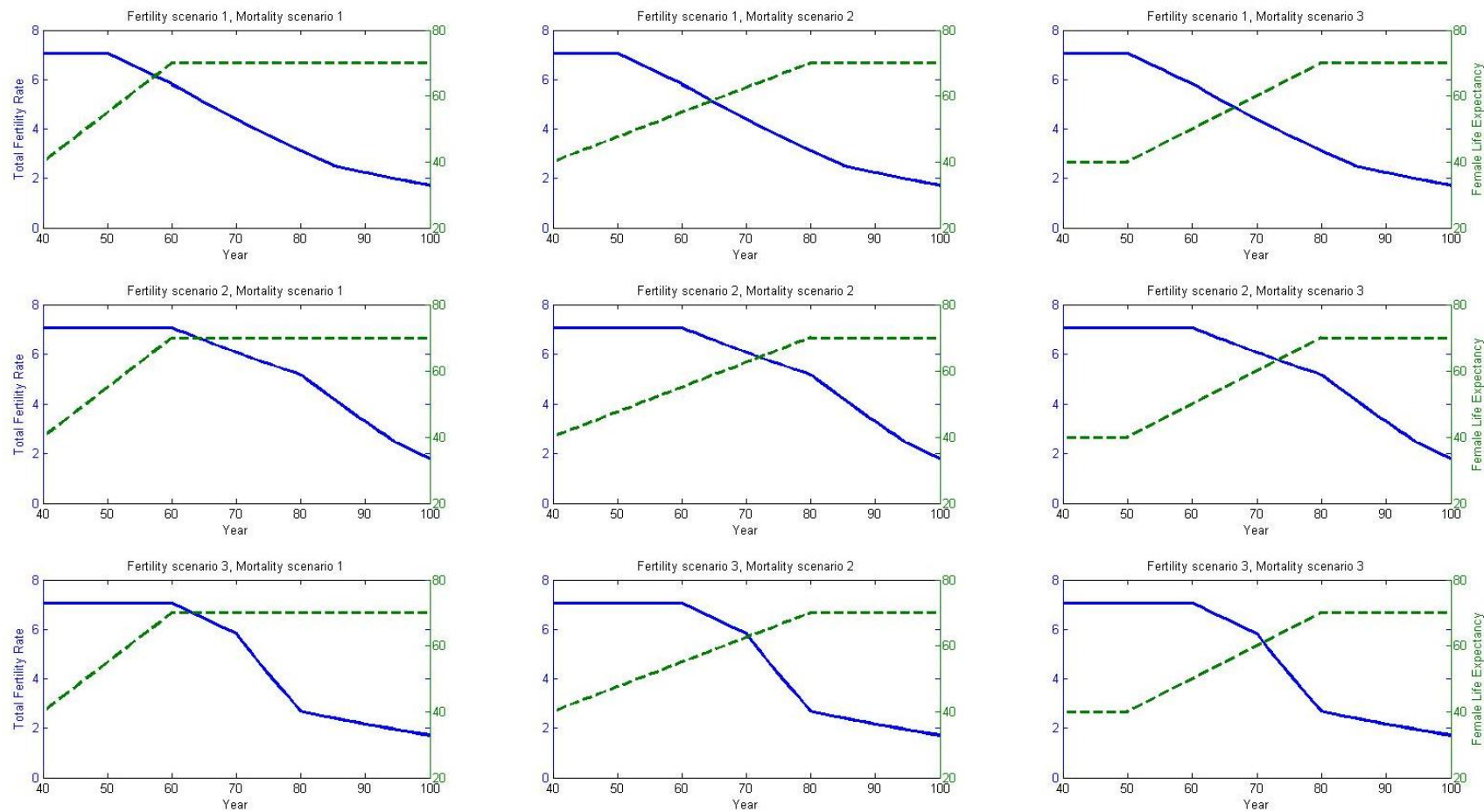
Table 2. Cross-classifications of the demographic scenarios considered.

Timing of onset		Tempo of transition	
		Gradual	Rapid
	Early	M2 F1	M1
	Late	F2	M3 F3

Note: Dichotomies only considered, refer to figure 1 for a true picture of the scenarios.

Table 3. Medians and interquartile ranges of features of kinship networks in year 100.

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

Note: Connectivity multiplied by 100.

Table 4. 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 5. Medians and interquartile ranges of features of kinship networks in year 150.

