BORDER DEMOGRAPHY AND BORDER MALARIA AMONG KAREN POPULATIONS ALONG THE THAILAND-MYANMAR BORDER

A Dissertation in
Anthropology and Demography
by
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ABSTRACT

International borders and the regions that encompass them sometimes have demographic and epidemiological characteristics that differ from non-border regions. The reasons for these differences are quite complex. International borders are sometimes the meeting point of different cultural and linguistic groups. They are the gates through which the “have-nots” pass as they attempt to achieve economic stability or increase their economic standing. Frequently, international borders are regions with special economic zones or with businesses that cater specifically to people on the other side of the border. Finally, these regions are also a bottleneck through which many human migrants pass. These and many other factors influence the age and sex structures of border populations; the movement patterns and spatio-temporal distributions of those populations; and furthermore, influence the disease burdens of these populations.

The international border between Thailand and Myanmar (formerly Burma) is an excellent case in point. In this dissertation I examine ethnic Karen border populations and their malaria burdens from a demographic, anthropological, ecological, and epidemiological perspective. The dissertation uses data collected through a U.S. National Institutes of Health grant (grant number: NIH U19AI089672) and the Southeast Asian International Center for Excellence in Malaria Research and is divided into two major themes: human demography and disease ecology. The first section concerns the demography of ethnic Karen populations along the Thai-Myanmar border. The second major theme concerns the ecology and epidemiology of border malaria in a Karen village along the Thai-Myanmar border.

My major findings are that household demography is a strong predictor of migration and that seasonal migration in Karen villages exhibits some degree of spatial synchrony.
Furthermore, I find that border malaria is at least partially related to problems associated with asymptomatic carriers, misdiagnoses, and the socio-political context that exists along this border.
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Chapter 3, “Household ecology and out-migration among ethnic Karen along the Thai-Myanmar border”, is a multi-authored work that has just recently been accepted for publication. I am the first author on this work, with James Wood, Shinsuke Tomita, Sharon DeWitte, Julia Jennings, and Liwang Cui all being coauthors (in this order). As first author, I conceived the project, helped to collect some of the data, created the statistical models and sensitivity analyses with the help of coauthors, wrote the first draft of the paper, and wrote the final revision of the paper.

Chapter 4, “Border malaria: detection, spatial patterns, and risk factors for infection in a malaria foci on the Thai-Myanmar border”, will also be a multi-authored paper but has not yet been submitted for review. I will be the first author on the paper, which will also include Stephen Matthews, Liwang Cui, Jeeraphat Sirichaisinthop, Jetsumon Sattabongkot, Guiyun Yan, and Guofa Zhou. I conceived this research project, did the statistical analysis and mapping, wrote the first draft, and will write the final draft when coauthors have provided comments and suggestions.
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I’ll close by noting that my biggest debt of gratitude must go to my wife (Amber) and son (Salem). They’ve endured my trips to the field, my workaholic tendencies, and my many arguments with computers and software programs. Both have been through lots of ups and downs through these years and they’ve helped me work my way through it, being sources of constant strength and support. I can’t imagine a stronger team anywhere on the planet.
CHAPTER 1: Introduction, goals, and organization

This dissertation is an attempt to understand the demography, the spatial and temporal population dynamics, and the malaria epidemiology of several ethnic Karen border populations along the Thai-Myanmar (formerly Burma) border. Population movement and ecology have previously been implicated as important factors in the distribution and spread of malaria in this region (Somboon et al. 1998; Bhumiratana et al. 2013; WHO 2010). The overarching goal was to better understand the potential relationships between these aforementioned factors and persistent border malaria in this region. This research was based on a National Institutes of Health grant for the Southeast Asian International Center for Excellence in Malaria Research (ICEMR). Demographic and epidemiological surveillance systems were established in four Karen study villages for the ICEMR project. Based on the resulting data, this research has implications for anthropological, demographic, geographic, disease ecology, and epidemiological research and theory. The dissertation is made up of three main chapters, presented as publishable manuscripts, as follows.

Chapter 2, “Human migration and spatial synchrony: spatial patterns in temporal trends”, touches on theory and method in spatial population science. This research looked at out-migration in the ICEMR study villages from two different temporal perspectives: age “risks” of migration and time-series migration. Borrowing some theory and methods from population ecology, I looked at potential spatial synchrony in both age and time-series patterns in migration across the four study villages (Bjørnstad et al. 1999).

Chapter 3, “Household ecology and out-migration among ethnic Karen along the Thai-Myanmar border” was an investigation into household and individual level predictors of out-migration in the aforementioned Karen study villages. Household level factors included
household size (number of household members) and the consumer-producer (C/P) ratio 
(Chayanov 1966) while individual level predictors included age and sex. Given that C/P ratios 
are notoriously difficult to estimate empirically (Kramer 2005; Lee & Kramer 2002), I included a 
sensitivity analysis of the model results with regard to the C and P weights.

Finally, Chapter 4 (“Border malaria: detection, spatial patterns, and risk factors for 
infection in a malaria foci on the Thai-Myanmar border”) was an attempt to better understand the 
phenomenon commonly referred to as border malaria in the literature about malaria in Thailand. 
Drawing on more detailed data from one of the four study sites, I investigated differences in 
diagnosis success between field microscopists, an expert microscopist, and PCR diagnosis. I 
then drew on the migration data used in Chapters 2 and 3 to test for a potential correlation at the 
individual and household levels between migration and malaria. Using a mixed effects logistic 
regression, I looked for risk factors in malaria infection (based on PCR-confirmed Plasmodium 
vivax cases), and looked at space-time patterns of infections by household within the study 
village. As far as I am aware, this is the most detailed, micro-scale spatial analysis of border 
malaria in this region to date.

Chapter 5 summarizes the dissertation, discusses some of the limitations in this work, and 
then points to some future directions for research that will address some of those limitations as 
well as build on and fill in some of the important gaps in this research.

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CHAPTER 2: Human Migration and Spatial Synchrony: Spatial Patterns in Temporal Trends

INTRODUCTION

Demographic research is almost always focused on temporal processes in populations. At its core, demography is concerned with changes in populations, frequently but not always focusing on fertility, mortality, and migration. These changes take place over some unit of time, meaning temporal dynamics are inherent and quite often are explicitly modeled in demographic analyses. However, these processes don’t take place in the absence of geography and demographers aren’t only interested in temporal dynamics, they are increasingly interested in spatial dynamics too (Wachter, 2005; Voss, 2007; Porter & Howell, 2012; Matthews & Parker, 2013). Things that are close in geographic proximity are often more alike than things which are geographically distal, and temporal trends are typically tied to the spaces and places in which they occur (Tobler 1970). Population densities in geographically proximate populations may rise and fall in synchronous fashion or conversely may have opposing patterns altogether. Mortality rates in neighboring regions can be extremely similar as can fertility and migration rates. This spatial synchrony or spatial covariation may be the result of several factors, including the socio-cultural characteristics of a region, the natural or built environment, or even epidemiological factors.

Perhaps migration offers one of the most readily available examples of demography as an inherently spatial science. Migration is unique as a topic of interest to demographers as it is necessarily a spatial process (Wachter 2005). That is, in order to migrate, one must physically move from one place to another. This spatial process is also somewhat defined by its temporal component. Some migrants move permanently while on the other end of the spectrum, many
people make almost daily physical moves to another location (e.g. to school, to work, etc). Both long and short term migrations\(^1\) occur heterogeneously across populations, with different age or sex groups moving at different rates, distances or even directions, and for different reasons. Furthermore, migration *rates* may cluster within or across regions, populations, and subpopulations (e.g. ethnicity or age groups). For a host of reasons, migration is therefore intrinsically wedded to other aspects of spatial demography.

Merging theory and empirical data is important for any scientific discipline. Theory in demography differs in its approach when compared to theory in other disciplines, perhaps because it describes general processes rather than attempting to explicitly describe why those processes occur at an individual basis. Some have even claimed that demography is a method without a theory (see Burch 2003). Perhaps, however, this comes from a narrow view of what theory is, as demography explains, usually through models, the ways that populations behave and the age schedules that are associated with life events in populations (Burch 2003). Malthus’ theory of population growth, Lotka’s model of stable populations, Thompson’s demographic transition model, and Henry and Coale’s work on fertility in “natural” populations are all examples of demographic theory (Malthus 1817; Thompson 1929; Lotka 1939; Henry 1961; Coale 1971). Demography does have theory; however that theory differs from the theory that most demographers learn in their sister, social science disciplines which are typically focused on the components of populations rather than the whole.

That most students of demography are dually trained, both in demography and in another social science disciplines, also makes demographers and demography unique because the field is inherently multidisciplinary. Demographers also have much in common with population

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\(^1\) Short-term migrations may also be referred to as human mobility or circular migration and in population ecology parlance, dispersal.
ecologists and population biologists. And while populations are a topic of interest that shouldn’t have to be married to another discipline in order to warrant study, this common arrangement leads to a deep understanding of the processes being studied\(^2\). Demography helps us understand population processes whereas our social science backgrounds help us understand, from more micro-level standpoint, why people do the things that they do. Ultimately, demographers are well-suited for deriving explanations for overarching population processes, and perhaps especially for merging theory with empirical data.

I therefore begin this chapter by drawing on some theory behind the mechanisms and causes of spatio-temporal population dynamics, using migration as a substantive topic. I look at both age-specific and repeated cross sectional data as two different focal points for understanding human migration and movement patterns. While short term movements aren’t typically discussed at the same time as migration, I am here considering all ranges of human movement, or dispersal in population ecology parlance, with permanent migration being a special subcategory of human movement. In order to illustrate the merging of empirical data and theory, I then draw on data on a highly mobile ethnic group (the Karen) in Southeast Asia. Then I close with a discussion on some new and old issues related to spatial demography, namely: issues of scale and future directions in spatial demography.

**Spatial Synchrony**

Populations that are related geographically can simultaneously be affected by macro-scale processes. For example, a contraceptive policy rolled out in a developing region might lead to decreasing fertility throughout that region. Separate, yet geographically proximate subpopulations within that overarching region may exhibit strong synchrony in decreasing

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\(^2\) Nathan Keyfitz, arguably among the most influential demographers, was a strong proponent of this line of thought. While his PhD was in Sociology, he collaborated with population scientists from quite a wide array of disciplines, including population biology (e.g. Keyfitz & Haswell 2005).
fertility rates even if other factors vary in those subpopulations. Furthermore, we might expect to see decreasing synchrony between subpopulations that are further and further away from each other, especially since at some point we would be comparing populations that are no longer covered under the same contraceptive policy. Essentially, we might expect to see time-series trends that are very similar for populations that are more proximate than those which are more geographically separated (spatiotemporal autocorrelation). Similar examples could be given using meteorological factors (rain and ambient temperature) in agricultural populations, epidemiological landscapes (which are also influenced by environmental factors), macro-scaled economic policies, political factors, and educational schedules, all of which can and likely do influence human demography.

Given a long set of observations (time series data) there are various methods, both parametric and nonparametric, for measuring correlations between distance and synchrony (Liebhold et al. 2004). Early methods for assessing synchrony included plotting and visually inspecting data. Another simple method is to look for correlations between time series data, using Pearson’s product-moment or Spearman’s correlation coefficients, or the lag-0 cross-correlation coefficient. Linear decay models have been used to investigate decreasing synchrony with increasing distance. A nonparametric model might be more suitable to complex distance–synchrony relationships. For example, Bjørnstad & Bolker created a method that compares smoothing splines across landscapes (Bjørnstad & Bolker 2000). Methods for detecting and measuring more complicated forms of spatial synchrony have also been created. For example, a plot of synchrony over distance sometimes reveals waves in distance-synchrony relationships (Lieberman 1993). Such waves can also move over time, leading to a phenomenon referred to as travelling waves, of which the speed and sometimes points of origin can be determined. Such
traveling waves have been applied to several substantive areas of research, including the 
epidemiology of measles, dengue, and influenza, as well as other host parasite and predator prey 
relationships (Bjørnstad et al. 1999; Grenfell et al. 2001; Cummings et al. 2004; Stark et al. 
2012). Some researchers have also used phase analyses to calculate correlations and measure 
lags between peaks in time series data (Cazelles & Stone 2003).

There are both mechanisms and causal factors that can lead to such synchrony. With 
regard to mechanisms, Moran\(^3\) showed early on that two populations with the same density 
dependent relationships (i.e. the relationship between population growth and population density 
is the same) can exhibit population synchrony through correlated density independent factors 
(such as meteorological events) (Moran 1953; Royama 1992; Bjørnstad et al. 1999; Hudson & 
Cattadori 1999). The so called “Moran effect” suggests that the correlation between the 
population densities \(p_d\) of two populations is equal to the correlation in their environments \(p_e\):
\[
p_{d} = p_{e}. 
\]
Moran was concerned with the population dynamics of the Canadian lynx \((Lynx 
canadensis)\) with regard to meteorological factors; however, it is not hard to imagine situations in 
which density independent factors (several of which I previously mentioned) influence the 
dynamics of human populations as well. Conversely, dispersal may also influence populations 
by making them more homogeneous, though this factor can be complicated by assimilation and 
acculturation in humans (Ranta et al. 1995). Some studies have shown that while migrants often 
arrive in a new nation with the fertility rates of their nation of origin, they quickly assimilate to 
the fertility rates of their destination (Parrado & Morgan 2008; but also see Frank & Heuveline 
2005). The same has also been shown with regard to health (Abraído-Lanza et al. 1999).

\(^{3}\) Patrick Alfred Pierce Moran also developed the Moran’s I statistic, a commonly used measure of spatial 
autocorrelation.
The causes of such synchrony are multifold and may be extremely complex. However, while causal factors in the synchrony of population dynamics have been among the most vexing of issues for population ecologists, some of the factors leading to spatial covariance and population synchrony in human populations are intuitive. Socio-cultural, economic, and political factors that influence population dynamics can be inferred through social science studies. The trick then becomes wading through the overabundance of information, the numerous different potential contributing factors, to arrive at an understanding of what led to the population dynamics of interest. However, when such dynamics co-vary spatially, we should at least be able to narrow down those factors which are shared by populations with shared dynamics. Are there external density independent factors that are shared by populations? Or are the populations in fact virtually the same because of the mixing of ideas and even population members?

Models that incorporate both space and time in demography have historically been lacking. Most explicitly incorporate time or space at the expense of the other. Arguably, models that incorporate a spatial component are far outnumbered by those with temporal components in demographic research. Spatial synchrony can perhaps offer a theoretical and methodological bridge, by simultaneously linking space and time, when spatially referenced time series data are available.

Is migration law-like? Mathematical descriptions of migration

Demography is now mostly a statistical science, but at least some of the founders of modern demography saw it as a mathematical science too⁴ (Burch 2011; Romaniuk 2011). Consider Lotka’s mathematical theory of stable populations and Keyfitz’s contributions with regard to sensitivity analysis, population dynamics, and applied demography (Lotka 1939; Romaniuk 2011).

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⁴ In fact, Lotka saw the study of human populations as being divided into mathematical demography and statistical demography.
Keyfitz & Caswell 2005). Another place where demographers have incorporated mathematical methods is in modeling age patterns of demographic events such as mortality, fertility, and finally migration; applying mathematical functions that describe the shape of age-specific curves in demographic processes.

Some life events have such strong age-specific characteristics that it makes sense to create a model schedule of events for comparisons and investigations into deviations from the norm. Mortality is probably the best studied of these model schedules; however, Rogers and Castro (1981) extended this approach to migration (Rogers & Castro 1981). Generalizing from the age profiles of internal migrants from several Western world settings, they created a set of four multiexponential model migration schedules. In the general model there are 11 parameters, seven of which specify the shape of the migration curve by age and four that describe the intensity of migration by age. The most common components of these models (see Figure 2.1) describe the decrease in high migration from early childhood (when children are moving with their parents in the formation of new households) and a rise in migration during the working and marrying ages. Some models also have “retirement” peaks in later age groups (Raymer & Rogers 2008).

Age-specific rates of migration aren’t the only thing that varies. The different components of these model schedules can be considered individually with regard to whether or not the reasons for migration in each component are the same as well as whether or not they consist of dependent (as with migration in very young ages) or independent (occupational migration) migrants. An analysis of the life course can therefore inform or explain a given schedule of migration. Finally, while this general pattern in age-specific migration may approach a socio-cultural universal, there are likely to be subtle differences in the migration
schedules of different regions of the world, which have different population structures, different societal norms, and different economic and political factors.

**Temporal Patterns in human migration and movement**

Humans (and other animals) make permanent, seasonal, monthly, even daily or hourly movements. Sometimes there are rhythms in those movements, with schedules based on seasons, daylight, and holidays leading to synchronous movements within and across populations. With regard to short-term movements, consider rush-hour traffic in which many people leave their households to spend much of the day in a location that may be many miles away from their household. Later in the afternoon swarms of people leave work to return home. College students may leave home in early fall and return in the winter. Agricultural workers follow seasonal harvests for their livelihoods, repeating harvesting cycles year after year.

Each of these suggested movement patterns are driven by macro-scale factors such as daylight and seasons, which are shared across large geographical spaces. This means that movement patterns may appear synchronous across those geographical spaces that share the same sunrise and sunset times, the same seasonal patterns, or the same time zones, or across regions with shared holidays and a number of other factors. While there are always exceptions to these trends and synchronies, these general patterns are quite predictable over time.

Space and time also intersect in other interesting ways, for example, with regard to interactions between frequency, distance, and travel times (Hägerstrand 1970). Trains, airplanes, highways, and automobiles have made it much easier to travel farther distances in shorter amounts of time. But constraints do remain. Travel distance is directly related to travel...

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5 Some holidays are highly localized (consider Juneteenth in Texas or Patriots day in Massachusetts and Maine), whereas others have an extremely broad range (i.e. New Year’s day, Christmas, etc.)

6 There is a literature concerning “Time Geography” that is relevant to this and is of general interest with regard to space-time interactions (Hägerstrand 1970).
time, though the relationship between these two factors has changed much over the last couple of centuries. Travel frequencies aren’t likely to be very high when travel time is very long (Hägerstrand 1970). For most people, short term movement patterns such as those that occur daily, are likely to occur relatively near the home (Wang et al. 2011). More long term patterns aren’t quite as constrained by this trend, and permanent moves are likely at present to be more constrained by social networks, information, and economic circumstances than physical ability (Pred 1977). While the ability to travel literally around the world is now much easier than it once was, doing so frequently remains unlikely.

**Why does migration happen?**

Migration occurs for many complex reasons, and a comprehensive examination of the motivations, drivers, and reasons behind migration is beyond the scope of this chapter. However, as previously mentioned, demographic analyses are frequently supported by drawing on social science theory in order to attempt to explain why people do what they do. In that spirit, I briefly touch on several theoretical explanations for migration motivations, but will only be able to scratch the surface. Early models for explaining migration focused on large areal units and comparative inequalities that either pushed would-be migrants away from regions with scarce materials or pulled them to regions that are relatively rich in materials (Muth 1971; Fields 1976). However, researchers noted the extreme heterogeneity in migration processes, even within the same migrant groups, destinations, and places of origin. Not all people migrate, not all migrants follow what appear to be logical migrant streams. The focus therefore shifted to individual-level theories that were still primarily focused on economic factors (Todaro 1980; Stark & Bloom 1985). Most of these models looked at the decision to migrate in a cost-benefit balancing framework, where the benefits (real or perceived) outweigh the costs of making a
move. However, while individual migrants can and do act as their own agents, they are also embedded in households, families, neighborhoods, communities, villages, and regions (De Jong & Gardner 1981; Portes & Sensenbrenner 1993). The context in which an individual would-be migrant lives, or is exposed to, matters in migration decisions. Context can be cumulative and can change over the course of a lifespan, as can individual wants and needs, meaning that a life course approach to understanding migration decisions is valuable (Howell 1981; Howell & Frese 1983). Further extensions in migration studies have considered social and cultural factors, as well as gender, in migration processes (De Jong et al. 1996; Curran & Saguy 2001). Each of these aspects may influence not only the decision to migrate, but also who migrates, where they go, when or if they will return, if they send home remittances, etc. Similar factors also influence general human movement patterns at very short (daily) or seasonal patterns (Winterhalder & Smith 1992; Wang et al. 2011).

Many of these considerations are arguably more about place than space, though there are clear interactions between the two. That is, the characteristics of a place can influence the migration situation in that place. As alluded to above, areas with relatively poor natural resources might act as “push” factors, leading people who live in such areas to migrate out at higher rates than in other regions. People living in unsavory conditions, for example, in areas with high crime, with warfare, with poor health conditions, etc., may also be more likely to at least attempt to move away. However, social scientists will note that this effect can be extremely heterogeneous, with some individuals remaining in such areas despite the obvious attractions of leaving.

Another related consideration that is perhaps more commonly discussed among mathematical demographers and population ecologists concerns density dependence in
migration. More than a few studies have looked at the potential for population density to influence all sorts of population processes (Wood et al. 1985, 2014; Relethford 1986; Caswell 2006). For example, regions with high population densities may have low per capita resources, leading to higher rates of out-migration, sometimes referred to as Allee effects (Allee & Bowen 1932). Some researchers have even proposed that finding marital partners will be more difficult under some density situations, which could also lead to either in- or out-migration (Mielke et al. 1994; Swedlund 2009). While such factors can influence human migration, they aren’t likely to be completely deterministic. Socio-cultural factors can be and are extremely powerful.

For example, post-marital residence rules influence out-migration and dispersal patterns. Historically speaking, most people did not move very far from their place of origin. Marriage was typically with someone from nearby, and neolocal households didn’t stray very far from the couples’ houses of origin (Wijsman & Cavalli-Sforza 1984; Coleman & Haskey 1986; Harrison 1995; Fix 1999). Transportation has changed this pattern, to some extent and especially in some societies, quite drastically (Harrison 1995). Virilocal\(^7\) post-marital residence patterns, in which newly married couples live either with or very near the male spouse’s family, will lead to interesting patterns in population dynamics, perhaps especially spatially. Most populations practice some form of exogamy, meaning that there are rules about who to marry and proscribing marriage with people who are too closely related. At the same time, most populations also practice some form of endogamy. Most people don’t marry people that are too different from themselves. Therefore we might expect to find situations in which individuals choose to marry people who don’t live too far away from their home or family of orientation, but far enough so as not to be breaking incest taboos. In a virilocal society, then, females who out-migrate at

\(^7\)Here I use the terms virilocal and uxorilocal rather than patrilocal and matrilocal, respectively. My reasoning is that the terms patrilocal and matrilocal assume a unilineal descent system, which is not always the case.
marriage are likely to move further away than are males. The opposite case would occur in uxorilocal societies, with dispersal being more geographically widespread for males than for females.

**SPATIAL AND TEMPORAL VARIATION IN KAREN MIGRATION**

**Ethnic Karen along the Thai-Myanmar border**

The Karen are the largest ethnic minority in Thailand, and one of the largest ethnic groups in Myanmar (formerly Burma) (Rajah 2008). They are primarily subsistence agriculturalists, meaning that they are largely dependent on the rice that they grow themselves, though they are far from isolated from the Thai economy. Their dependence on agriculture means that work is highly seasonal, with high intensity working periods at the beginning and end of the rainy season, corresponding to land clearing, planting, and harvesting crops (Kunstadter 1972, 1983).

The Karen have also been engaged in low-intensity warfare with the Myanmar government (Lee et al. 2006) for around half a century but have been at peace for the last year. Many Karen fled their ancestral lands in Myanmar for the relative safety of Thailand. In some cases, thousands of Karen refugees have flooded across the border in short periods of time, crowding into large refugee camps along the Thai-Myanmar border (TBC 2004). There are also much smaller movements, with individuals, families, and villages relocating across the border.

In all cases, there are reasons to return to Myanmar for various amounts of time. For example, many Karen have family and friends remaining on the Myanmar side of the border. Holidays and down times in the agricultural year are times when Karen from Thailand may travel back to Myanmar to celebrate and to visit friends and family. Furthermore, some Karen actually farm plots of land in Myanmar. The international border is only marked by a relatively
small river in many regions, and unused land on the Myanmar side of the border can offer a source of rich soils for farming.

Finally, some movements among adolescents and children are related to schooling. As agriculturalists, the Karen of Thailand mostly inhabit rural areas in Northwestern Thailand. Schooling is important to the Karen; however, there are few local schools for students beyond age 14, when secondary schooling begins. This means that many children travel to regional secondary schools and frequently stay in school dorms for the duration of the semester. As previously mentioned, migration motivations and dynamics may vary by age group. In the case of adolescents in secondary school, there is seasonal migration that does not exactly correspond to seasonal migration in adults who are tied to the land.

The long international border (over 2000 kilometers) between Thailand and Myanmar is difficult to police, and the region is known as a hub for the illegal trade of narcotics (the “Golden Triangle”), precious gems, lumber, cattle, and humans (Lintner 2000). This means that there is a relatively large amount of clandestine movement across the border, not only by merchants in the black market economy but also by Karen who simply walk across the unguarded border to visit Myanmar. It also means that for many reasons this place, which has no well-defined borders, provides a contextual environment that is highly conducive to heavy flows of human migrant traffic. Much of this movement is temporary, but there can be considerable variation in the duration of travels. Since the Karen are tied to the land because of their dependence on agriculture, much of this movement can be expected to occur seasonally.

**Analysis and results of Karen out-migration**

My research among the Karen of Thailand looks at the influence of household and individual-level factors on demography and epidemiology. In 2011, as part of a large, National
Institutes of Health initiative for understanding and controlling malaria in this region, demographic and epidemiological surveys were undertaken in each of four Karen villages along the Thai-Myanmar border. The villages are arranged from North to South with about 35 kilometers separating the northernmost from the southernmost village (Figure 2.2, Table 2.1). Full censuses are taken twice yearly and every other week a mobile health team moves through the villages, going house-to-house, asking about any new additions to households (in-migrations or births) as well as any missing individuals from households (out-migrations and deaths). Those who have moved out of a household and aren’t expected to return within a month are coded as out-migrants. These are the individuals (out-migrants) who are in the subject of the following analysis, with time-series data for 13 months.

The temporal component of migration is multi-dimensional: migration may occur more frequently during certain times during the life-span as well as during certain times of the year. We can therefore think about temporal trends in migration from both cohort (age-specific) and repeated cross-sectional perspectives. While there are general trends in both sets of temporal dynamics (age and the calendar year), the difference between the two is striking. Age schedules of migration strongly conform to each other, whereas the time series trends are more loosely coupled. That is, correlations are much stronger between the life span data of the four study villages when compared to the time series migration data from those same villages.

From Figure 2.3 we can see a small dip in out-migrations in children approximately five years old, followed by a steep rise in migration rates among those around age twenty. Afterward, migration rates slowly taper off throughout the rest of the life span. These data conform relatively well to those plotted in Figure 2.1, as expected from previous work on model schedules of age-specific migration (Rogers & Castro 1981). Comparisons across the villages
indicate that peak migration rates are lower in the two villages with smaller overall population sizes, but that the temporal dynamics are largely mirrored across all four villages. This could potentially indicate some density dependence in out-migrations with regard to age. At least some previous research has indicated density dependence in migration rates (Wood et al. 1985; Relethford 1986; Mielke et al. 1994; MacDonald & Hewlett 1999; Umezaki & Ohtsuka 2002).

Table 2.2 lists pairwise Spearman’s rank correlation coefficients for age-specific rates of out-migration between the villages, indicating high correlations between all combinations of the four villages. \(P\)-values for these correlations are likely to be unreliable because of both spatial and temporal dependence. Conversely, the seasonal dynamics of out-migration appear to vary more widely across villages, perhaps especially among those which are furthest apart geographically (Figure 2.4). The two villages that are closest together (3 and 4) appear to have the most consistently correlated trends (from Figure 2.4 and Table 2.3), followed by village 2 and 1.

I then created a distance matrix based on spatial coordinates (distances between each combination of village centroids); a difference matrix based on average village elevation, between each average village elevation; and correlation matrices for both age-specific and time series out-migration between each village (correlograms for each matrix are shown in Figure 2.5). Next I used Mantel tests to look for correlations between the distance, difference, and migration correlation matrices. Mantel tests provide a means of statistically testing for correlations between matrices. In this case, the tests looked for correlations between sets of vectors which were assigned to each village, with the vectors indicating relationships between villages based on geographic distance, as well as correlations between elevation, age-specific out-migration, and time series out-migration. The Mantel tests provide both a correlation coefficient and \(P\)-value. I used a Monte-Carlo permutation approach for calculating \(P\)-values.
Each matrix was permutated 9,999 times and the original test statistic (coefficient) was compared to the distribution of permutated test statistics in order to calculate the $P$-value (Tables 2.4, 2.5).

