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A Comparison of Spatial and Social Clustering of Cholera in Matlab, Bangladesh

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Abstract

Infectious diseases often cluster spatially, but can also cluster socially because they are transmitted within social networks. This study compares spatial and social clustering of cholera in rural Bangladesh. Data include a spatially referenced longitudinal demographic database which consists of approximately 200,000 people and laboratory-confirmed cholera cases from 1983 to 2003. Matrices are created of kinship ties between households using a complete network design and distance matrices are also created to model spatial relationships. Moran's *I* statistics are calculated to measure clustering within both social and spatial matrices. The results show that cholera always clusters in space and seldom within social networks. Cholera is transmitted mostly through the local environment rather than through person-to-person contact. Comparing spatial and social network analysis can help improve understanding of disease transmission.

Keywords

cholera transmission; social networks; neighborhoods; Bangladesh

Introduction

Infectious disease transmission can be influenced by neighborhood-level socio-environmental circumstances as well as by personal interactions that allow pathogens to spread among individuals. Social network analysis can be used to understand disease transmission between people, places, and other “nodes” within a network (Wasserman & Faust, 1994; Hanneman, 2001; Klovdahl et al, 2001). Beyond simply recognizing the existence of ties, these methods can also focus on the nature of connections themselves, examining features such as size, density, boundedness, and shortest paths between nodes (Smith and Christakis, 2008). The edges and arcs in a network are often assigned attributes based on qualities such as kinship or friendship, physical interactions between individuals, or the reported strength of the tie, i.e. “strong” versus “weak” (Granovetter, 1973). Also of

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interest in social network research are the larger social forces at work that determine the resulting network, such as customs or kinship (Wellman, 1988), and how the positioning of actors in relation to other entities and within the larger system of relationships—i.e., their “embeddedness”—affects observed actions and outcomes (Granovetter, 1985). Network analysis, as described by Emirbayer (1997), can be thought of as a non-substantive approach that focuses on the changing nature of relations, rather than on the fixed attributes of the individuals or entities that are linked to one another.

Within the field of geography, network analysis has gained the attention and interest of researchers. At least to some degree, physical-environmental settings and features will influence how individuals and institutions are sorted, grouped, and subsequently interact (White, 2008). The integration of geography and network analysis is visible in various ways, such as predicting the formation of relationships as directly related to physical distance, or measuring the modification of distance on social influence (Zenilman et al, 1999; Christakis and Fowler, 2007; Faust et al, 1999). Recently, curiosity regarding additional theoretical concepts has resulted in works that simultaneously consider ideas of network embeddedness or social influences in conjunction with space and physical location (Radil et al, 2010; Liu et al, 2010). Actor-Network Theory, a relational approach that includes both human and non-human entities as “actors,” has gained ground amongst geographers studying topics varying from restaurant location to wildlife topologies (Bosco, 2006). Within the subfield of economic geography, which already has a history of frequent engagement with the market-based theories of Polanyi (1944) and Granovetter (1973; 1985), the interplay of network, relational, and spatial analysis has led to discussion and debate on the emergence of entirely new conceptual paradigms (Ettlinger, 2003; Sunley, 2008; Hess, 2004).

In health research, network analysis is valuable for examining the diffusion of some diseases, particularly those that spread non-randomly through a population. Much of the previous research on networks and health has focused on HIV/AIDS and other sexually transmitted infections (Jaffe et al, 1983; Auerbach et al, 1984; Bell et al, 1999; Wylie et al, 2007; Ghani et al, 1997; Aral et al, 1999) as well as on contagious illnesses such as tuberculosis and influenza (Fitzpatrick et al, 2001; Klovdahl et al, 2001; Cook et al, 2007; Cliff et al, 1988) or health outcomes associated with social processes, such as obesity (Christakis et al, 2007). In these studies, the networks used have various defining characteristics. They may, for example, consist of single individuals as nodes and physical and/or social contacts as ties (Jaffe et al, 1983; Auerbach et al, 1984; Bell et al, 1999; Ghani et al, 1997; Aral et al, 1999; Fitzpatrick et al, 2001; Christakis et al, 2007). Locations and places represent nodes in a network, with the movement of populations between them acting as linkages to facilitate diffusion (Sabel et al, 2010). This has been documented at varying spatial scales, such as within cities (Wylie et al, 2005; Klovdahl et al, 2001) or across much larger areas, e.g. the spread of epidemic influenza across Iceland (Cliff and Haggett, 1981; Cliff and Haggett, 1988).

This study investigates cholera transmission in rural Bangladesh from 1983 to 2003, using a kinship-based social network where small household clusters act as nodes and are connected by individual migrations. Understanding how the diffusion of the pathogen responsible for cholera is facilitated by common daily interactions and behaviors can inform prevention efforts for this disease and those of a similar nature. The local aquatic environment provides the habitat for the bacteria responsible for cholera thus the disease clusters in space (Emch, 1999; Ali et al, 2002a; Ali et al, 2002b). The occurrence of direct person-to-person transmission, meanwhile, is considered rare by some and supported by others (Pollitzer, 1959; Tamayo et al, 1965; Swerdlow and Issacson, 1994). By taking a network-based approach, this research contributes to the discussion of dominant forms of transmission while introducing a new approach to examine cholera diffusion. Specifically, the

concentration of cholera within a network is compared to the clustering of the disease in space. We hypothesize that a potential route for cholera is through contaminated food and water shared between individuals in residential settings, yet that the dominant form of transmission is through contact with the bacteria in the local environment. Evidence of clustering among social contacts, however, would lend support to the former.

Background

The study area is Matlab, Bangladesh, which is located approximately 50 km southeast of Dhaka at the confluence of the Meghna and Ganges Rivers (Figure 1). The population of Matlab is approximately 200,000 and the people reside in clusters of patrilineally-related households called *baris*. A *bari* may contain anywhere from one to a dozen households, with an average of five or six (Ali et al, 2005). Since 1966, the International Center for Diarrheal Disease Research, Bangladesh (ICDDR,B) has administered a surveillance system in Matlab, monitoring the population and recording demographic and health-related events (D'Souza, 1981). This database offers a unique opportunity to examine the relationships between environmental and population factors and health outcomes. Diarrheal diseases such as cholera are a significant cause of morbidity and remain endemic to the region (Black et al, 1981; Emch, 1999; Emch et al, 2002). Aquatic phytoplankton and zooplankton provide a reservoir for the cholera-causing *Vibrio cholerae* bacterial pathogen (Islam et al, 1990; Islam et al, 1993; Nalin et al, 1977; Nalin et al, 1996; Huq et al, 1983; Epstein et al, 1993; Colwell, 1996). *V. cholerae* are able to inhabit brackish, coastal, and fresh water environments for significant periods of time due to the presence of these reservoirs. Cholera can be transmitted through contaminated surface water, which is used by the population for bathing, washing clothes and dishes, cooking, and sometimes drinking (Emch, 1999; Hoque et al, 1996). Furthermore, unsanitary latrines are responsible for surface water contamination.

Cholera transmission occurs through the fecal-oral route and the pathogen is able to survive naturally in aquatic environments (Colwell et al, 1977; Colwell et al, 1990). Two forms of transmission have been described, known as primary and secondary (Miller et al, 1985; Craig, 1988; Franco et al, 1997). Primary transmission is the result of direct contact with the pathogen from the aquatic reservoir; this often occurs as seasonal events encourage growth of the bacteria in the environment, raising the risk of contact. Secondary transmission is the result of subsequent spread from infected human hosts to other susceptible individuals through fecal contamination. Secondary transmission occurs through person-to-person contact that is driven by human activity leading to contamination of shared food and water sources (Birmingham et al., 1997; Acosta et al., 2001; Shaprio et al, 1999; Swerdlow et al., 1997; Spira et al., 1980). Secondary transmission can also occur when people eat contaminated food from a restaurant or street vendors (Weber et al., 1994; Ries et al., 1992; Koo et al., 1996).

Most secondary transmission in Matlab likely occurs with food and water acting as vehicles of transmission (Quick et al., 1995; Gunn et al., 1981). Interaction between people may occur within or outside of the household, with acquaintances and neighbors. Equally likely and perhaps more common, however, is contact with family members and kin. The continuing importance of family in Bangladeshi society despite fertility decline and modernization lends support to the argument that the family remains an important institution in an area such as Matlab, and that activities in daily life, such as labor and meals, often take place in the presence of related individuals (Amin, 1998; White, 1997). Rural areas also more likely adhere to traditions such as *purdah*, the confinement of women to the home, limiting female social contact to family members (Amin, 1997). If cholera is to spread via

consumption of water or food contaminated by others, there is a significant chance that the transmission is within their family.

Individuals are more likely to interact with others who are closer to them in space than those located further away (McPherson et al., 2001). The spatial distribution of family in Matlab is not random; rather, when a son who marries moves out of his father's household, he is likely to either live in a household within the same *bari* or establish a *bari* of his own that is geographically close as a result of land partition customs (Quisumbing and Maluccio, 2000). Therefore, due to the traditional importance of family and customs such as *purdah* the social network of an individual in Matlab is likely significantly composed of kin.

Data

A combination of health, demographic, and geographic data are used to examine the social and spatial clustering of cholera in Matlab. Since 1966, the ICDDR,B has administered a Health and Demographic Surveillance System (HDSS) in the study area which has a population of approximately 200,000 people. Each resident, upon entry into the study area, through either birth or in-migration, is assigned a unique identification number within the database known as a Registration ID (RID). The individual is linked through this ID to a *bari* and household. Since a person can live in one *bari* initially but then relocate to another, every *bari* of residence for an individual is recorded in the HDSS, including dates of in- and out-migration. Community health workers visit each *bari* in Matlab twice a month and record data on births, deaths, and migrations. Individuals who are sick are referred to and treated at the ICDDR,B hospital at no cost to the patient. Data on laboratory-diagnosed cases of diarrheal diseases are recorded at the hospital and then linked to demographic information for individuals, their *baris*, and households. Individual-level study data include the *bari* of residence of all Matlab residents between January 1st 1983 and December 31st 2003, dates of in- and out-migration, and all laboratory-confirmed cholera cases. A geographic information system (GIS) database of Matlab was used to link cholera cases to a *bari* location (Emch et al, 2002).

Methods

Social networks were constructed and used to model kinship relationships because they are likely to engage in some form of interaction, either within or outside of the household. A kinship-based social network was built using the longitudinal HDSS which makes it possible to “track” an individual from *bari* to *bari* over time within the Matlab study area. The assumption guiding this network is that when an individual moves, he or she maintains interaction with the previous *bari* of residence due to existing relations. Though the original migration is directional, the resulting interaction between the two *baris* is mutual; therefore the social connections are non-directional. These inter-*bari* migrations are primarily based on kinship, i.e. marriage into a different family. Specifically, the actors in this network are people with some kinship-based relationship that will foster movement between physical residences. Using the migrations of related individuals between *baris* as evidence of a social connection is more precise than simply assuming all related individuals interact with one another, as previous cohabitation may create closer bonds. Naturally, this type of network will not capture all social interactions in the lives of the Matlab population since kinship is not the only reason individuals are connected to one another. Yet both rural communities and lower socio-economic settings are described as particularly family-oriented due to familial visits, customs, and expected support (Guest and Chamrathirong, 1992; Hollinger and Haller, 1990).

The kinship network is based on individual-level migrations linking *baris*, which are the “nodes,” or units of analysis in the network. Each individual-level migration from *bari* x to *bari* y creates a social linkage between those two *baris*; each linkage of this type is called a dyad. A complete list of all dyads, or an edgelist, can be represented in graphical or matrix form. In a social adjacency matrix, or any matrix created on the basis of adjacency, 1 represents the presence of a single, non-directional social connection between two *baris* and 0 represents no social connection. The use of 1 or 0 to represent linkages was due to the relatively small variation in the strength of connections, as there was an average of less than 1 migration to or from a *bari* per year. Given greater variation, the weights matrix would be re-evaluated based on differences in levels of communication and influence (Leenders, 2002). Multiple social networks were first constructed for each year; i.e., the linkages between *baris* for 1983 were not considered when constructing the social network for *baris* in 1984, and so forth. This approach was chosen to account for uncertainty regarding how long an active social linkage based on a migration may last. Each year was first analyzed independently in order to investigate trends over time. To account for connections created between *baris* that may have remained over time, a cumulative network was then created. A cumulative network is one that considers all social connections during the entire study period. Beginning in 1983, connections created during each year remained throughout the remainder of the study period. These accumulated network connections and all known cholera cases were then used to predict clustering of cholera rates across *baris* in 2003.

Clustering of cholera in space at various neighborhood scales was also examined in order to compare the effects of the local environment. To determine spatial clustering of cholera, for each *bari* all other *baris* located within a 500, 1000, and 2000 meter buffer were identified. This information was used to make three different distance-band spatial matrices of all *baris*, where 1 represented a common neighborhood between two *baris* and 0 represented no common neighborhood. These three different buffers, or “neighborhoods,” were used in order to compare spatial clustering at various scales. Previous research in Matlab on cholera and other diseases has used similar neighborhood scales. Because of variation in population density and environmental features, using more than one type of buffer size allowed for comparison of the scales at which cholera is most likely to cluster.

The total number of *baris* evaluated in both the social and spatial analysis was 8,873. The dependent variable of interest was the rate of cholera in a *bari* during a specific year, aggregated from all individual recorded cases. For the entire 21-year study period, there were 8,765 cases of cholera in Matlab. Individual-level cholera cases were assigned to a *bari* for each year using the unique RID of the individual diagnosed with cholera. For every *bari*, the total number of cases that year was divided by the total population of the *bari* to produce a cholera rate. For each year, there was thus an $n \times 1$ vector of *bari*-level cholera values. An additional vector was created containing the value of change in the cholera rate for each *bari*, or the difference between the rate of the current year of interest and the previous year.

For each year, the four $8,873 \times 8,873$ matrices, one of social adjacency and three representing the different shared spatial neighborhoods, were row-standardized into weights matrices. This gave both social affiliates and spatial neighbors equal “weight” in terms of their influence on a particular *bari*. Standardization also permitted for comparison of both the social and spatial models. The matrices could then each be multiplied by either the $n \times 1$ vector of cholera rates per *bari* or the vector of change in cholera rate, generating a lag operator which represents the average rate of cholera or cholera change in neighboring *baris*, or those either socially-affiliated (social lag) or spatially connected (spatial lag).

The global Moran's I statistic was used to identify both the social and spatial clustering. Typically used as a measure of spatial autocorrelation, Moran's I can also be applied to

detect clustering within other types of networks representing elements such as language or cultural variables (Dow, 2007). In this case, the result provides a global measure of the degree of clustering of *baris* with similar cholera rates, in a traditional spatial application but also within the social network. The term “global” refers to average clustering within the entire social network or geographic area, as opposed to a “local” measure, which is used in spatial analysis to identify the relationship between a specific value and the average of the neighboring values. Note therefore that the tests here only reveal global trends. Moran's *I* produces a coefficient ranging from -1 (indicating perfect dispersion) and 1 (indicating perfect correlation), with a value of zero implying a random spatial pattern. The measure was used in this study as an indicator of overall clustering of similar cholera rates. Clustering of the change in cholera rates across *baris* was also tested, i.e. whether those *baris* connected socially and spatially saw similar changes in rates of cholera from the previous year. Z-scores for significance were Monte Carlo simulation-derived using 10,000 runs, under a null hypothesis of no network autocorrelation either in geographic or social space. The test was run for each of the twenty-one years using the social connectivity matrix as well as the three spatial distance matrices. Additionally, the Moran's *I* was run for the cumulative social network consisting of connections created between 1983 and 2002 to test for clustering in 2003. Each separate analysis produced both the coefficient representing the extent of clustering and a z-score for significance for each year of the data. The cumulative network produced a single coefficient and z-score for 2003. The analyses were done in Stata 9 and MATLAB 7.7.0.

Results

The densities of the individual networks were relatively sparse, which is assumed to be a result of higher inter-household migration than inter-*bari* migration; that is, there may be more movement occurring between the households within a *bari* than between *baris* themselves. Table 1 shows cholera incidence in Matlab during the twenty-one year study period; the number of cases varied dramatically from 47 cases in 1990 (0.24/1000) to 1147 (5.53/1000) in 1993. Figures 2 through 4 show the z-scores of spatial autocorrelation at the three neighborhood levels. Z-scores of more than 1.96 indicate a very strong probability of clustering in space. Significant spatial clustering ($p < 0.05$) of both cholera rates and yearly change in cholera rates for *baris* occurred at the 500-meter neighborhood for all years with the exception of 1990 (Figure 2). The results were similar for spatial clustering at both the 1000-meter and 2000-meter neighborhood scales (Figures 3 and 4); at 1000 meters, all years showed significant clustering of cholera rates except for 1990, and all years showed significant clustering of change in cholera rates. At 2000 meters, clustering for both variables was significant at the $p < 0.05$ level for all years except 1990 (Figure 4).

The global Moran's *I* statistic was then used to assess the degree of clustering of cholera across *baris* connected by the kinship-based social network, as well as clustering of yearly change in cholera rates across socially connected *baris* (Figure 5). Significant social clustering of cholera rates between connected *baris* was found during only three years, 1989, 1993, and 2000. Clustering of change in cholera rates occurred only in one year, 1989. The cumulative social network used to predict clustering of cholera rates in 2003 was not significant.

Discussion and Conclusions

This study compares spatial and social clustering of cholera. Previous studies suggest that neighborhood-level factors are important predictors of cholera incidence, affecting populations through both primary and secondary transmission dynamics. In order to measure the impact of secondary transmission, especially through contact between households linked

by kinship, connected *baris* were identified to create a social network. The global Moran's I statistic was used to measure and compare both types of clustering within two different types of matrices, representing space and social connectedness. The results illustrate that spatial clustering of cholera is much more prevalent in Matlab than clustering socially. This is likely due to socio-environmental risk factors at the neighborhood scale, such as water and sanitation environments and population density. The same is generally true for clustering of differences in cholera rates from the previous year, providing further evidence that local effects matter. This finding is robust across spatial scales suggesting that common environmental and demographic effects are important in both smaller and larger neighborhoods.

Clustering of similar cholera rates in the social network of *baris* was less common, although there were three years in which it was significant. Clustering in change of cholera rates from the previous year also occurred in two of those years. During two of the three years in which there was social clustering, average rates of cholera across *baris* were not exceptionally high, though 1993 did see the highest rate of cholera during the study period, which may explain the dramatic differences in clustering during that year.

The main limitation of this study from a social-networks perspective is that only kinship connections were measured. However, the comparison between social clustering and spatial clustering suggests that the local environment is of greater importance than social connectivity in cholera transmission. Furthermore, the possibility exists that the observed clustering in space is a result of not only environment, but also social interaction with non-kin. The spatial network may thus, effectively, also capture a social network.

Improved understanding of disease transmission dynamics is critical for public health. While improvements in sanitation, socioeconomic status, and education have helped reduce rates of diarrheal disease in Bangladesh and other countries in the developing world, it remains a priority to identify specific pathways of transmission and thus develop effective intervention methods. This research introduces a way of analyzing if and how social interaction may contribute to cholera occurrence within rural Bangladesh. This approach can also be used for other infectious diseases.

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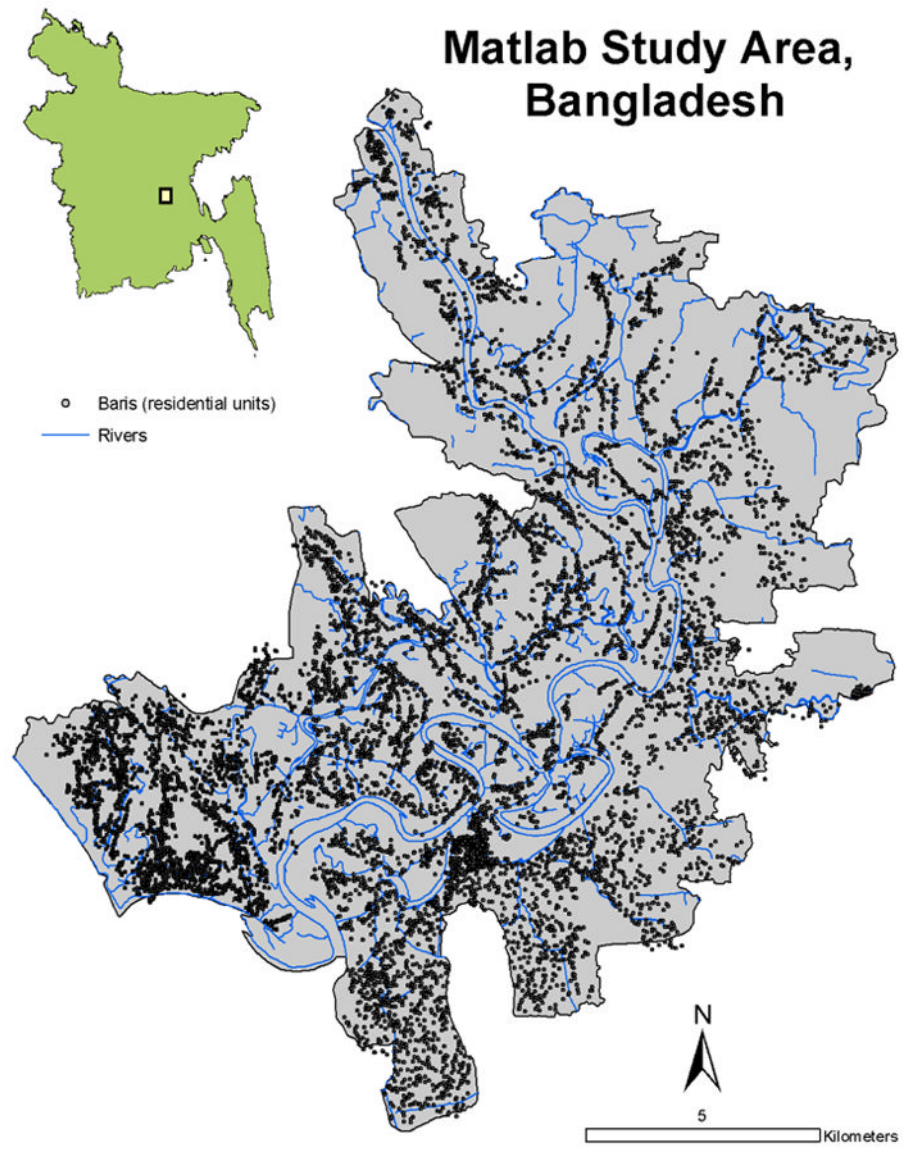


Figure 1. Study area map

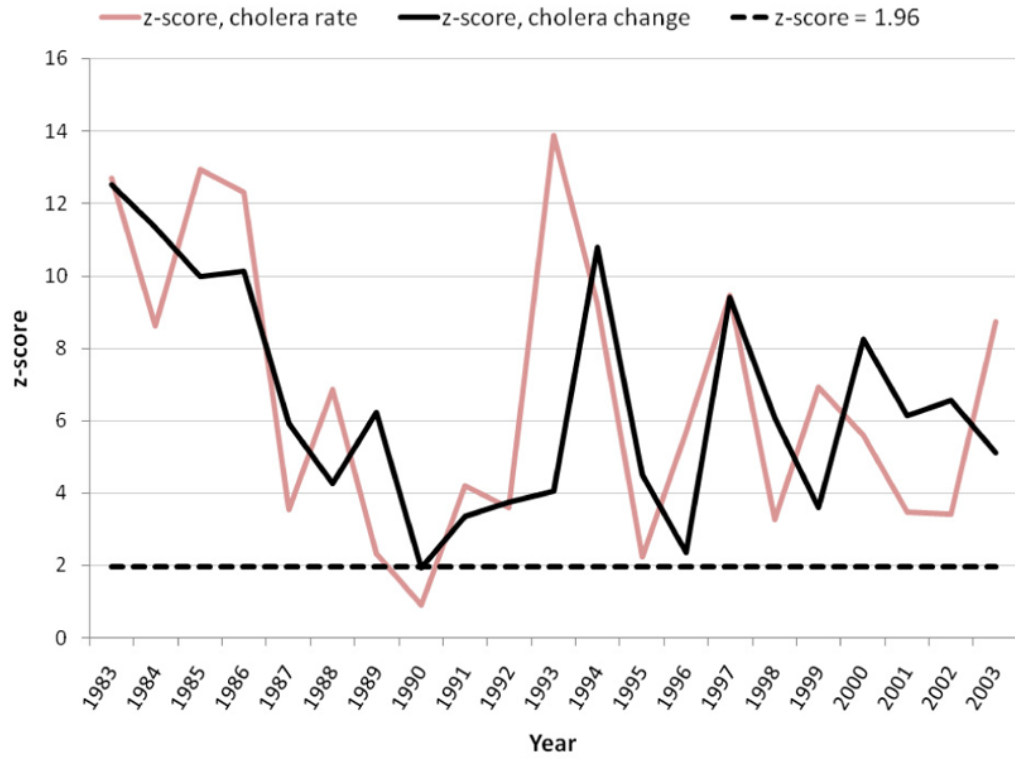


Figure 2. Significance of spatial clustering of cholera rates and change in cholera rates, 500-meter neighborhoods

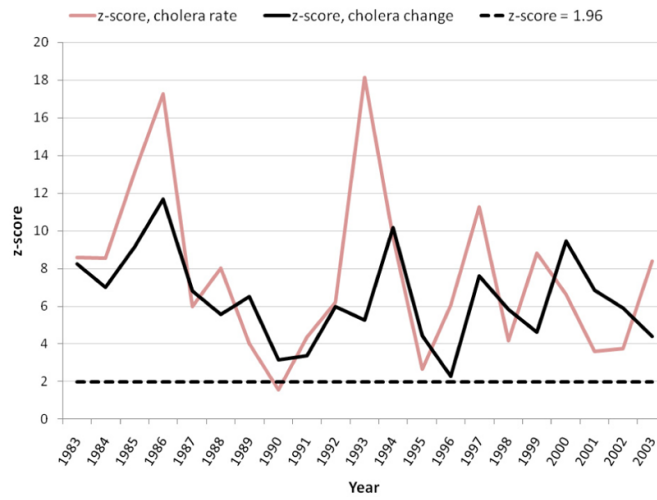


Figure 3. Significance of spatial clustering of cholera rates and change in cholera rates, 1000-meter neighborhoods

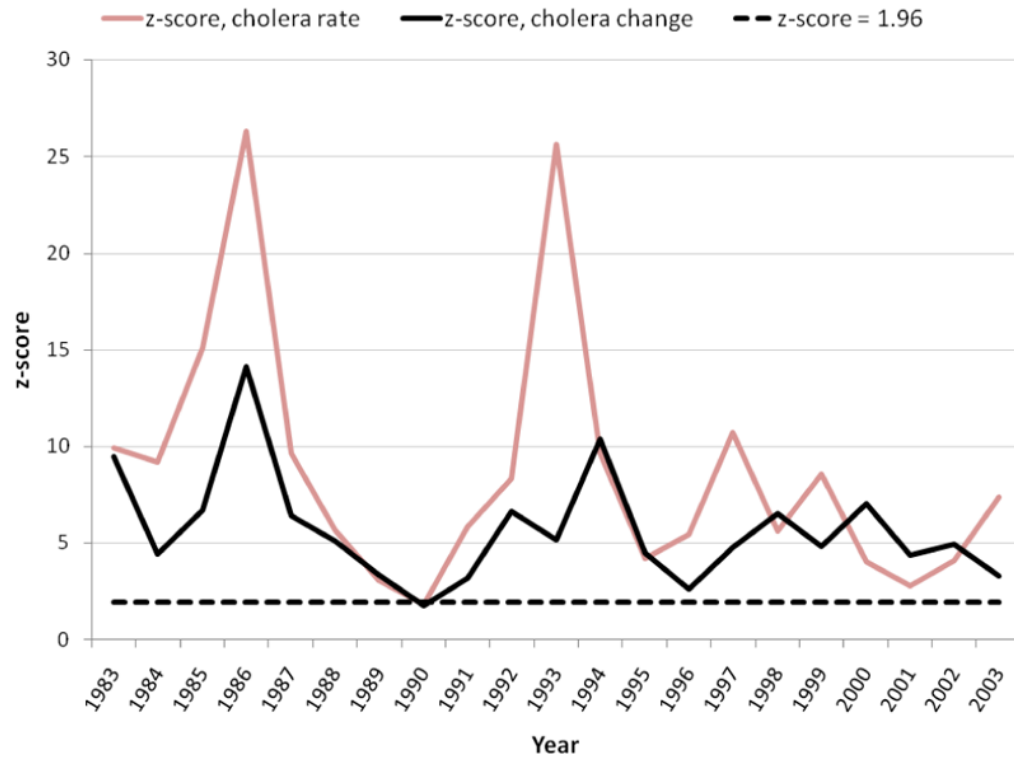


Figure 4. Significance of spatial clustering of cholera rates and change in cholera rates, 2000-meter neighborhoods

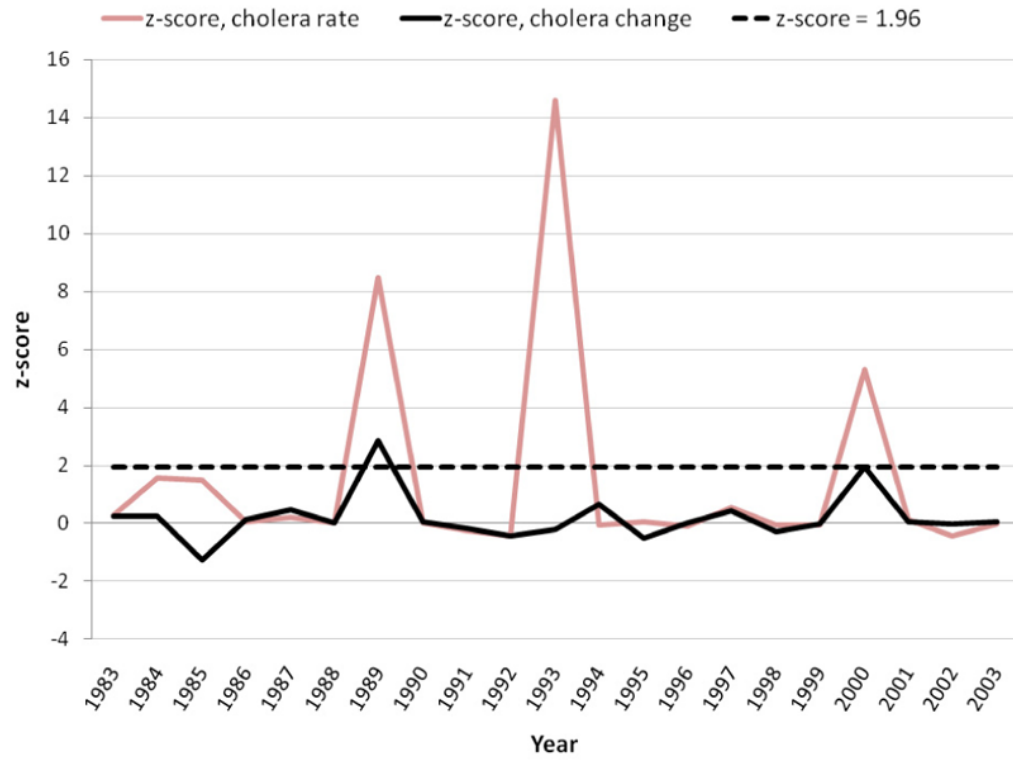


Figure 5. Significance of social clustering of cholera rates and change in cholera rates

Table 1
Number of cholera cases, total population, and incidence by year

Year	# Cholera Cases	Total Population	Incidence per 1,000
1983	825	181,224	4.55
1984	452	182,779	2.47
1985	467	183,354	2.55
1986	788	185,857	4.24
1987	414	189,649	2.18
1988	342	192,362	1.78
1989	63	194,833	0.32
1990	47	196,777	0.24
1991	229	199,145	1.15
1992	722	199,450	3.62
1993	1,147	207,332	5.53
1994	739	207,848	3.56
1995	371	208,459	1.78
1996	267	210,279	1.27
1997	509	211,157	2.41
1998	591	213,073	2.77
1999	255	214,344	1.19
2000	120	214,370	0.56
2001	99	203,922	0.49
2002	167	205,709	0.81
2003	151	206,953	0.73