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

Note: Connectivity multiplied by 100.

Table 6. 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.
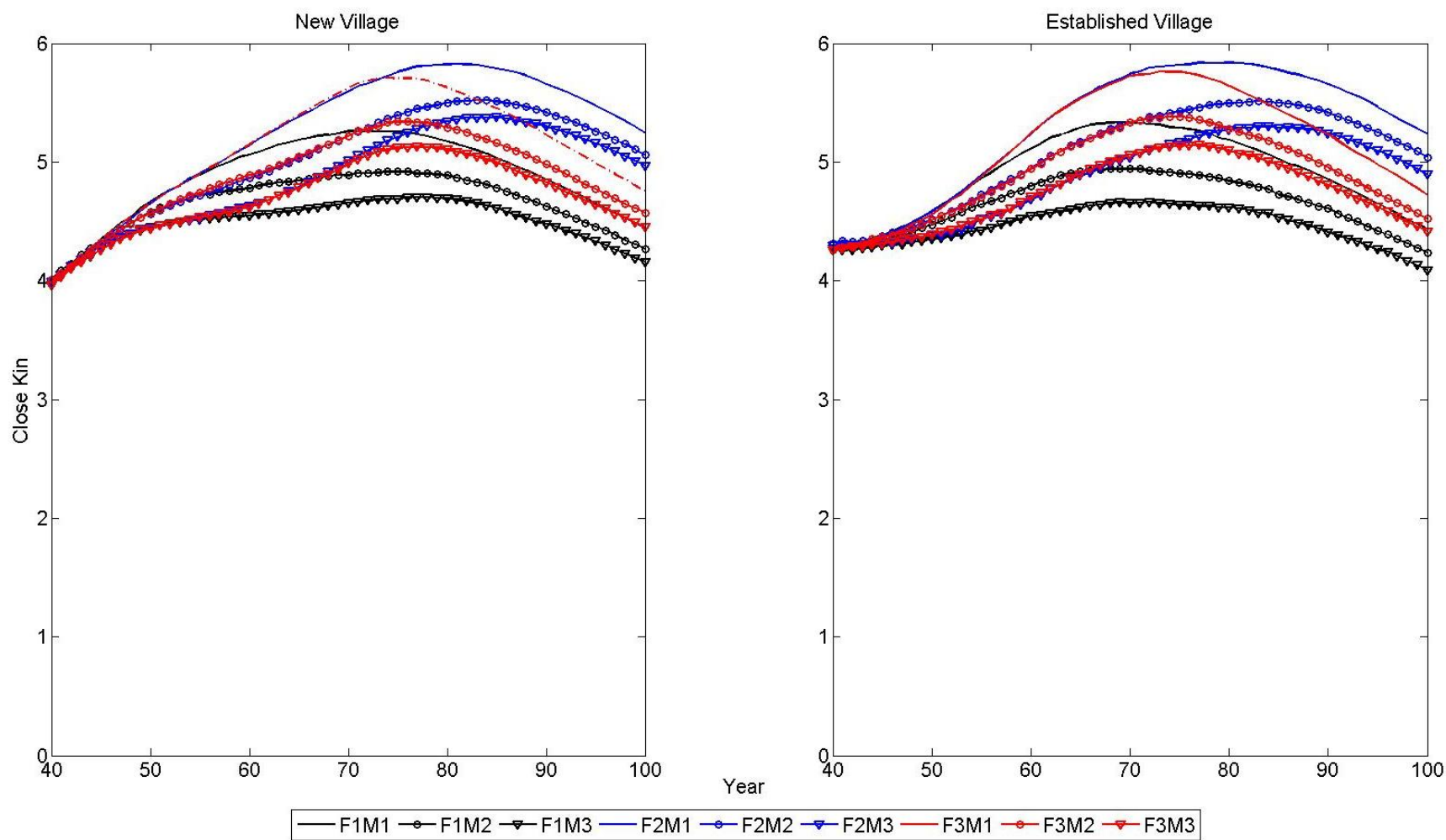
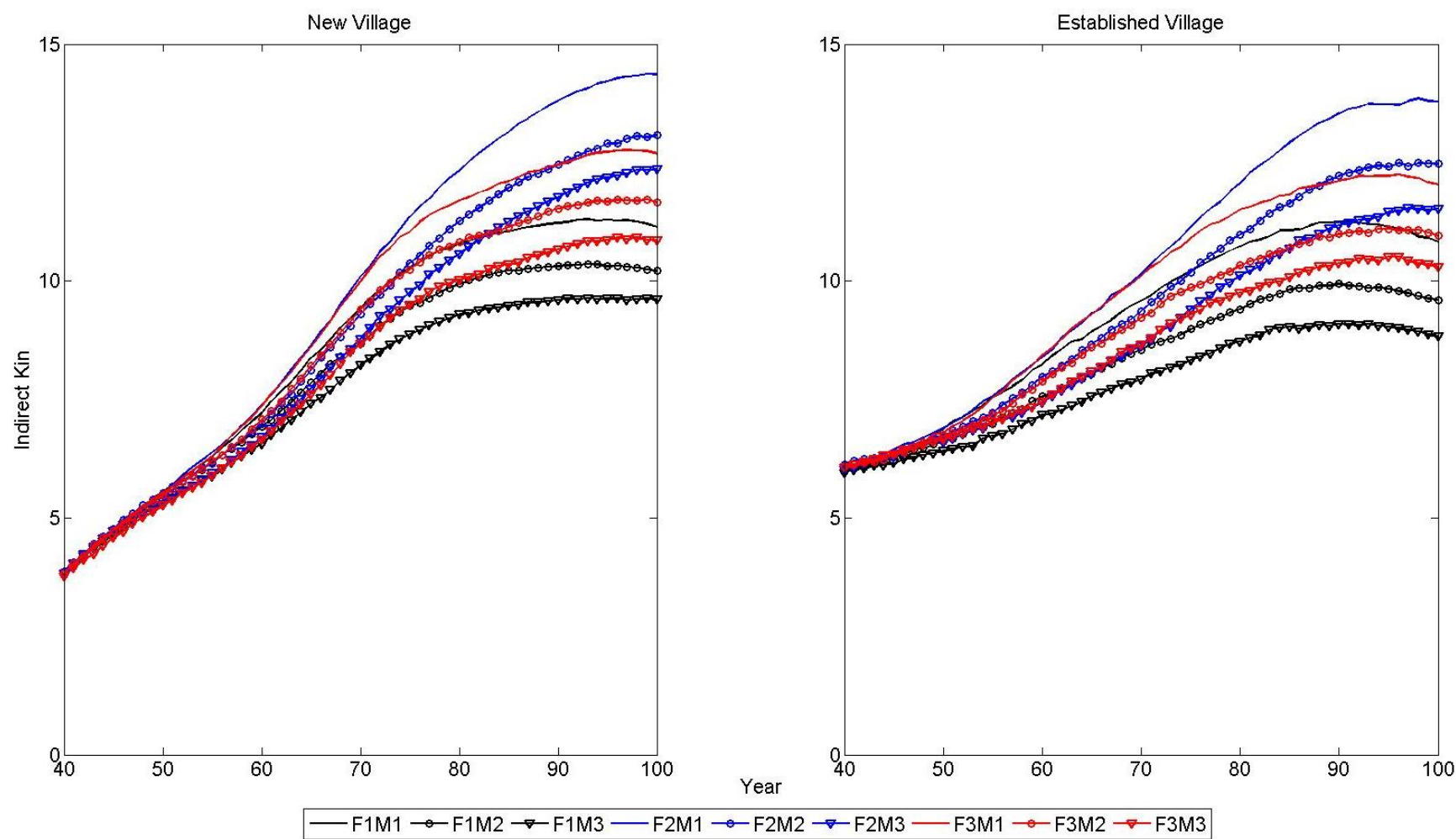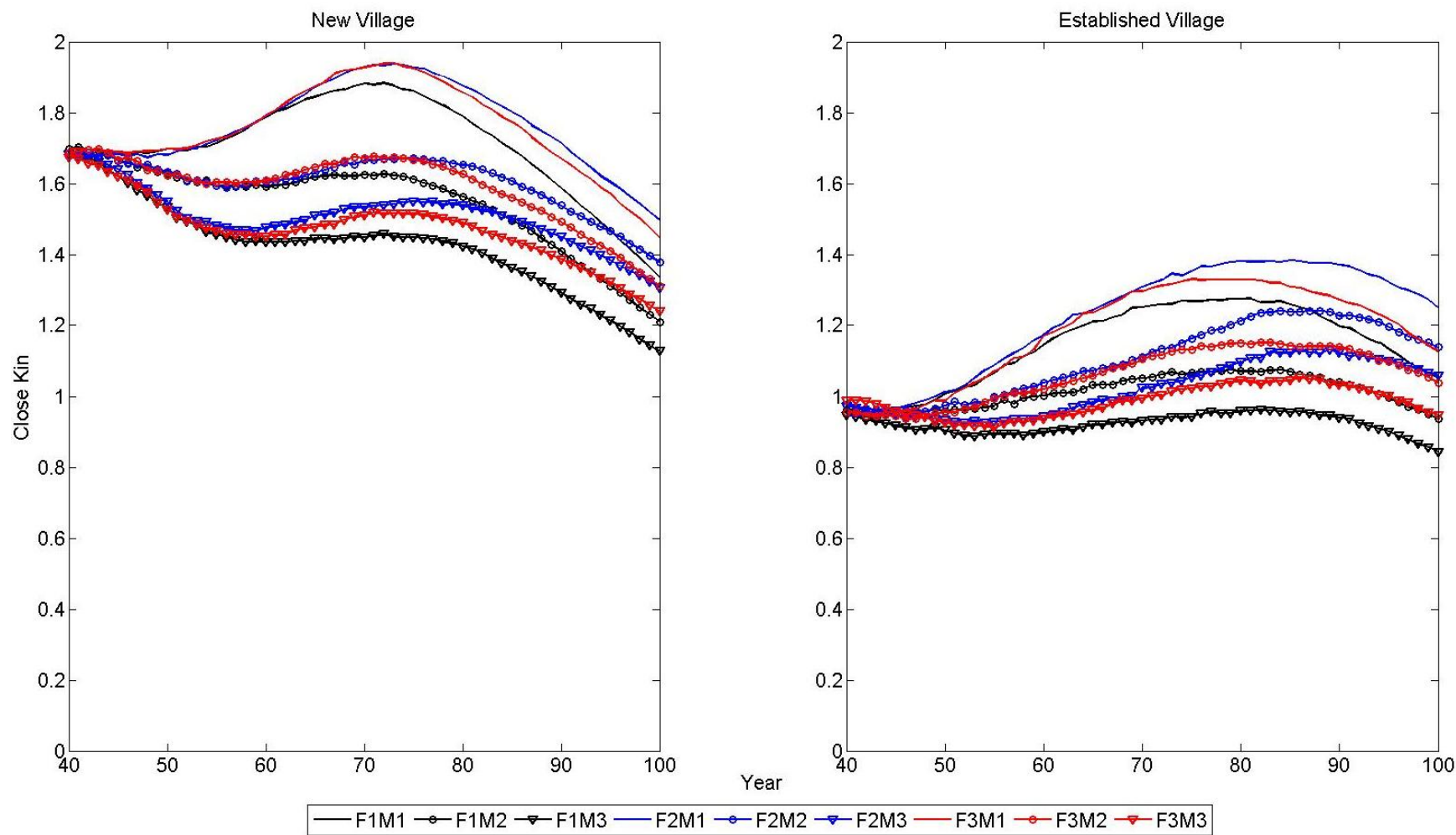**Figure 3. Trends in indirect kin over time by fertility and mortality scenario and initial village.**

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.

Region/ country	Total fertility (If)	25% (If)	40% (If)	Years 10% to 40%
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

T able A1 continued.

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
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

T able A1 continued.

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 heterogenous 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[11] – 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 terms of fertility preferences is also treated as heritable[12]. 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:

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

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

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11 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.

12 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.

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 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 nQx 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[13]. The specific life expectancy

parameters used in each scenario can be seen in figure 2.

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

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13 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.

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[14]. 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

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14 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.

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 20th 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 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) $R_a = \dfrac{N_a}{P_a}$,

where N_a is the number of migrants of a given age and sex, P_a is the number of

individuals of a given age and sex in the population, and R_a 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) $N_a = P \times M \times N_a$,

where *P* is the total population, *M* is the proportion of the population that are migrants

(the parameter which I later manipulate), and N_a 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[15], 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) $R_a = \dfrac{P \times M \times N_a}{P_a}$,

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

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15 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.

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

neither of these can be done it is assumed that the children are hosted by distant kin or

friends of the family[16]. 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[17]) 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

16 Note that these chidlrens' 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 to be assigned to parents.

17 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.

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 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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