**Discussion**

The age-specific patterns in migration indicated in these data are roughly shared with many other societies (consider the model schedule in Figure 2.1). Macro-level factors that extend further than the units of study in this brief analysis probably influence these trends in age-specific out-migration. This is interesting for a variety of reasons that I previously alluded to, perhaps especially because it points to law-like patterns in the behavior of human populations. Also, while these patterns are shared across so many societies, the components of the migration schedule can generally be broken down into different causal factors for each component of the model schedule. Migration for the very young is likely to occur for different reasons than migration in the elderly. Very young children are typically moving with their parents, school-aged children may be moving out to go to school, young adults are likely to move out for marriage or work, and elderly people may move back in with family members or to new places after retirement. My findings with regard to the Karen villages in this study further add credence to the idea that age-specific migration is almost law-like in its shape across the life span.

While the figures illustrating time series migration treat the populations within the villages as homogeneous, the motivations and drivers of such migration may vary. Perhaps the two biggest factors to consider in the Karen case are seasonal migration, which occurs during times of the year when there is little agricultural work, and the timing of the school year for secondary students (Figure 2.6). Migration that corresponds to the agricultural calendar is hereafter referred to as “seasonal” migration. Such seasonal migration in these populations can mostly be subdivided into two main types: occupational and marital. Seasonal marriage has been
noted in many agricultural populations, with peak marriage times occurring during lulls within the agricultural calendar, frequently following the harvests or livestock birthing seasons (Kussmaul 1985; Wrigley & Schofield 1989; Coppa et al. 2001; Gonzalez-Martin 2008). Occupational migration is also likely to occur during these downtimes, with Karen adults sometimes selling their labor or engaging in various forms of trade (Rajah 2008). Conversely, migration of secondary school children out of the household necessarily follows the school calendar (Figure 2.6). School calendars are roughly coordinated throughout Thailand, meaning that there should be a relatively synchronous out-movement of children as they begin the school semester. Children in rural areas may be more likely than those in urban areas to attend boarding schools and live in or near the school since there are fewer local schools in those regions. In summary, the rising peak in age-specific migration rates (from around age 12 – 17), occurs for different reasons (probably schooling) than does migration from 18 until older ages (probably post-marital residence and occupational migration).

While the study villages aren’t very far removed from each other geographically, meteorological patterns can vary widely across such relatively small regions. If migration is seasonal, as it appears to be, and if meteorological factors in more proximal villages are more similar than in more distal villages, the patterns shown here may simply coincide with shared macro-level drivers: the Moran effect. One assumption behind the Moran effect is that the population process being observed is density dependent. As previously mentioned, several studies have indicated density dependence in migration patterns. For example, in very small populations there will be a limited amount of potential mates, meaning that marriage aged adults will need to move out in order to find marital partners (Relethford 1986). Conversely, in areas with large populations there may be resource shortages, also potentially leading to out-migration.
(Umezaki & Ohtsuka 2002). Clearly population density is unlikely to be the only important factor in migration, and it may even result in differing dependence relationships in different regions, societies, and cultures (Ohtsuka et al. 1985). However, with regard to the Moran effect, we might expect that different populations with the same density dependencies will experience synchrony in population processes (in our case, migration) when a common macro-level factor affects those same populations. While not confirmatory of density dependence, in the data presented here the largest peaks in age-specific migration are seen in villages with the largest populations (3 and 4, see Table 2.1).

Finally, villages 3, 4, and at least part of 2 share a common secondary school in another village further south of village 4. Children attending secondary school in village 1 also move out to live in dorms when school is in session, but they go to different schools. There may be variations in academic calendars in these different schools, though those differences are unlikely to be large.

**SCALE (IN BOTH SPACE AND TIME)**

It has been argued that issues of scale, specifically scale and pattern, are the “central problem of ecology” (Levins 1992). I would argue that it is also at least a central problem in demography, not just spatial demography. While I have already briefly mentioned issues of scale, especially with regard to macro-level drivers in spatial synchrony, the issue isn’t limited to space and definitely warrants further discussion. Issues of scale with regard to spatial analysis have been known for some time. For example, ecological analyses have famously been poor predictors of individual outcomes (the ecological fallacy) and the spatial unit that is chosen in a study will almost certainly influence the outcomes of that study (themodifiable areal unit problem) (Robinson 1950; Openshaw 1984).
Scale is also important in temporal dynamics, and the choice of scale can likewise influence analytical results. Some population processes, for example, occur at temporal scales much larger than even typical longitudinal studies (let alone cross sectional studies). Evolutionary changes in populations and population adaptations to climate changes via resettlement and changes in subsistence strategies are but a few examples. Some processes occur at the temporal scale of multiple generations or even longer, rather than a more typical temporal units such as years used in demographic analysis. Other processes occur in very short temporal intervals. As previously mentioned, rush hour traffic is the byproduct of short term, quite predictable, human movements. A study on such short term human movements would be impossible if data were collected or analyzed at longer time scales. Likewise, what happens hourly may not have as much relevance for evolutionary change in human populations.

This concept isn’t new to demography. For example, Lotka showed that populations will ultimately reach a stable equilibrium growth rate over time. However, Lotka (and Coale) were also concerned with short term dynamics, and were leery of focusing solely on long-term equilibria, especially when considering demographic dynamics that occur in shorter wavelengths (Lotka 1939; Coale 1972; Caswell 2007). Likewise, applied ecologists have had similar concerns in that the dynamic behavior frequently encountered in nature or over a person’s lifespan has less to do with long term (asymptotic) dynamics than with short term (transient) dynamics (Koons et al. 2005; Ezard et al. 2010). Sensitivity and perturbation analyses, along with tests of ergodicity, have indicated that while asymptotic dynamics tend to be insensitive to initial conditions, transient dynamics are very much influenced by the initial state (Caswell & Werner 1978; Caswell 2007). In short, what is important in long-term dynamics might have less importance in short-term dynamics, and vice versa.
Clearly, scale is important for both spatial and temporal analyses. But how do we know which scale, or since we are considering spatio-temporal analysis, which scales, are the correct ones to use? There is no simple answer. In the previous study I chose villages as my units of analysis, assuming that each village is a separate population. I have also used bi-weekly migration rates on the one hand, and age-specific rates\(^8\) on the other, as temporal units. Other analysts might choose to lump all villages within the region, and others still might instead use the entire district, province, or even nation as their spatial unit. Many demographic analyses conveniently use the year as the basic unit of time.

Probably, the choice of spatial and temporal units should be informed by both the study question at hand and theoretical knowledge. In my case, I am interested in potential synchronous behavior across four study villages, at relatively fine-tuned moments in time. Other researchers might instead be interested in larger units and larger populations and processes that occur over longer periods of time. At least theoretically, a prior understanding of the scale at which processes occur should aid in deciding at which scale that process is investigated. It is also important to consider that fine-scale data can potentially be aggregated. It may be impossible to adequately disaggregate data collected at very long intervals.

Take, for example, a hypothetical situation in which household wealth directly influences household member out-migration. If a researcher looked at daily household spending and earning she might find equivocal results whereas if the researcher were to look at monthly or yearly savings she might find a strong, dose-response-like association. This is because the effects of wealth aren’t generally instantaneous, they happen over a period of time. Perhaps it is important to consider here that the daily information could potentially be aggregated up to the

\(^8\) With 5-year age groups in order to control for potential age-heaping in self reported ages among survey respondents.
appropriate temporal scale of months or years but disaggregation is unlikely to work as well. Theory would probably tell us a priori that the effect of wealth (or a lack of it) on the chances that a person migrates is a process that would probably take months or more before leading to an actual migration result. In the absence of a theoretical response, a related approach would be to specifically test for the effects of different time scales – with the end result being theory building or improving.

Conversely, there are methods and techniques that have been designed for defining “natural” populations. Wombling, for example, is a technique that is sometimes used to help define natural boundaries via changes in traits such as allele frequencies in populations (Womble 1951). Briefly, a bilinear function is applied to lattice data in order to create a smooth surface and to calculate vector gradients or surface slopes. Wombling has scarcely been applied to demographic research (but see Bocquet-Appel and Jakobi 1996). However, it has been proposed that wombling could be used with survival data, with wait times as the quantitative trait of interest: “wombling for wait times”.9

I leave it to the readers and researchers to decide whether it is more appropriate to define a population a priori or via direct methods such as wombling. Such a decision will depend, once again, on the research question at hand. As wombling is a method for defining “natural” borders, and therefore populations, it will necessarily identify relatively homogeneous populations. If heterogeneity within a population is actually what is of interest, then it might not be an appropriate approach.

Regardless, the spatial unit that is chosen is critical for research design and will influence analysis outcomes. A real problem in spatio-temporal analyses, and perhaps especially in

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9 Ottar Bjørnstad gave a talk on “wombling for wait times” at an NSF meeting on “Challenges in Modeling the Spatial and Temporal Dimensions of the Ecology of Infectious Diseases” at Ohio State University (Sep. 18, 2012).
demography, is that disaggregated units like the ones used in this chapter are frequently unavailable. Furthermore, the choice of spatial and temporal unit is sometimes driven not by theory or research question but instead by census tracts, ZIP codes, largely arbitrary district, county, provincial borders (Matthews 2011). Countless large-scale demographic analyses are flawed by the inability of demographers to draw data at the correct spatial (and temporal) scale. Conversely, there are real limits to the ability to collect fine-scaled data on large populations, meaning that such data for the types of populations that most demographers enjoy studying are simply unavailable. I’m not sure that these problems can be assumed or ignored away.

CONCLUSIONS

GPS and “big data” are both increasingly available to population researchers. Arguably, both have the possibility of strongly influencing the future landscape of demography and spatial demographic research. Data that were once only time stamped may now also have spatial references, meaning that spatial relationships can be analyzed in themselves or that unobserved spatial heterogeneity in processes can at least partially be controlled. Furthermore, increases in data availability mean that research projects and topics that were once almost impossible are now increasingly feasible. An obvious example mentioned earlier concerns near real-time human movement patterns which can now be mapped using GPS units or cell phones.

Yet, the availability of such data also presents hurdles that must first be overcome. Chief among these hurdles are the technological and computational burdens associated with extremely large datasets. These technological issues are quickly being addressed and in my opinion, will not remain a significant issue for long. However, demographers who intend to use big data will almost certainly need to learn new approaches to data management, wrangling, and analysis.
Furthermore, big data doesn’t only have technological problems; there are tangible theoretical issues as well. Perhaps most of these issues are related to the nature of secondary data use in research. Demographers are probably more comfortable with using secondary data sources than are many researchers in other fields, but issues of data quality, hidden biases, and operationalization remain. Also, having more data isn’t always a cure for problems that are inherent in research questions or design. But with the hype surrounding big data, it is quite possible for researchers to think it is such a cure. A carefully designed study, with a small but properly collected and representative dataset, will probably always be superior to the use of extremely bulky, biased, secondary data for ad hoc research questions – no matter how big the size of the latter dataset.

Along with new data collection methods and ultimately new datasets comes the need for new developments in ethics and policy. Current ethics policies are likely to be based on research scenarios from the past (Howell & Porter 2010). Some issues remain the same, but the vast changes in the potential amount and variety of data collected now make confidentiality and safety in research today much different. While ethics policies first need to be updated to deal with modern realities, perhaps a framework that inspires such policies to continually be updated, as research approaches and data capabilities change, should also be considered. Changes in technology and research are now occurring so quickly that by the time ethics and policy are changed to address these changes, it will likely already be time to change them again.

These issues aside, new forms of data also provide new opportunities, not just for addressing theoretical issues but also for creating new methods. Not that long ago, true spatio-temporal analysis, that is, statistical approaches that equally dealt with space and time, were virtually non-existent. Most space-time analyses addressed either space or time explicitly, and at
the expense of the other dimension. This is no longer the case – methods for dealing with space
and time simultaneously have been proposed, are increasingly available in standard statistical
software programs, and continue to develop and emerge. Spatial synchrony, introduced earlier in
this chapter, is just one example. Wavelet analysis and wombling are other approaches that are
quite relevant to space-time modeling.

Aside from borrowing techniques used in other disciplines, the time is also ripe for the
emergence of new methods for analyzing large space and time datasets. Here, with a lot of
cumulative experience as data scientists, spatial demographers could have a big role to play.
Software packages such as R, which are free and open source, make experimenting and
operationalizing new analytical approaches quite approachable, even for researchers with little
training in computational sciences. Ultimately, for ambitious and inspired researchers and
methodologists with an eye toward the future and with something to offer, the horizon appears to
be wide open.

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**Figure 2.1** A typical model schedule for age-specific migration from Stockholm, 1974 (Reproduced from Rogers & Castro, 1981).

**Figure 2.2** Study villages
Figure 2.3 Age-specific migration across the study villages. a. raw data, b. raw data fit to a smoothing spline function with 10 degrees of freedom.

