As a PhD candidate in Biological Anthropology and Demography my overarching research area is disease ecology. While an undergraduate student I received training in mosquito ecology [1], environmental health, epidemiology, and biostatistics. In my graduate training I have built on this background with training in demography, population ecology, molecular ecology, and population genetics. Methodologically I utilize survival analysis, spatial statistics (including econometrics), and network analysis. Previously I have done research on the timing and duration of dengue fever outbreaks [2], temporal trends in historical tuberculosis mortality, and the population genetics of drug resistant malaria parasites [3]. I am associated with the Center for Infectious Disease Dynamics at Penn State University (PSU) and I am currently working as a statistical consultant with the Research Computing and Cyberinfrastructure group at PSU. Over the last year I have been working with the Geographic Information Analysis Core at the Population Research Institute (PSU), where I have been aiding Dr. Stephen Matthews on a special collection for the journal Demographic Research on “Future Directions in Spatial Demography.” My research experience and interests are a good fit for the “Challenges in modeling the spatial and temporal dimensions of the ecology of infectious diseases” workshop.

In my dissertation research I am collaborating with a large, multidisciplinary NIH project (Southeast Asia International Center of Excellence for Malaria Research) and my research focuses on malaria dynamics in Southeast Asia, especially along the Thai-Myanmar and China-Myanmar borders [4,5]. This area is known as a hot spot for drug and multi-drug resistant malaria. Furthermore, it appears that drug-resistant strains of malaria may spread via human migrants; with infectious, asymptomatic carriers moving drug resistant strains from one region to another [6].

The spatial distribution of malaria in this region is extremely patchy. For example, within Thailand there is very little malaria except along international borders with Cambodia, Laos, and Myanmar. This spatial distribution is most likely the result of complex interactions between human and mosquito ecology, the physical environment (altitudinal gradients, land cover, etc.), climatological factors (especially precipitation and ambient temperature), as well as the socio-political situations in these border areas. In my dissertation research I intend to investigate and model the hypothesized importance of human migration in malaria dynamics and the distribution of drug-resistant parasite strains. Time and space are inherently important in my conceptual and analytical model.

Attending the "Challenges in modeling the spatial and temporal dimensions of the ecology of infectious diseases" workshop is important for my current and future research for several reasons. One reason is that being around people with similar interests will broaden my knowledge base and methodological tool-kit. Seeing what others are doing, as well as discussing and receiving feedback on my research, is important for improving my research techniques. I also hope that my experiences and insights can help other attendees.

Another important factor is networking with fellow scientists. Building relationships with scientists of like mind is important not only for my current research but also for future collaborative, and potentially occupational, opportunities. Networking with well-seasoned professionals will expose me to potential mentors while networking with my peers may lead to future collaborative efforts.

There are several important issues with regards to spatio-temporal modeling with which I am interested. Perhaps foremost among these is the simultaneous inclusion of both
space and time in mathematical models. While there are many well-developed methods for modeling space or time, models that use both explicitly are much fewer (and are computationally demanding.) However, this may change in the near future as the growing use of parallel and grid-enabled computing may provide the computational power necessary for such models [7].

Another issue that I am very interested in has to do with ecological systems with multiple generation times. For example, in malaria ecology we are concerned with the human host, the mosquito vector, and the parasite. The populations of each of these three organisms are structured by either age or stage and the generation times and reproductive mechanisms in each are largely different. This means that the populations of each component of malaria epidemiological cycle have temporal (and spatial) dynamics on different scales. Having different generational times not only effects demographic factors such as population growth and dispersal but can also influence population genetics (which is related to drug resistance in parasites, for example).

A third issue with which I am interested concerns population projections. Projections have sometimes been used in both demography and ecology, however many such projections are concerned with long-term dynamics. Transient dynamics can be very important in disease ecology, especially when focusing on systems with multiple generation times, some of which are very small in comparison to human generation times. Matrix population models are well suited for dealing with such projections; however the inclusion of a spatially explicit component appears to largely be lacking [8].

Finally, spatial analysis has some inherent and very important ethical considerations. In my own dissertation research I am attempting to measure migration patterns among migrants that are political refugees and/or internally displaced. Some of these migrants move back and forth across the Thai-Myanmar border illegally. Others are sometimes engaged in fighting the Burmese military. Both migrant groups have legitimate concerns about being followed. Therefore some major considerations in my research are: 1.) How to model hidden migration streams, and 2.) how to do so in a way that won’t cause any harm, perceived or real, to my study subjects. While I have some ideas about how to do so, largely by indirectly measuring migration, I would welcome input from the many expert disease ecologists that are sure to attend this workshop.

LITERATURE CITED: