Arthur Getis

A. Current and Prospective Research Interests

I am engaged in a series of related research projects in fields as diverse as demography, disease transmission, and economic well being. This work is held together by my consuming interest: the role of spatial patterns for understanding social and economic processes and the development of techniques for spatial analysis. A component of each of the research projects is spatial. With the subject matter of this meeting in mind, let me briefly address the spatial research embodied in the disease transmission projects.

Together with colleagues at UC Davis and in Peru and Thailand, we are attempting to better understand the transmission of dengue fever. In a nutshell, transmission takes place when a female *Aedes aegypti* mosquito blood-feeds on a viremic human, one who harbors one or more of the four dengue viruses, and then soon after blood-feeds on a human who was never before infected by the particular virus held by the mosquito.

The Peru study data has been collected, but the Thailand study is only now getting underway. For Peru, several research papers have been written and several more are planned. The first papers concern the entomological characteristics of disease transmission. The papers now being prepared investigate the serological characteristics of disease transmission and the interaction of entomology and serology.

Here, I will report briefly on some aspects of the entomological research, which represents an assessment of disease risk. Entomology includes a study of the life history strategies of the mosquito vector and a study of the human propensities to facilitate disease transmission. For all practical purposes, only the *Aedes aegypti* is the vector of dengue, and only humans are the sources of the blood the mosquitoes need for oviposition (egg laying). Thus, our study is of the symbiotic relationship between insect and human. As one might expect, given the short range of flight of the mosquito (it flies only about 50 meters from its pupa site) and short life span (about 12 days), the possible susceptible humans will be found in areas near oviposition sites.

Perhaps the chief finding of our studies points toward individual households, more or less spatially separated from other households, as the major source for mosquitoes. More often than not, these households contain elevated numbers of unlidded, outdoor, water-holding containers. Although we know that the spatial aspects of the pattern of mosquitoes (adult and immature) and the pattern of humans (particularly children; who are most likely not to have been infected by any dengue virus) are the key to understanding the transmission of the disease, we have not been able to show a direct link between mosquitoes and infected individuals.

It is for that reason that we have engaged in the Thailand project. In that country, we hope to collect data in such a way that the link between serological and entomological characteristics of a household are less subtle and more obvious. Since the beginning of the Peruvian study five years ago, new technology has made it possible to identify the existence of a viremic individual within 24 hours after becoming viremic. In addition, our sampling scheme goes beyond the household to consider other possible sites for disease transmission.

B. New Types of Spatial Analysis

In our Peruvian study, we engaged in a series of what may be called descriptive spatial pattern identifiers. These included K-functions (global statistics) and G_i clustering statistics (local statistics). These enabled us to identify statistically significant clusters of entomological or serological variables. From these, we could assign probabilities to the likelihood that a particular household might become a site for disease transmission. While we engaged in this project, several other spatial analytical devices were developed but not thoroughly explored. These include spatial filtering and AMOEBA (A Multi-directional Optimal Ecotope-Based Analysis), and spatial modeling using compartments. All of these will be employed in the Thailand study. Spatial filtering allows for the identification of that part of a variable unaffected by spatial association with near neighbors and that part affected by spatial association. AMOEBA allows for the detailed creation of the spatial weights matrix, now a basic part of the regression modeling which requires georeferenced variables. The compartment models include specifications for disease transmission.