Figure 2.4 Trends in crude out-migration in the study villages over the survey period: a. raw data, b. raw data fit to a smoothing spline function with 10 degrees of freedom
Figure 2.5 Correlogram indicating: a. distances between villages, b. correlations in elevation between villages, c. correlations in out-migration over time between the study villages, and d. correlations in age-specific out-migration between the study villages. Darker shades indicate higher correlations, lines pointing up and to the right indicate positive correlations.
Figure 2.6 Agricultural and school schedules.
Table 2.1 Village Characteristics

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<th>Village</th>
<th>Altitude (meters)</th>
<th>Population</th>
<th>Households</th>
<th>People/House</th>
<th>% Female</th>
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<td>5.56</td>
<td>51</td>
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Table 2.2: Spearman correlation coefficients for age-specific migration rates between the study villages

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<th>Spearman's</th>
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<th>Village 2</th>
<th>Village 3</th>
<th>Village 4</th>
</tr>
</thead>
<tbody>
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<td>Village 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
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<td>Village 2</td>
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<td>Village 3</td>
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<td>Village 4</td>
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<td>0.93</td>
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Table 2.3: Spearman correlation coefficients for period-specific migration rates between the study villages

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<th>Village 2</th>
<th>Village 3</th>
<th>Village 4</th>
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Table 2.4 Mantel test results for age-specific migration

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<th>P-value</th>
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<td>Elevation</td>
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Table 2.5 Mantel test results for time series migration

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CHAPTER 3: Household ecology and out-migration among ethnic Karen along the Thai-
Myanmar border

INTRODUCTION

Studies of migration in small-scale, indigenous agricultural populations are important not
only for demographic research, but also for understanding the mechanisms behind the
distribution of populations across landscapes and the spread of infectious diseases (Fix 1999;
Ferrari et al. 2008; Stoddard et al. 2009). For example, because migration, like many
demographic behaviors, is not uniform by age (in many populations, age-specific migration rates
tend to be highest among young adults and their dependent children), migration can have
significant impacts on the age structure of both the source and receiving populations (Rogers &
Castro 1981). For certain infectious diseases, such as malaria, migration across international
borders is a key factor of pathogen reintroduction and constitutes a major challenge for the
elimination of infectious diseases (Tatem and Smith 2010). However, migration in small
agricultural populations remains an understudied demographic processes, especially in
developing countries and remote regions (Massey and Espana 1987; Curran 2002; Entwisle et al.
2008). Detailed migration data in rural developing areas can be difficult to come by for several
reasons. First, some migration is illegal, making documentation difficult. Second, migration
opportunities may arise suddenly, meaning that people with no prior intention to migrate may
quickly change their minds. Third, a lack of resources and physical infrastructure (roads, etc.)
makes it difficult to carry out migration surveys. Fourth, many migrants in Sub-Saharan Africa,
Southeast Asia, and Latin America are also ethnic minorities who live on the margins of society,
meaning that taxpayer money is unlikely to be directed toward their concerns.
A variety of cultural, social, epidemiological, political, and economic factors can influence migration decisions (Muth 1971; Fields 1976; Todaro 1980; De Jong and Gardner 1981; Stark and Bloom 1985; Sassen 1988; Portes and Sensenbrenner 1993; Curran and Saguy 2001). Socio-cultural norms dictate marriage patterns with respect to both age and post-marital residence rules. The epidemiological landscape of a region might influence settlement and migration patterns, and could potentially lead to out-migration from a region that is especially burdened with disease. In modern times, national governments are likely to have legal restrictions on where a person can travel and settle. Foreign nationals, for example, may need special documentation for moving legally across international borders and even with documentation may be restricted in their ability to settle in foreign nations. And, of course, the importance of economics cannot be overemphasized in migration decisions. Migrants in poor rural areas may be drawn to relatively wealthy urban areas (Muth 1971; Fields 1976; Todaro 1980; Stark 1991). Even within relatively homogeneous rich or poor regions there can be spatial heterogeneity in resources, potentially leading to micro-level movement.

Demographic researchers have attempted to use migration models to describe the migration process, and those models can be classified broadly by their unit of analysis. For example, several early models were macro in scale, focusing on the economics of entire nations or even multi-national regions (Muth 1971; Fields 1976). In the latter case, poor nations may act as sources of migrants whereas wealthy nations may act as sinks for them. Over time, the focus on macro-scale models was largely replaced by a focus on micro-, individual-scale models (Sjaastad 1962; Lee 1966; Todaro 1980; Stark and Bloom 1985). This change of focus largely followed the realization that migrants are not homogenous. That is, not every person in a poor region migrates and, in fact, some people who live in wealthy regions migrate as well. A variety
of factors have been considered in micro-level models, including the lure of increased capital and the escape of poor economic conditions, as well as the draw of migration flows that are already in place (e.g. cumulative causation) (Massey and Espana 1987; Massey 1990; Bohra-Mishra and Massey 2011). Finally, some more recent models have realized that there is an important middle ground in the level of focus with regard to migration models. Individuals live in households, communities, villages, cities, and regions; these higher levels of organization, and the interactions within them, should not be ignored (De Jong and Gardner 1981; Portes and Sensenbrenner 1993). All these factors are likely to be important in influencing migration decisions.

With regard to anthropological demography, perhaps the most fundamental demographic unit to consider is the household. Households are clearly composed of distinct individuals, but individuals do not have their own demography, and economic strategies are arguably made mostly at the household level,\(^\text{10}\) perhaps especially within small-scale, indigenous farming communities in developing-world settings (Netting 1982, 1993; Wood 2014). In such populations, individual well-being, which in the most basic sense means the ability feed oneself, can be attributed largely to household farming success or failure. In the absence of alternative subsistence strategies, individuals who live within farming households that are experiencing shortages in food or other resources suffer the consequences of those shortages. Conversely, individuals who live in households with an abundance of resources are likely to benefit from that abundance.

Household surpluses and shortages are not only a function of agricultural production, they are also related to the demographic structure of the household. One measure of the

\(^{10}\) Remittances to households are also an important factor, meaning that even family members outside of the household can contribute to household economies.
demographic structure of a household is the consumer-producer (C/P) ratio. A.V. Chayanov (1925, 1966) was probably the first person to calculate C/P ratios and include them in a model of household economics. Chayanov was largely interested in Russian peasants and was essentially looking at dynamics in peasant productivity over the long-term (several decades) and in terms of large-scale population and economic dynamics. However, Chayanov’s C/P ratios are also a measure of individual household well-being in a Malthusian sense, as they can also indicate inadequacies of productive capacity within the household resulting from changes in household age and sex structure over time.

A few studies have actually looked at C/P ratios with regard to household dynamics and household wellbeing over time (Lee and Kramer 2002; Hammel 2005; Lee and Campbell 2007; Sparks, Wood, and Johnson 2013; Jennings et al. 2011). For example, households that have recently been established by a newlywed couple will have low C/P ratios. In many rural and agricultural societies, offspring will be born into a household within a few years of its establishment, resulting in a fairly rapid increase in the C/P ratio. As those offspring grow into adolescence, they begin to contribute more to the household economy, and the C/P ratio decreases once again. Finally, assuming that all offspring eventually move out as the original household founders age, the original founders will enter into senescence and once again the C/P ratio will increase as they are less capable of contributing to their own household economy than they were as young adults (Lee and Kramer 2002; Hammel 2005).

Household characteristics can therefore have profound implications for household members. For example, the age and sex structure of a household may be important with regard to migration decisions. For individuals who live in resource-poor households, migration may offer a new source of economic subsistence. Conversely, individuals from poor households may
not have the resources necessary (travel costs, etc.) for migrations. Ultimately, a household's membership size, relative wealth, and the age and sex of inhabitants may be important with regard to household-member nutrition, longevity, marriage practices, and potentially migration (Gage et al. 1996; Garnier et al. 2003; Madhavan et al. 2009; Hadley et al. 2011). At the same time, migration itself will influence the household’s subsequent C/P ratio, and this fact may play a part in the decision to migrate.

**Objective**

Previous research in the developing world has shown that household characteristics such as dependency or C/P ratios, household size, and relative household wealth are strong predictors of demographic and health outcomes. For example, some research has indicated that households may regulate their size and age structure, especially with regard to working-age adults, through the migration of their members (Katz 2000; Madhavan et al. 2009; Hadley et al. 2011). Not all household members contribute equally to the household economy and not all consume equally from the household bounty. As an extreme example, migrants who are away from home yet sending back remittances may consume none of the household’s food store while still contributing to that store. Households with relatively limited and constrained resources, and with more consumers than producers, may also be more likely to have household members either suffer poor nutrition or move out of the household (Benefice, Cames, and Simondon 1999; Garnier et al. 2003). Furthermore, households with excess producers may also be more capable of coping with the loss of extra producers. How household economic crises (e.g. the loss of household producers) are handled is likely to be construed, in part, through cultural and societal norms.
Of course, not all migration or population movement is the result of household crises. Historically, some populations have been mobile for subsistence reasons. For example, many hunter-gatherers engage in seasonal mobility strategies to exploit game and other resources while avoiding resource depletion in any one area (Lieberman 1993). Similarly, some pastoralists migrate with their livestock in pursuit of fresh pastures. Also, many young adults leave home in order to establish their own households or to join other households through marriage, regardless of subsistence strategy. In regions where schooling is available but not local, school-age children may move out of the household at the beginning of the school year or term. The demographic profile of the household members who move out in each of these cases is likely to vary according to the reason the person has left and by cultural norms (Rogers and Castro 1981; Behrman and Wolfe 1984; Jacobsen and Levin 1997; Curran and Saguy 2001). In this paper we explore the potential influences of household and individual characteristics in household out-migration in four ethnic Karen villages along the Thai-Myanmar border in Tak Province, Thailand. We use mixed-effects survival models to examine the influence of various covariates on the hazard of leaving a household (out-migration).

**Study population**

The Karen are one of the largest ethnic minority groups in both Myanmar and Thailand and they inhabit both sides of the Thai-Myanmar border. An accurate census in Myanmar has not been conducted since the 1930s, and current estimates of the total Karen population vary between 3 and 7 million (Barron et al. 2007; United Nations High Commissioner for Refugees 2007). Over the last half century the Karen have been engaged in periodic warfare with the ruling government in Myanmar (Burma), and at times there have been mass evacuations of Karen from the Myanmar side of the border to the relative safety of Thailand. Many Karen
therefore live in refugee camps on the Thai side of the border, whereas others continue to live in rural agricultural villages or in cities in both Myanmar and Thailand. As of January 2013 over 100,000 Karen were living in refugee camps on the Thai side of the border (The Border Consortium 2013). According to the 2010 Thai Census, approximately 440,000 people reported usually speaking Karen in their homes (Office of National Statistics, Thailand 2010).

The Karen are subsistence farmers who have, over the last several decades, also become more engaged in Thailand’s market economy. While the bulk of agricultural efforts for most Karen in this area remains irrigated-rice production for household subsistence and local consumption, some now grow produce for export and others hire themselves out as agricultural laborers. Several researchers have done work on Karen socio-cultural patterns, health, and demography (Kunstadter 1972, 1983; Nakano 1980; Skeldon 1985; Walker 2001; Omori and Greksa 2002; Lee et al. 2006; Rajah 2008). Most of the detailed demographic work concerning the Karen was conducted by Kunstadter and colleagues during the mid- to late-20th century. Kunstadter’s work was broadly focused on population dynamics and agroforestry (Kunstadter 1972, 1983). Little work has been done on migration among the Karen, but Kunstadter suggested that Karen migration was limited in its geographic range (1972). Males commonly moved out of their villages for marital purposes, typically moving to or near their female spouse’s family household. Labor exchanges between households related by kinship were also common and would occur seasonally according to the agricultural calendar (Figure 3.1). Household formation is also heavily influenced by cultural norms. The “ideal” household, according to research done by Kunstadter and fieldwork conducted by the author, consists of a married couple and their children, as well as the spouse of their youngest married daughter and
the children from that marriage. Older daughters and their families may also live nearby (Kunstadter 1984).

Most of these generalities hold true today, though the political and economic realities under which the Karen currently live obviously influence migration and movement patterns. The international border is extremely porous and movement across it is frequent. Karen villagers from the Myanmar side visit weekly markets on the Thai side and many of the Karen who live on the Thai side frequently visit relatives and friends on the Myanmar side. Also, the abundant resources in Myanmar, including lumber, precious gems, and cattle, lead many people (some of whom are Karen) to move across the border surreptitiously. Some even maintain farming plots on the Myanmar side of the border. Such extra-legal movement can be difficult to document and quantify. Finally, while the Karen are primarily subsistence farmers, they are not isolated from the larger Thai and Myanmar economies. Rather than being tied solely to the household and its agricultural plots, household members are aware of, and take advantage of, outside economic opportunities. Many will exploit these outside opportunities in order to diversify the household economy, providing a buffer against instability in household food stores and income. Those migrants who remain tied to their agricultural households are likely to migrate during off-peak times of the year, when agricultural work is less strenuous and their labor is not immediately needed (Figure 3.1).

METHODS

Data

Our data come from a U.S. National Institutes of Health-funded project that is aimed at controlling malaria in the Greater Mekong Subregion of Southeast Asia (Cui et al. 2012; Cui et al. 2012). Four study villages have been selected along the Thai-Myanmar border, ranging in
size from 500 to 2000. All the study villages were on the Thai side as access to the adjacent part of Myanmar is restricted. The villages were selected because of their history of malaria caseloads (this area has some of the highest estimated incidences of malaria in Thailand) as well as their willingness to participate in the research. Full demographic surveys have been carried out in the villages twice, listing the number of individuals in each household by name, sex, and self-reported age and assigning a unique identification code to each individual and to each household. Follow-up surveillance, which began in October 2011, is conducted every two weeks and will continue for several years. The data used in this paper cover the period October 2011 through November 2012. During the surveys, healthcare fieldworkers moved through each of the villages, going from house to house recording health status and changes in household size and composition (which were coded as resulting from birth, death, in-migration, or out-migration). When a household member who had been given an identification code during the initial census was not present in a household, the field workers asked other adult household members about their status. Remaining household members were specifically asked how long the absent household member was going to remain away from the household. Household members who were not expected back within four weeks were coded as out-migrants. Our migration data are therefore interval-censored, in that we know a migration occurred during a two-week window, but we do not know exactly when in that two-week window the migration occurred. Covariates included individual, survey week, sex and age, the number of individuals within a household, and the household C/P ratio (estimated as discussed below). Since a household’s size and C/P ratio are affected by the subtraction of a household member resulting from out-migration, we included a two-week lag for those two household predictors to avoid simultaneity effects.
We acknowledge that our measure of migration (based on leaving for an expected one month period of time) is relatively arbitrary and that there are several other household-level factors that are not included in our data that are likely to be important with regard to migration decisions. The goal of the project (so as to distinguish it from this specific research) was to analyze temporal age and sex patterns in malaria infections within and across the study villages rather than to analyze demographic outcomes.

Statistical analysis

We used piecewise mixed-effects logistic regression to model the hazards of individual out-migration with respect to household-level predictors. The logistic model, including a random intercept, is:

$$\log \left( \frac{p_{it}}{1 - p_{it}} \right) = \alpha_{hi} + \beta_1 x_{i1} + \ldots + \beta_k x_{ikt}$$

where $p_{it}$ is the conditional probability that the $i$-th individual will move out of his or her household ($hi$) during a particular two-week observation window $t$, $\alpha_{hi}$ is a random-effect intercept allowing for unobserved heterogeneity among households, and the $\beta$s are the estimated regression coefficients for the covariates ($x$). The random intercept $\alpha_{hi}$ is assumed to have a normal distribution with mean $\mu_\alpha$ and variance $\sigma^2_\alpha$, “hyperparameters” to be estimated directly from the data. We used the transformation $100(e^\beta - 1)$, to estimate the percent change in the odds of an out-migration event for every unit increase in that particular covariate.

Since migration intensity may vary over the study period, possibly increasing after agricultural work is done, we tested two different specifications for time, linear and quadratic, using Akaike information criterion (AIC) and Bayesian information criterion (BIC) to assess the two specifications. The linear effect of time proved to be a better fit. Furthermore, migration
patterns, motivations, and drivers can vary strongly by age (Rogers and Castro 1981). We therefore stratified our model by age groups, running separate models for those aged 0 – 12, 13 – 69 and 70 plus (Table 3.1), in order to account for age in our models. Finally, we standardized household C/P ratios (mean = 0 and standard deviation = 1) to facilitate interpretation of model estimates. The lagged household covariates were used to examine potential correlations between the household size and C/P ratio from the previous survey (two weeks prior) and their effects on the probability that a household member had moved out by the time of the current survey.

**C/P weights and sensitivity analysis**

Some previous studies have used dependency ratios (usually defined as the ratio of household members ages < 15 and > 65 to those ages 15-65) as an indicator of household demographic pressure on economic and demographic behavior (Reyna 1976; Hadley et al. 2011). However, dependency ratios assume that children and elderly household members do not contribute to the household economy but only take from it. There is a wealth of literature indicating that this is not the case (Caldwell 1976; Cain 1977; Lee and Kramer 2002), though the contributions of children are usually smaller than those of their parents (Kaplan 1994; Stecklov 1999). Thus, to calculate the C/P ratio of each household, each household member is assigned a weight for C and for P (separately) according to their age and sex. The resultant C/P ratio of a household is arguably a better measure of household economy than is the dependency ratio. Furthermore, a high C/P ratio can indicate Malthusian stress within the household, where there is more consumption need than there is production capacity.

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11 Since migration occurs for a variety of reasons, it is an oversimplification to treat migration events as identical. A competing risks model might therefore be a better model for understanding different types of migration. However, our data do not allow us to classify different migration types. We know that an individual has left the household, but we do not actually know why. We hope to rectify this deficiency in future research.
A particularly vexing and intractable problem with regard to this weighting scheme, however, is the question of how we actually estimate C and P for one particular study population. At least one intensive ethnographic study has attempted to create precise calculations for the C/P ratio (Kramer and Boone 2002; Lee and Kramer 2002; Kramer 2005), but even this excellent effort is in many ways deficient and therefore unconvincing. Given the importance of C/P ratios and the unknown nature of the actual weights, we created a set of rather arbitrary but plausible weights for each of eight age and sex groups (Table 3.1) for both consumption and production, i.e. a total of 16 weights. Our initial weights were roughly based on Karen Kramer’s intensive ethnographic work with the Maya (Kramer and Boone 2002; Lee and Kramer 2002) as well as Nakano’s fieldwork with the Karen (Nakano 1980). We then implemented a “bootstrap-like” simulation method to test the sensitivity of our model results to errors in our assumed C/P ratio weighting scheme. Each simulation drew pseudorandom numbers for weights based on a uniform distribution; we based ranges for the uniform distributions on Lee and Kramer’s (2002) empirical data from the Maya (Table 3.2). Pseudorandom numbers were drawn for each age and sex group and separately for C and P, weights were then applied to those age and sex groups, and the survival models were estimated using the randomly-drawn weighting scheme. At the end of a model run, the process began again, with a new set of pseudorandom weights assigned to each age and sex group. Each simulation was run for 500 iterations for each age stratum of the survival model. The results from our simulations consisted of a distribution of coefficient estimates for the effect of household C/P ratio on the log odds of out-migration.
RESULTS

Summary statistics

Out of 181,073 distinct observations from the censuses and prospective demographic surveillance, our dataset included 1,604 out-migration events, 924 (58%) of them male and 680 (42%) female. Figure 3.2 illustrates the age and sex patterns of out-migration across the four study villages. At most ages, males migrate more often than females. However, this pattern is most pronounced between the ages of 15 and 50. Female out-migration peaks around age 15 whereas male out-migration peaks around age 20. After age 15, female out-migration quickly decreases whereas high male migration is sustained between ages 15 and 25. These age- and sex-specific patterns in migration follow well-described age-specific schedules of migration in an almost universal pattern (see Rogers & Castro 1981).

Survival models

The effect of time (survey week) in each of the models was negligible (Tables 2.3 – 2.5). Sex, household C/P ratio, and household size all showed relatively strong effects. For children under age 13 (Table 3.3), the effect of household C/P ratio was both strong and positive ($\hat{\beta} = 0.12; 95\% \text{ CI: } 0.08, 0.16$), that is, it increased the odds of an out-migration event. The effect of household size was also strong and positive. The addition of one household member resulted in a 30% increase in the odds of a household member under age 13 moving out. Not surprisingly, sex appears to have no effect on out-migration in children.

In stark contrast to the model for children, the model for working-age adults (ages 13 through 69 (Table 3.4)) indicated a strong negative relationship between household C/P ratio and out-migration ($\hat{\beta} = -0.63; 95\% \text{ CI: } -0.73, -0.53$). The effect of household size remained strong and positive, indicating a 24% increase in the odds of an out-migration with the inclusion of one
more household member. Also, an individual’s sex was a relatively strong predictor of out-migration within this age group, with females being about 39% less likely to move out when compared to males.

Our model for elderly out-migrants (Table 3.5) suffered from a small number of cases, with only 19 out-migrations over the study period. Standard errors and coefficients were too similar to warrant direct interpretation of our model results with this age group.

In summary, in our models for children and adults, households with more members were more likely to experience individuals moving out. Also, the effect of C/P ratio is strong in both child and adult out-migration, but the direction of the effect differed (positive for children, negative for working-age adults). Finally, working-age females were much less likely to migrate out than were working-age males.

Sensitivity analysis

Our sensitivity analyses indicate the robustness of our survival models with regard to the effect of C/P ratio on out-migration (Figures 3.3 – 3.5). Across the 500 simulated models for children under age 13, the mean effect size for C/P ratio was 0.15 (min = 0.02 and max = 0.33) (Table 3.6, Figure 3.3). If we were to take 0.15 as the true coefficient size, it would indicate a 16% increase in the odds of an out-migration with an increase of one standard deviation in a household C/P-ratio. We should note than such an increase in the C/P ratio is an extremely large change. The mean coefficient size for working-age adults was -0.61 (min = -1.24, max = -0.01) (Figure 3.4). The mean coefficient size indicates a 46% decrease in the odds that an individual will move out with an increase of one standard deviation in household C/P ratio. Finally, our simulation results with regard to elderly out-migrants further indicates the lack of predictive
power for this model stratum (Figure 3.5). The distribution of estimated coefficients straddles zero, with an average coefficient of -0.05 (min = -3.95, max = 1.94).

CONCLUSIONS

Several previous researchers have investigated potential influences of C/P ratios on various demographic and economic outcomes. However, our model specifically investigated the relationships between household dynamics and C/P ratios, over time, with regard to out-migration. To our knowledge, this is the first time that this substantive topic has been investigated.

Our statistical models revealed several interesting things. For example, it appears that at least some of the migration at younger ages in our study villages is related to schooling (Figure 3.1). While there are local primary schools, older students must travel from their natal villages to attend secondary schools. Some secondary schools are boarding schools, meaning that children will reside at the school location until the end of the term. Most migration at younger ages is dependent on adult (parental) migration. In our dataset there were very few cases of children under age 5 who moved out without there also being one or two adults from the same household who moved out – which we interpret as parents leaving with their dependent children. We found no difference in sex with regard to out-migration in children less than 5, and we believe that this is an intuitive finding: parents take both sons and daughters with them.

Larger households and households with higher C/P ratios were more likely to experience childhood out-migration. This finding may be related to the age structure and family dynamics of household members as well as socio-cultural patterns and norms. For example, many households in our study villages consist of multiple nuclear families. As those families grow, one family may move out to create its own household. Previous research in Karen villages
indicates that having more than two reproductive-aged couples in a single household is undesirable (Kunstadter 1984; Rajah 2008). An older daughter whose nuclear family is sharing her parent’s household may be required to move out when a younger daughter subsequently marries and moves in. In such cases, there are often young children who also move out with the couple. We expect that such households would include more household members and have higher C/P ratios (with more children and elderly household members).

Conversely, our model for adults found a strong association between sex and out-migration. Migration in working-age adults within our study population can be broadly split into two groups: those related to marriage and postmarital residence, and those related to occupation and economic opportunities. Both have gender- or sex-specific patterns. For example, the Karen have traditionally been uxorilocal (Rajah 2008); that is, males who marry are likely either to join the household of the female spouse’s family of orientation or to establish a new household near her family’s house. However, this pattern does not fully explain the out-migration we are seeing in our study villages. It is likely that many of the young females (around 15 years old) who are moving out are also doing so for marriage, despite uxorilocality. This may be consistent with a society that is acculturating to surrounding socio-cultural groups, and with traditions that are either changing or are loosely enforced. Furthermore, while postmarital residence probably does explain some of the out-migration we are seeing, it may be a small fraction of the total. For example, those adults who are moving out with children are also leaving households with high C/P ratios. Since they (adults moving out of households with their children) make up a small minority of the overall group of adult out-migrants, the effect of the C/P ratio on adult out-migration continues to be negative.
Much of the adult out-migration in our dataset is probably attributable to economic factors and, in some cases, to breaks in the agricultural calendar. Our models suggest that, aside from being mostly male, adult out-migrants are more likely to come from households with more household members and low C/P ratios. We interpret both of these household-level factors to reflect the household economy, more specifically, the household work force. Households with few “producers” and many dependents, and therefore a high C/P ratio, are unlikely to have “extra” workers who are free to move out for any reason. In other words, households with high C/P ratios are already constrained to the point that the loss of a household producer could have severe consequences. For example, households with a single parent and several children, or with elderly grandparents taking care of their grandchildren, are unlikely to have adults move out.

These findings are relevant to migration theory that deals with migration, economics, and household level factors. For example the New Economics of Labor Migration (NELM) model proposes that migrations are the result of household-level decision making and, furthermore, that it can be viewed as a means of diversifying risks in households and regions where the year-to-year maintenance of household food stores is unstable (Stark and Bloom 1985). With regard to our findings, households with high C/P ratios may be those with the greatest risk but they are also households with the smallest capabilities of diversifying risk. That is, households with high C/P ratios are those in which there are few or no adults left to leave a household in order to seek alternate sources of food or money. Conversely, households with “extra” working-age individuals appear to be most capable of sending migrants and potentially increasing household well-being. While we are not able to completely address this conjecture in our model, it is at least imaginable that a continuum in household wealth exists and that there is a threshold below which households that need to increase household wealth are unable to do so.
This pattern is also potentially related to the growing literature on poverty traps (Collier et al. 2003; Dasgupta et al. 2005; Bowles et al. 2007; Bonds et al. 2010). Individuals who live in households that have fallen below a threshold level of poverty are essentially “trapped” in a cycle of poverty owing to a lack of resources, health conditions, civil conflict, and environmental degradation. Poor children who grow up with fewer resources are likely to suffer lifelong consequences of such conditions. As they age and form their own households, they are likely to take those conditions with them, establishing a new household with children that are likewise reared in a resource-poor environment, in a household that is perpetually trapped in poverty, ultimately continuing an inter-generational cycle of poverty.

Furthermore, while we found our model strata that dealt with elderly (70 plus) out-migration to be unreliable because of the dearth of out-migration events in that age group, this lack of mobility may in itself may represent an interesting finding. If the elderly in these populations are less mobile, they may also be less able to seek healthcare treatment or other important services.

Finally, while our data do not cover a long enough period to examine seasonal patterns, there is some evidence that migration peaks during off times in the agricultural year (Figure 3.1). In our study population, adult males work heavily during the planting and harvesting seasons but may have more free time during the rest of the year. During slack seasons males may engage in hunting, fishing, lumbering, or other forms of subsistence or cash labor. There are potential epidemiologic implications for this migration pattern. Previous research in SE Asia has indicated that working age males are at increased risk of infection by some forms of malaria (especially *Plasmodium falciparum*) (Wiwanitkit 2002; Lin et al. 2009). There are multiple ways that this could be related to migration. For example, migrants that live in regions with no
malaria can travel to malarious areas, become infected, and transport the disease back to their places of origin. Conversely, migrants who live in malarious regions may transport the disease to regions without malaria when they travel (Le Menach et al. 2011). Further research will investigate this potential link between malaria and migration.

Also, in at least some agricultural populations, even marriage patterns are shaped by the agricultural year. Marriage seasonality reflects the seasonality of agricultural work, with marriages primarily occurring during relatively slack times of year following the harvesting of crops or the birthing seasons of livestock (Kussmaul 1985; Wrigley and Schofield 1989; Coppa et al. 2001; Gonzalez-Martin 2008). Marriage seasonality affects not only birth seasonality (Johnson, Ann, and Palan 1975; Abeysinghe 1991; Matsuda and Kahyo 1994; Garcia-Moro et al. 2000; Grech et al. 2003; Greksa 2004), but also the temporal patterns of postmarital migration. Future research in this study population will investigate the potential for yearly, seasonal patterns on the timing of out-migration in this region.

There are several limitations to the present study. Perhaps foremost among these is the definition of migrants used in our data: household members who are not expected to return to the household within the next four weeks. There are at least two main problems with this definition. First, migration intentions do not always match migration actions. Second, migrations that occur for shorter periods of time are both important and frequent in our study populations. What our study therefore misses are long-term migrations that were not intended (or expressed to other household members) and short-term, circular migrations. Our guess is that, if we did include these migration events in our data, it would not greatly change our model results with regard to household and individual level predictors of migration. However, given a longer set of
observations, and the missing short-term migrations, we might expect to uncover strong
seasonality in migration that would largely match the agricultural calendar.

Another major limitation to this study is the absence of information about household wealth,
landholding, or savings. These factors are obviously important with regard to household well-
being and could influence migration decisions. In our model we included uncensored household
characteristics as a single random effect in an attempt to account for these types of unexplained
heterogeneity. It is our opinion that the inclusion of such covariates would almost certainly
provide deeper insight into, and more information about, the influence of different household-
level factors on out-migration, but that their inclusion would not qualitatively change our current
model results.

Our models indicate that in addition to the age and sex of the individual, household-level
factors such as the number of household members and C/P ratios can be strong predictors of
individual-level out-migration. We also argue that while C/P ratios are notoriously difficult to
calculate because of the weighting system involved, they are an improvement over dependency
ratios and, with a little ethnographic insight, can be robustly estimated. Furthermore, our
sensitivity-analysis approach to analyzing potential relations between C/P ratios and out-
migration is novel. Our simulation results indicate a range of potential outcomes, under various
weighting schemes, and therefore give us a way to understand the sensitivity of our model results
to our model inputs.

Finally, a potentially interesting insight from these data and models concerns the unit of
time. It makes sense that household dynamics shift over time, as the age structure of household
members also changes. However, our data and models suggest that household dynamics also
shift over very short intervals (two-weeks) and that those shifting dynamics are also related to demographic forces such as migration.

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Figure 3.1: Net out-migration, agricultural and school calendar. Image adapted from Nakano (1980), migration data come from the present study and the agricultural and school schedules come from field work done by D.M.P.
Figure 3.2: Age-specific migration rates by sex
Figure 3.3: Distribution of simulated coefficient estimates for the effect of C/P ratio on out-migration in children under age 13
**Figure 3.4:** Distribution of simulated coefficient estimates for the effect of C/P ratio on out-migration in individuals between the age 13 and 69
Figure 3.5: Distribution of simulated coefficient estimates for the effect of C/P ratio on out-migration in adults over age 69.
Table 3.1: Weighting scheme for C (consumption) and P (production) by age and sex group

<table>
<thead>
<tr>
<th>age group</th>
<th>consumption</th>
<th>production</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>male</td>
<td>female</td>
</tr>
<tr>
<td>0_4</td>
<td>0.2</td>
<td>0.2</td>
</tr>
<tr>
<td>5_12</td>
<td>0.5</td>
<td>0.5</td>
</tr>
<tr>
<td>13_69</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>70_plus</td>
<td>0.9</td>
<td>0.9</td>
</tr>
</tbody>
</table>

Table 3.2: Range of weights for simulations. A uniform distribution was used to draw pseudorandom numbers from the weight ranges listed below. The ranges for weights are drawn from (Kramer and Boone 2002)

<table>
<thead>
<tr>
<th>age group</th>
<th>consumption</th>
<th>production</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>male</td>
<td>female</td>
</tr>
<tr>
<td>0_4</td>
<td>0 - 0.4</td>
<td>0 - 0.4</td>
</tr>
<tr>
<td>5_12</td>
<td>0.3 - 0.7</td>
<td>0.1 - 0.1</td>
</tr>
<tr>
<td>13_69</td>
<td>0.8 - 1.2</td>
<td>0.9 - 0.9</td>
</tr>
<tr>
<td>70_plus</td>
<td>0.7 - 1.1</td>
<td>0.5 - 0.5</td>
</tr>
</tbody>
</table>

Table 3.3: Model results for children under age 13 (note that after Bonferroni correction, only P-values less than .0167 would be considered statistically significant)

<table>
<thead>
<tr>
<th>Covariate</th>
<th>Coefficient</th>
<th>Standard Error</th>
<th>t-value</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Survey Week</td>
<td>0.0031</td>
<td>0.0058</td>
<td>0.5400</td>
<td>0.5868</td>
</tr>
<tr>
<td>C/P Ratio</td>
<td>0.1219</td>
<td>0.0408</td>
<td>2.9900</td>
<td>0.0028</td>
</tr>
<tr>
<td>House Size</td>
<td>0.2595</td>
<td>0.0486</td>
<td>5.3400</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Female</td>
<td>0.0443</td>
<td>0.1371</td>
<td>0.3200</td>
<td>0.7469</td>
</tr>
</tbody>
</table>

Table 3.4: Model results for those aged 13 to 69 (note that after Bonferroni correction, only P-values less than .0167 would be considered statistically significant)

<table>
<thead>
<tr>
<th>Covariate</th>
<th>Coefficient</th>
<th>Standard Error</th>
<th>t-value</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Survey Week</td>
<td>-0.0018</td>
<td>0.0030</td>
<td>-0.6100</td>
<td>0.5395</td>
</tr>
<tr>
<td>C/P Ratio</td>
<td>-0.6275</td>
<td>0.1000</td>
<td>-6.2800</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>House Size</td>
<td>0.2140</td>
<td>0.0258</td>
<td>8.3100</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Female</td>
<td>-0.4940</td>
<td>0.0652</td>
<td>-7.5700</td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>
Table 3.5: Model results for those over age 69 (note that after Bonferroni correction, only P-values less than .0167 would be considered statistically significant)

<table>
<thead>
<tr>
<th>Covariate</th>
<th>Coefficient</th>
<th>Standard Error</th>
<th>t-value</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Survey Week</td>
<td>0.0511</td>
<td>0.0477</td>
<td>1.0700</td>
<td>0.2838</td>
</tr>
<tr>
<td>C/P Ratio</td>
<td>0.1869</td>
<td>0.6352</td>
<td>0.2900</td>
<td>0.7686</td>
</tr>
<tr>
<td>House Size</td>
<td>0.1890</td>
<td>0.1631</td>
<td>1.1600</td>
<td>0.2467</td>
</tr>
<tr>
<td>Female</td>
<td>-0.1680</td>
<td>1.2070</td>
<td>-0.1400</td>
<td>0.8893</td>
</tr>
</tbody>
</table>

Table 3.6: Summary statistics for simulation results

<table>
<thead>
<tr>
<th>Model</th>
<th>mean</th>
<th>median</th>
<th>standard deviation</th>
<th>min</th>
<th>max</th>
</tr>
</thead>
<tbody>
<tr>
<td>0 to 12</td>
<td>0.15</td>
<td>0.16</td>
<td>0.06</td>
<td>0.02</td>
<td>0.33</td>
</tr>
<tr>
<td>13 to 69</td>
<td>-0.61</td>
<td>-0.59</td>
<td>0.25</td>
<td>-1.24</td>
<td>0.01</td>
</tr>
<tr>
<td>70 plus</td>
<td>-0.05</td>
<td>0.01</td>
<td>0.65</td>
<td>-3.95</td>
<td>1.94</td>
</tr>
</tbody>
</table>
CHAPTER 4: Border malaria: Detection, spatial patterns, and risk factors for infection in a malaria foci on the Thai-Myanmar border

INTRODUCTION

Though the global malaria situation appears to be improving, the disease remains one of the biggest threats to populations living within the tropical world. In 2012 the World Health Organization (WHO) estimates that there were 207 million cases of infection and 627,000 malaria-related deaths (WHO 2013). In much of the Greater Mekong Subregion which includes Cambodia, Laos, Myanmar, Thailand, Vietnam and China’s Yunnan Province, malaria is now confined to patches in very specific areas. The malaria landscape is quite heterogeneous, with many of these patches occurring in hilly, forested areas and international borders. In Thailand, there has been little-to-no indigenous malaria in most of the central plains for several decades. In sharp contrast, international borders with Cambodia and Myanmar (formerly Burma) continue to have endemic malaria.

Myanmar has until very recently had little public health infrastructure and the heaviest malaria burden in the region (WHO 2010; Cui et al. 2012). The malaria problem along the Thai-Myanmar border is therefore sometimes considered a spill-over effect, with population movement from Myanmar being implicated as a driving force in the continued persistence of malaria in the region. Furthermore, the prevalence (from case reports) in some areas within Thailand appears so low that, in the absence of reintroduction from a reservoir source, it might be expected to die out in the presence of freely available antimalarials.

Conversely, the ecology along this border is likely conducive to persistent malaria regardless of this population movement. The area is heavily forested, hilly, and mountainous. There are at least three mosquito vector complexes within the region, meaning that vector
abundance is complex and almost omnipresent (Sinka et al. 2011). The border region is also home to many different ethnic minority groups who are collectively referred to as “Hill Tribes”, with the largest group being the Karen. These groups differ from both the Thai and the Burmese in many ways. They have different cultures, languages, demography, ecologies and subsistence patterns and they tend to be economically poor. They frequently live in very remote areas that are far from clinics and hospitals and are difficult for health workers to reach, especially during the rainy season (from May to November). Until very recently, several of these groups have also been at war with the Myanmar government, meaning that they have been isolated along the Myanmar border and many have lived as refugees on the Thai side of the border. The situation is one in which environmental, socio-political, and economic factors combine to form a perfect storm that is quite favorable to continued malaria transmission.

Along the Thai-Myanmar border, Tak Province has consistently had the highest numbers of malaria infections, both *Plasmodium vivax* and *Plasmodium falciparum*, for several years (Zhou et al. 2005). Within Tak Province, Tha Song Yang district (the administrative unit containing the study village in the inset map, Figure 4.1) typically has the heaviest malaria burden. However, most malaria surveillance in the region has been through passive case detection (PCD) where cases of malaria are recorded at hospitals, clinics, and malaria posts. These types of data are convenience samples, in that they are collected from the most convenient population possible: those who are symptomatic and seek treatment at a health care facility. These individuals are unlikely to be representative of the entire population at risk of infection meaning that samples from PCD are prone to self-selection by patients because not all subgroups in a population seek treatment equally (Byass 2008; Peters et al. 2008). Furthermore, the population at risk is undefined, meaning that biases that are likely to be present in this
convenience sample are impossible to assess. In particular, patients at these hospital and clinics frequently come from across the international border and sometimes from far away. In Thailand, the significantly better health services plus the free treatment policy from the government for malaria patients regardless of nationality may have offered additional attractions to draw people from Myanmar to seek malaria treatment across the international border. Since an understanding of the baseline population that these patients come from is completely lacking, it is not possible to accurately calculate risk factors for infections, prevalence, or incidence rates from these data. Finally, populations with endemic malaria frequently have asymptomatic carriers who can act as reservoirs for the continued persistence of malaria, even in cases where all symptomatic persons are cured (Macauley 2005). Information about such asymptomatic carriers is therefore extremely important for malaria control and elimination. These problems make it difficult or impossible to assess the representativeness of PCD cases for the catchment population, even when that catchment population is well-defined.

As many nations in the GMS are progressing toward regional malaria elimination, a better understanding of malaria epidemiology is essential. In the present study we aimed to acquire this knowledge through active case detection (ACD). By combining frequent site visits, field diagnostics and laboratory evaluation by PCR, the reliability of case numbers was assessed, which allowed the identification of spatio-temporal patterns of malaria and risk factors (including migration) for malaria infection. Since many cases on the Thai side of the border are in Myanmar nationals or are classified as imported cases, we were also interested in the potential for indigenous, rather than imported, malaria to be present on the Thai side of the border, particularly with regard to submicroscopic malaria and asymptomatic carriers.
METHODS

Study site and population

The study site is located along the Moei River on the Thai side of the international border (Figure 4.1). The international border runs along the southwestern quadrant of the study hamlet. It is located on the side of a hill with a difference of over 100 meters in elevation from the lowest to the highest household. A drainage system runs from the northeast to the south-central part of the hamlet. A natural spring exists under the hamlet and villagers use it as a source of drinking and bathing water. The water runs through a series of small waterfalls and pools, along the drainage system, and ultimately makes its way into the Moei River (Supplementary Figure 4.1). Most of the hamlet has been cleared of underbrush and throughout there are eroded water ways and puddles that fill during the rainy season. The study hamlet (Village 1 in Figure 2.2) had approximately 547 inhabitants, 48% of which were male, at the beginning of this study in July 2011. The hamlet is mostly composed of ethnic Karen people. Approximately 78% of the inhabitants self identified as being Karen while 7% claimed to be Thai and 16% did not respond. Conversely, 18% had Thai citizenship, 66% had no citizenship (neither Burmese nor Thai) and the same 16% did not respond.

ACD Surveys

The protocol of this study has been reviewed and approved by the institutional review boards of the Pennsylvania State University and the Thai Ministry of Health. Informed consent was obtained from the head of each participating household. A full scale demographic survey was conducted and each villager who agreed to participate was given a unique identification code. Demographic variables include sex, self-reported age, and nationality. Households were also given identification codes and their spatial coordinates were recorded. Household
demographic surveys have been conducted almost weekly, beginning in October 2011. These surveys note both additions to a household (through in-migrations or birth) and subtractions from a household (through outmigration or death). Individuals who move into a household and stay for a month or longer are coded as in-migrants (from the week that they originally entered the household). When a household member has moved out of a household, the study team asks other remaining household members when that person will return. If they are expected to be away for a month or more they are counted as an out-migrant.

Three mass blood surveys (MBS 1 - 3) were also conducted in the study hamlet in July and December 2011, and May 2012. During these surveys, thick and thin blood films were made for each available participant, and these films were immediately checked at the nearest malaria clinic for malaria infection by microscopy. In addition, about 100μl of finger prick-blood was spotted on Whatman 3M filter paper, air dried and stored individually in silicon desiccant for subsequent PCR detection of malaria parasites. Persons with malaria-positive slides were then visited by public health workers and administered antimalarials according to official Thai protocol. Slides and filter papers were marked with villager and household identification codes and were stored for subsequent analyses (including slide positivity confirmation by expert microscopist, parasitemia counts, and PCR confirmation of infection).

**Malaria Diagnosis**

Malaria infections were diagnosed by microscopy using Giemsa-stained thick and thin blood smears at a malaria clinic near the field site. The results were read again by another expert microscopist with over 20 years of experience. For molecular analysis, a nested PCR method with a 2 X 2 mm disc punched from each filter paper blood spot serving as the DNA template was performed. The primary PCR was performed using genus-specific primers for the rDNA
gene, while nested PCR used primers specific for each of the four human malaria species and *Plasmodium knowlesi*, which is also known to also occur in this region (Putaporntip et al. 2009).

**Slide sensitivity and specificity**

Diagnoses were compared between the three different methods (field microscopy, expert laboratory microscopy, and PCR). We calculated the sensitivity (the proportion of PCR positive people who were identified as positive by microscopy) and specificity (the proportion of PCR negative people who were diagnosed as negative by microscopy) between field microscopy and expert microscopy, field microscopy and PCR, and expert microscopy and PCR. Because of the very low numbers of diagnosed cases from field and expert microscopy, we did not calculate the positive and negative predictive values.

**Risk factor analysis**

We used mixed effects logistic regression to look for statistically significant risk factors for *P. vivax* infections. Because of the small number of *P. falciparum* cases, we were not able to conduct the same analysis for falciparum malaria. We tested for both household- and individual-level factors on the individual risk of vivax infection. Individual-level covariates included age group, sex, nationality (in this case, Thai versus those who reported being stateless) and migration status (whether the individual had moved into the study village prior to being infected). Household level covariates included: the mean household size, for the household with which an individual was associated, during the surveys prior to infection; household dependency ratio (ratio of young (age 0 to 12) and elderly (over age 69) household members to working age (age 13 to 69) household members); and whether or not a person had moved in or out of the household during the study period. We also included a random intercept for each household to attempt to control for unexplained heterogeneity at the household level.
We experimented with different specifications for age groups and the inclusion of interaction terms between age and migration, dependency ratio and household size, and nationality and migration. The final model was chosen based on Akaike Information Criterion scores, a measurement of model fit that is penalized by the inclusion of more parameters. Where possible, odds ratios for falciparum risk factors were calculated using contingency tables.

**Spatial analysis**

We mapped the distribution of PCR-confirmed vivax cases by household for each of the MBS individually and combined. We then tested for both global (entire study site) and local (around household clusters) spatial autocorrelation. We used a k-nearest neighbor approach (using both $k = 2$ and $k = 3$) for assigning spatial weights matrices. In order to test for global spatial autocorrelation we used both the Moran’s I statistic and join-count statistics. For the Moran’s I test we standardized cases in households by the household size. Since our study site included many households with no cases, and therefore many households with 0s, we also calculated join-count statistics (which are designed for binary data). For the join-count based test of global autocorrelation we transformed the data into a binary format ($1 = $ a household had 1 or more infections during a given mass blood survey; $0 = $ a household had no infections during the mass blood survey). These global tests were then followed by a test of local spatial autocorrelation (LISA: local indicator of spatial autocorrelation) using the standardized household cases (Anselin 1995).

**RESULTS**

**Malaria diagnosis**

The results of our comparisons between the three diagnostic approaches (field microscopy, expert microscopy, and PCR) are given in Table 4.1 and Table 4.2. There were
stark differences between each approach (Table 4.1). Assuming PCR as the truth, field microscopy missed over 88% of all malaria cases during the three mass blood surveys and the expert microscopist missed over 50% of all cases. Using expert microscopy as the gold standard, field microscopy still missed over 75% of all cases. Both microscopy approaches missed all of the mixed infections (5 in total).

The sensitivity and specificity of both field and expert microscopy are given in Table 4.2. Briefly, both methods were specific but not sensitive. For vivax infections, field microscopy had a 2% sensitivity and expert microscopy a 6% sensitivity. For falciparum infections both fared slightly better, with field microscopy having 5% sensitivity and expert microscopy having 37% sensitivity. Using expert microscopy as the standard, field microscopy had a 17% sensitivity for vivax infections and 12% sensitivity for falciparum infections. All specificities approached 100%, meaning that most cases diagnosed as PCR negative were also considered negative by microscopy.

**Risk factors**

Using mixed effects logistic regression, we analyzed potential household and individual level factors (modeled as dummy variables) for increased risks of infection by *P. vivax* (Table 4.3). We also tested different interaction terms between age and migration, dependency ratio and household size, and nationality and migration. None of these interactions were statistically significant and models that included the interaction terms had higher AIC scores than did models without. These interaction terms were therefore excluded from our final model. The age groups that provided the best model fit were: 0 to 4, 5 to 14, and 15 and above. The single most important covariate in our logistic regression model was “nationality”. Individuals who had no nationality had over 8 ½ times the odds of vivax infection (model-adjusted odds ratio, Table 4.3)
and also around 8 ½ times the odds (unadjusted odds ratio) of falciparum infection. We found no statistically significant difference in infections by sex or migration status. Furthermore, household size, household dependency ratio, and living in a household with other migrants did not appear to increase an individuals’ risk of infection. We did find a small effect of household elevation on the risk of individual infection. For each increase in household elevation of one meter an individual appeared to have about a 13% decrease in the odds of vivax infection. Finally, children aged 5 to 9 appeared to have the greatest risk of infection. We are cautious in over-interpreting these results with regard to age groups because there are few case numbers and there isn’t a clear age pattern in our data (Figure 4.2).

**Spatial patterns**

Maps of *P. vivax* cases by household indicated wide variation across the MBS (Figure 4.3). In particular, cases during the MBS2 (during the dry season) were fewer and tightly clustered near a few year-round water sources (documented during a follow up field visit). Spatial clusters were detected by both Moran’s I and join-count statistics in MBS2 and MBS3. However, clusters in MBS3 were only detected when using k=3 nearest neighbors for the spatial weights matrix. LISA statistics indicated potential local autocorrelation in each map – with two local clusters in MBS1, two in MBS2, and potentially four in MBS3. Combined, these tests indicate tight spatial clustering during the dry season (MBS2) and an expansion of cases in the wet season (MBS1 and MBS3). The clusters that are present in the dry season remain in the wet season, but spatial autocorrelation is less evident in the wet season because of the increase spread of cases throughout the village.

A bivariate map showing households with vivax cases, combined from the three mass blood surveys, and the nationality of household members further indicates the relationship
between this covariate and malaria infections (Figure 4.4). Cases cluster tightly near the drainage system and year-round water sources, as well as in households that are composed of individuals with no Thai nationality.

**DISCUSSION**

Timely identification of malaria infected people and prompt treatment are essential to eliminate the transmission source, especially in regions entering the malaria elimination phase. In many malaria hypoendemic areas, the presence of asymptomatic patients who may serve as the parasite reservoirs requires that ACD efforts need to be installed and enhanced. Currently, field epidemiological surveys of malaria infections mainly rely on microscopy. Malaria diagnosis by microscopy in Thailand is the norm; with any patient presenting at a malaria clinic, malaria post, or hospital first being diagnosed by microscopy. However, parasite densities in asymptomatic parasite carriers are often below the detection limit of microscope (normally above 50 parasites/μl blood) (Ouédraogo et al. 2009; Harris et al. 2010; Steenkeste et al. 2010; Okell et al. 2012). Several studies have indicated that low density infections are more easily missed in diagnoses (Coleman et al. 2002; McKenzie et al. 2003). Patients attending clinics are usually symptomatic and presumably would have higher parasitemias when compared to infected individuals who are either fully or partially asymptomatic (Coleman et al. 2002; Byass 2008). Therefore in ACD, microscopy may miss more cases than would normally be missed. The results from the diagnostic portion of our study indicate that over 80% of malaria cases are missed through microscopy. In addition, the accuracy of microscopic diagnosis is also dependent on the skill and training of the microscopist (Raghavan 1966; Trape 1985; Payne 1988). In our study, we found that individuals with low parasitemia were more likely to be
missed by the field microscopist when compared to the expert microscopist. This also highlights the need for strengthened training of microscopists in malaria diagnosis.

PCR method has at least an order of magnitude higher sensitivity than microscopy. Although PCR may not be suitable to serve as the point-of-care method in malaria diagnosis, PCR has been increasingly used in malaria detection, in particular in epidemiological surveys. While the presence of DNA doesn’t necessarily indicate the presence of living parasites, parasite DNA is unlikely to persist in a host for longer than a few weeks or even days (Jarra & Snounou 1998). In our study, we also found that PCR has a much better performance than microscopy. Those that are missed by both field and the expert microscopists may be related to low parasitemias. It is noteworthy that five PCR-confirmed cases were mixed parasite species infections, all of which were missed either entirely or partially (a single diagnosis) by both field and expert microscopy. Failure to diagnose mixed infections has previously been discussed in the literature, with mixed infections in Thailand frequently being diagnosed as single infections or with vivax infections emerging shortly after treatment for falciparum malaria (Looareesuwan et al. 1987; Siripoon et al. 1997; Tjitra et al. 2008; Douglas et al. 2011). Potential scenarios leading to this phenomenon include: the patient had a preexisting infection when a new infection occurred, and the new infection had not yet emerged from the liver stage at the time of diagnosis; or, there may be antagonistic effects between different parasite species (potentially even different strains of the same parasite) within a single host (Siripoon et al. 1997). Infection by one species may suppress parasitemia levels or emergence of blood stage parasites in a subsequent infection. In areas of co-existence of parasite species, misdiagnosis will inevitably lead to improper treatment of the cases.
Malaria cases in endemic areas often occur in hotspots, with close spatial associations with vector-breeding habitats, and in certain “high-risk” subsets of the population (those with higher exposure to vector-breeding habitats). Some previous work in the Greater Mekong Subregion has indicated that malaria clusters along the international borders and is associated with forests and forest edges (WHO 2008; Cui et al. 2012; Bhumiratana et al. 2013). It is also found to be associated with adult males (Erhart et al. 2005; Lin et al. 2009). In addition, migration and population movement are important for malaria epidemiology in this region (Singhanetra-Renard 1993; Erhart et al. 2005; Markwardt et al. 2008; Delacollette et al. 2009; WHO 2010; Kitvatanachai & Rhongbutsri 2012; Bhumiratana et al. 2013; Ward et al. 2013). While our analysis doesn’t refute these suggestions, it certainly describes a different scenario and further points to heterogeneities in the malaria ecology of this region.

Age patterns weren’t entirely clear and none of the age groups showed statistical significance in our statistical model. However, most cases occurred in the 5 to 9 age group (Figure 4.2). This pattern suggests that at least some transmission is occurring in or near the hamlet or schools, places where children spend most of their time. Furthermore, most studies that have mentioned migration as either a risk factor for infection or as a risk factor for population health have not directly tested for an effect of migration with regard to the risk of malaria infection and have instead been anecdotal (but do see Somboon et al. 1998). In our investigation we were able to look directly for associations between migrations and malaria infections, as well as a potential influence of living in a “migrant household”, on the risk of malaria infection. We found no evidence to suggest such an effect (Table 4.3).

On the other hand, we did find a large effect of having no citizenship on the risk of vivax infection (Table 4.3, Figure 4.4). Presumably, this risk factor isn’t directly associated with
nationality but with other indirectly related circumstances and factors. This particular study location is home to a group of stateless Karen who previously fled Myanmar for the relative safety of Thailand. These same villagers are relatively poor and live in hastily constructed, open household structures which are tightly clustered together on a landscape that is prone to flooding and holding pools of water. There are several other potential factors leading to this clustering. For example, these individuals may share behavioral traits or norms, including a lack of bednet use or occupational and subsistence strategies that might differentially put them at greater risk of infection. Furthermore, these individuals may have different immunological histories, coming from a region that typically has higher prevalences of malaria, potentially leading them to have acquired or even inherited immunity (Louicharoen et al. 2009). Interestingly, while almost all of the villagers with vivax infections did not have citizenship, around 14% of the ethnic Karen did have Thai citizenship.

The spatial ecology of infections in this study site also provided novel insight into the distribution of cases in a border malaria setting at a micro-level that is, to our knowledge, the first of its kind in this specific region. Our evidence points toward small pockets of relatively high transmission of vivax, and potentially falciparum, malaria that may be indigenous to the study hamlet. Cases appear to cluster in hotspots, potentially near water sources. Assuming that the pattern we see in this short time interval continues over longer stretches of time, we hypothesize that: infections occur year round in the village, during the dry season they cluster near year-round water sources, and during the wet season they expand as do mosquito breeding habitats. However, during the wet season villagers also spend more time outside the village, preparing fields for the agricultural season, planting seeds, tending the fields, and finally harvesting their crops. Especially during the harvest, some agricultural workers spend nights in
small huts or shacks in the fields. This space-time change in ecology means that many villagers are exposed to different potential mosquito vectors at different times of the year. The apparent spatial expansion of cases in the study site during the wet season may also be related to this seasonal ecological shift. Furthermore, we found several individuals with cases across consecutive MBS. Until further genetic studies are done on these samples, we cannot rule out the possibility that these individuals weren’t newly infected but were instead carrying an infection over many months (at least 5). If these assumptions are true, these “asymptomatic” carriers in this study village with low-level parasitemia and long-term infections are potential reservoirs of parasites. If mosquito vectors also exist within the study village, these individuals should be sufficient for malaria to persist even in the absence of parasites being imported.

There are several limitations to this study. Malaria cases were detected in three cross sectional waves rather than longitudinally and only consist of roughly a year’s worth of time. It is possible that the spatial patterns and the risk factors that we find in our data differ from year to year. Furthermore, the relatively small number of cases and the small size of the population make analysis difficult at best. A full analysis of the *P. falciparum* data here was not possible because of the low number of cases. This is a common problem in this region, where low transmission and small population sizes dominate. Also, while we found no association between migration and risk of vivax infections, our measurement of migration may not be sensitive enough to capture important movement patterns. The study hamlet is located on the international border and residents are likely to move back and forth over short time intervals (even within a single day). Such movements are not recorded in our data. Finally, this study would have greatly benefited from more in-depth surveys of the human residents, including subsistence strategies and household structure, as well as surveys of local mosquito populations.
Future research will look at the genetic relatedness and phylogeography of parasites within the village in order to better understand the dynamics of malaria transmission in this border setting. This future research will enable us to 1) investigate the potential for parasites to be spreading in a true contagious pattern (Are household members and neighbors sharing the same parasites? This would be expected if mosquito vectors were present within households and “neighborhoods”), and 2) whether patients who had infections across multiple MBS were in fact carrying the same parasite across those surveys (rather than being reinfected). Such studies will also help us to better understand the potential for human migrants to repeatedly import parasites from outside of the region into malarious areas on the international border.

In conclusion, there are likely several factors that lead to the large proportion of missed cases in this study, but regardless of those reasons the implications are profound. A major implication is that major parasite reservoirs may exist on the Thai side of the international border, contrary to the thought that parasites are being introduced from Myanmar. That is, importation is possible, but not necessary, for continued transmission here. Our interpretation of the spatial patterns and the clustering of cases in 5 to 9 year olds is that these patterns are indicative of indigenous transmission. This study also points to the potential for many infected persons to have low parasitemia, low symptoms, and chronic malaria infections. Such persons may be important reservoirs in this malaria system. Finally, while Thailand is a low transmission area compared to regions such as Sub-Saharan Africa, there may be small hotspots of high transmission driving the low level of transmission that seems to persist when considering larger geographic scales. That is, transmission levels are directly related to the spatial units that are used to classify them, and those spatial units are frequently arbitrarily chosen (e.g.
administrative units may not be drawn with respect to meaningful ecological or demographic zones).

ACKNOWLEDGEMENTS

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Figure 4.1: *P. vivax* cases per 1000 people by province and subdistrict in Tak Province (inset map) (2009)
Figure 4.2: Apparent age distributions of *P. vivax* cases by method of detection
Figure 4.3: Mass blood survey plots (A. MBS 1, B. MBS 2, C. MBS 3) The dates of the MBS are indicated on the timeline beneath (D). Meteorological data (D) from a near-by weather station are plotted to illustrate seasonality (blue indicates precipitation and red indicates ambient temperature). Village location indicated in inset map, Figure 4.1.
Figure 4.4: Distribution of nationality/citizenship by household and *P. vivax* cases. Village location indicated in inset map, Figure 4.1.
Supplementary Figure 4.1: Map of study site indicating locations of households, drainage systems, Moei River, and year-round water sources (location of village indicated in inset map, Figure 4.1)
Table 4.1: Cases diagnosed by field microscopy, expert microscopy and PCR

<table>
<thead>
<tr>
<th></th>
<th>P. vivax</th>
<th>P. falciparum</th>
<th>mixed (Pf + Pv)</th>
<th>total</th>
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<tbody>
<tr>
<td>field microscopy</td>
<td>6</td>
<td>2</td>
<td>0</td>
<td>8</td>
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<tr>
<td>expert microscopy</td>
<td>18</td>
<td>16</td>
<td>0</td>
<td>34</td>
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<tr>
<td>PCR</td>
<td>55</td>
<td>20</td>
<td>5</td>
<td>70</td>
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Table 4.2: Sensitivity and Specificity of tests

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<th>specificity</th>
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<tr>
<td>field micr. versus PCR</td>
<td>P. vivax</td>
<td>0.02 (0.00 - 0.10)</td>
<td>1.00 (0.99 - 1.00)</td>
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<tr>
<td>expert micr. versus PCR</td>
<td>P. vivax</td>
<td>0.06 (0.01 - 0.17)</td>
<td>0.99 (0.98 - 1.00)</td>
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<td>field micr. versus PCR</td>
<td>P. falciparum</td>
<td>0.05 (0.00 - 0.26)</td>
<td>1.00 (0.99 - 1.00)</td>
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<td>expert micr. versus PCR</td>
<td>P. falciparum</td>
<td>0.37 (0.16 - 0.62)</td>
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Table 4.3: Mixed effects logistic model: risk factors (treated as dummy variables) for PCR-diagnosed *P. vivax* infections

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<tr>
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<th>SE</th>
<th>z value</th>
<th>OR</th>
<th>p value</th>
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<td><strong>individual level</strong></td>
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<tr>
<td>child (0 to 4)</td>
<td>0.81</td>
<td>0.59</td>
<td>1.37</td>
<td>2.24</td>
<td>0.1696</td>
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<td>child (5 to 14)</td>
<td>0.29</td>
<td>0.58</td>
<td>0.49</td>
<td>1.33</td>
<td>0.6211</td>
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<tr>
<td>adult (15 plus)</td>
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<tr>
<td>female</td>
<td>-0.26</td>
<td>0.34</td>
<td>-0.76</td>
<td>0.77</td>
<td>0.4466</td>
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<td>male</td>
<td></td>
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<td>Thai</td>
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<td>0.70</td>
<td>3.10</td>
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<td>0.78</td>
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<td>migrant house</td>
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<td>stand. deviation:</td>
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CHAPTER 5: Discussion and future directions

The common theme of this research has been the very thing that splits two other worlds: the international border between Thailand and Myanmar. It is an invisible line, and in perhaps most places along the border you wouldn’t know it existed if you didn’t have maps, signs, and the occasional border patrol or police officer working near it. But the implications of this border, socially, environmentally, demographically, and epidemiologically are quite real. This dissertation was therefore an attempt to better understand the demography and malaria epidemiology of this region.

The study population here consisted mostly of ethnic Karen, living in settlements along the Thai side of the Moei River, which marks the international border for most of Tak Province. The Karen are experiencing considerable change at present. When the Southeast Asian International Center for Excellence in Malaria Research (ICEMR) project began, they were still actively at war with the Burmese military. Shortly after this project initiated the demographic surveys, an agreement between the Myanmar government and several Karen rebel groups to halt military action was signed (Naing 2011; Anonymous 2012). Some Karen refugees on the Thai side were waiting for something like this to occur before returning home. Others prefer to keep their homes in Thailand but now go back to visit friends, families, and their birthplaces with greater ease and more frequency. Ultimately what all of this means is that this region is quickly undergoing a lot of change. This change will, and perhaps already has, influence the demographic features of the region, making travel to the Myanmar side less dangerous (though landmines and other artifacts of war remain). Both sides of the border are rapidly developing now too. Towns are growing, roads are being paved, and more tourists and potentially money will follow.
Malaria has generally been considered a rural disease, though urban malaria is an increasing concern in some areas (Aleme et al. 2011; Siri et al. 2010; Hay et al. 2005). As towns grow and more jobs become available, it is likely that people from the country-side will move into these emerging urban centers, and these growing populations may have to worry less and less about malaria. Conversely, if human population movements and migrations do drive malaria dynamics or the spread of drug resistant malaria (Ward et al. 2013; Martens & Hall 2000; Le Menach et al. 2011; Bhumiratana et al. 2013), then as transportation across the border and beyond becomes much easier, that potential for spread may increase. But this is speculation, and I’ll return to my original thought: What is certain is that things are rapidly changing and this dissertation was an effort to gain an understanding of demography and malaria epidemiology along this border, at this point in time.

Chapter 2 was a theoretical, methodological, and empirical study that focused on spatial social science using migration as an example. In this chapter I touch on an array of topics related to spatial demography but they are all tied together around a common theme of migration. Demography is in some ways a peculiar field. Today most demographers are strictly social scientists and their respective fields tend to have a body of theoretical knowledge that differs strongly from that of demography. In fact, it has sometimes been argued that demography is a method without theory whereas anthropology (my own social science field) is all theory without any method. I don’t think this statement is entirely true, but it does address an interesting issue with theory in demography in that demography doesn’t necessarily divorce method and theory. As a statistical and mathematical science, the quantitative approach and description of

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12 However, urban areas are the prime habitat for Aedes mosquitoes and dengue fever outbreaks, meaning that mosquito borne infectious disease will probably remain a major public health threat for these populations.
populations has a body of theoretical knowledge as well. Populations usually act in fairly predictable ways, some of which have been well described by demographers.

In Chapter 2 I discuss Moran effects, spatial synchrony, and migration, examples of the marriage between method and theory in population science. Moran effects and spatial synchrony are borrowed from population ecology and essentially refer to clustering in population processes across landscapes (spatial synchrony), which is sometimes influenced by macro-scale factors that are shared across those landscapes (Hudson & Cattadori 1999; Bjørnstad et al. 1999). For example, if environmental conditions are shared across many populations, then you might expect population growth to be similar across those populations, even if they are different populations.

Agricultural populations tend to be tied to seasonal variation in meteorological factors (such as precipitation) and ultimately to the agricultural calendar (Coppa et al. 2001; Greksa 2004; Johnson et al. 1975). I looked at temporal trends (both age patterns and time-series patterns) in migration among four Karen study sites along the Thai-Myanmar border. Age patterns in migration were almost identical across the four study villages, as ought to be expected from the work done by Rogers and Castro several years ago (Rogers & Castro 1981). Conversely, villages that were closer to each other had more similar time-series trends. I hypothesize that this effect is related to shared macro-scale factors (the Moran effect) such as precipitation, elevation, and ultimately the agricultural calendar. Migrations are more likely to occur during down times in the agricultural calendar, and villages that are closer will have agricultural calendars that are more closely in sync.

Chapter 3 looks at household- and individual-level predictors of out-migration across four Karen study villages. The essential goal of this research was to learn which types of individuals are most likely to migrate out and what types of households are most likely to have
individuals migrate out. Individual-level predictors were in line with the theory and literature from mathematical and empirical demography. Migration is most common at very young and young working ages, and tends to be slightly higher among males in the young working ages than among females (Rogers & Castro 1981). Household-level predictors, however, were important in different ways for different age and sex groups. Households with high consumer/producer (C/P) ratios (Chayanov 1966), with more “consumers” than “producers”, were more likely to have children move out regardless of their sex. However, those same households were less likely to have adults move out, especially female adults.

The experience that I’ve gained from working and living around these, and other, Karen populations provides insight into these findings. Migration at very young ages is dependent on adult migration, with children moving with their parents or caregivers. Older children in rural parts of Tha Song Yang District who attend secondary school are typically forced to travel relatively long distances because such schools are only located near larger towns and cities. Many of these children attend a large Catholic School several hours’ drive away from the study sites discussed in this dissertation, where housing is provided for children from poor households. These children move into dorms for the semester and return when school is over.

The negative relationship between household C/P ratios and out-migration comes because a high C/P ratio represents a household that is already stretched to its limit with regard to production. A household with many children and very few working-age adults is unlikely to be able to deal with the loss of one of those adults. In these data, these households tend to be single-parent households with several children. There is no one left to move out until the children are old enough to go to secondary school. Furthermore, there remains a cost even when
children leave the household for schooling. Some resources may be diverted toward such children (school uniforms etc.) and their labor (production) is lost.

This study is the first that I am aware of to actually look at C/P ratios with regard to out-migration. Furthermore, it is novel in that it shows household level associations with migration at very short time intervals, approximately every 2 weeks. Many population-level researchers only focus on long-term dynamics, but some have noted the importance of short-term (“transient”) dynamics in population processes (Caswell & Werner 1978; Caswell 2007). This research, and the data gathered by the ICEMR project, therefore offers a unique view of migration dynamics in a rural, agricultural population.

One problem with studies that incorporate C/P ratios is that the weighting system for C/P ratios is notoriously difficult to derive empirically (Kramer 2005; Lee & Kramer 2002). While the goal of this research was not methodological, an innovation regarding C/P ratios was developed through it, based off of previous work by Jennings (2010). Through the use of simulations and a bootstrap-like approach I showed that the weighting system for C/P ratios, as long as it is reasonably chosen, isn’t overly important with regard to model outcomes. As long as absurd weighting systems (e.g. weighting infant production over that of young adults) aren’t used, then these model results remain robust.

Chapter 4 was an attempt to better understand the border malaria phenomenon (Wiwanitkit 2002; WHO 2010; Cui et al. 2012; Bhumiratana et al. 2013). Both in the literature and on the ground, the story has long been that border malaria is largely the result of population movements and migration (Bhumiratana et al. 2013; Kitvatanachai & Rhongbutsri 2012). Given the unique migration data that have been generated by the ICEMR project, and the focus of the
ICEMR project on malaria in this region, it seemed natural to look for connections between migration and malaria.

Somewhat to my surprise, however, I was unable to find any associations between individual risks of malaria and migration, either at the individual or the household level. On the other hand, what I did find was that a large fraction of malaria cases are missed by microscopy (in this case, around 80% were missed by field microscopists) and that in this study site, malaria cases are almost completely clustered in people with no official citizenship. These are individuals who, because of socio-political context of the region, have no citizenship on either side of the border and are therefore stateless (Kunstadter 2013; UNESCO 2011). Some of these individuals are considered foreigners even though they have lived on Thai soil for decades.

In this particular study site, most of these individuals appear to be people who fled violence in Burma over the last several decades. The area was set up as a make-shift camp, with most villagers intending either to move into official, legal refugee camps or to move back home if peace were to one day come. Houses more closely resembles the shacks that are sometimes built in agricultural fields so that workers can stay overnight in the fields during prime work times. These houses are clustered tightly together on soil that is prone to flooding and waterlogging. The individuals inhabiting these houses have little-to-no rights and are disproportionately poor. These factors are likely related to their higher risk of malaria infection, either through living near mosquito vector sources in housing that does not protect against mosquitoes or through exposure to vectors through shared subsistence strategies.

Since most of the cases clustered in the 5 to 9 year old group, it also seems likely that transmission is occurring in or near the village. It is also possible that these individuals have

\[13\] At the household level I looked for an effect of living in a household where there were migrants other than the person at risk of infection.
immunity (acquired or inherited) and so they are less likely to show strong symptoms and to seek antimalarial treatment. While I did not find a risk associated with the actual act of migration, this population is made up of people (or relatives of people) who migrated across the international border at some point in the not so distant past. Combined with my hypothesis that they are being infected on the Thai side of the border, it is ironic that “foreigners” are carrying parasites, but that they are possibly getting those parasites on Thai soil.

All of these factors contribute to a better understanding of border malaria and border demography in this region. However, there were several weaknesses to this work, mostly centered on problems of measurement. Measuring things like migration and malaria infection can be extremely difficult, especially in rural agricultural populations. The definition of migration in the ICEMR data was people who either intended to stay out of their home or to move into a home for longer than a month. Clearly lots of relevant movement occurs in shorter intervals (Martens & Hall 2000; Stoddard et al. 2009; Somboon et al. 1998) but measuring such shorter intervals in four different villages in relatively remote areas would have been extremely labor intensive. Furthermore, our findings using PCR rather than microscopy indicate that many malaria cases are actually missed. That I did not find a direct link between migration and malaria could be because there is no link, or because I didn’t have sensitive enough measurements of migration and/or malaria.

**FUTURE DIRECTIONS**

These weaknesses are probably an excellent place from which to approach future directions.

Future migration work will look at movement patterns that occur at much shorter time intervals than were recorded in the initial ICEMR demographic surveys and will also incorporate
destinations of migrants. In this way, the frequency, distance, and direction of movement patterns can be measured. Such work will probably have to focus on one or two villages rather than all four study sites, but the quality of resultant data should be worth the loss of extra study sites. Given that strong seasonality in migration patterns has already been observed in these populations (Chapter 2), I suspect that the same will show up in future studies.

I will also pursue further sensitivity analyses of the data used in Chapters 2 and 3, this time testing for model sensitivity with regard to both spatial and temporal units. Building off of the data set used in Chapter 3, and the theoretical discussion in Chapter 2, I will test for model sensitivity with regard to more aggregate temporal units than were used in the original analysis (based on two–week intervals). Furthermore, I will begin to explore the potential for different spatial units to influence model outcomes. It is possible that C/P ratios should be based off of clusters of closely related houses rather than individual ones. Family members frequently live near each other and share in economic expenses, labor, and consumption. While I don’t have data about relatedness between households, I can use spatial coordinates to cluster household groups and to eventually look for variations in model outcomes with C/P ratios based on different aggregate units. In future surveys I will also collect household network data, documenting connections between houses so that I can more accurately aggregate clusters of houses.

Another exciting line of work that will build off on dissertation will be to look at the genetics of the parasite samples that have been collected in the ICEMR project. By sequencing microsatellites in the parasites collected from infected persons I will be able to study the genetic relatedness of parasites across space and time (Anderson et al. 2000; Pearce et al. 2009). This work will be important for understanding the transmission of malaria in this region and will add
to our understanding of the potential role of human movement patterns in malaria dynamics. For example, are parasites introduced into a village by multiple people (migrants) who have transported them from geographically different regions? Or are they relatively homogeneous across all cases? Are parasite populations the same year after year, indicating that they never really go away, or is there a new population or a bottleneck in every dry season? Furthermore, is there clustering of clonal (or near clonal) parasites by spatial hotspots within villages? If family members share parasites, despite their age or sex, then this provides another line of evidence that transmission is occurring in or near the village.

Finally I hope to expand my field work in this part of the world across the border into Karen and Shan States. Similar work on migration dynamics, malaria, and other infectious diseases across different cultural groups and in different settings will enhance the work I’ve begun here and will provide some novel data against which theory can be tested and revised and new methodological approaches can be incorporated. My work in the field thus far has already provided many valuable contacts through which this work will be born. Given the quickly changing nature of this region, it will be fascinating to watch this region develop, change, and probably grow.

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