GIS for Health and the Environment

Development in the Asia-Pacific Region

With 110 Figures
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Preface

“As the world becomes more integrated through the trade of goods and services and capital flows, it has become easier for diseases to spread through states, over borders and across oceans — and to do serious damage to vulnerable human and animal populations.”


The global cost of communicable diseases is expected to rise. SARS has put the world on alert. We have now Avian Flu on the watch. Recognizing the global nature of threats posed by new and re-emerging infectious diseases and the fact that many recent occurrences originated in the Asia Pacific regions, there has been an increased interest in learning and knowing about disease surveillance and monitoring progresses made in these regions. Such knowledge and awareness is necessary to reduce conflict, discomfort, tension and uneasiness in future negotiations and global cooperation.

Many people are talking about the GIS and public and environmental health. The way we make public policies on health and environmental matters is changing, and there is little doubt that GIS provides powerful tools for visualizing and linking data in public health surveillance. This book is a result of the International Conference in GIS and Health held on 27-29 June 2006 in Hong Kong. The selected chapters are organized into four themes: GIS Informatics; Human and Environmental Factors; Disease modeling; and Public health, population health technologies, and surveillance.

As evident from the chapters, the main problem in GIS-based epidemiological studies is the availability of reliable exposure data. There is also a huge problem of showing adequate responsibility and ability to meet public concerns, such as protection on privacy and quick response systems. There has been some works done in search of the right approach in bringing together and reconciling market and public interests. Talking to each other and sharing critical information are getting increasingly important. Much work remains to be done to improve the GIS-based epidemiologic methods into tools for fully developed analytical studies and, particularly, the need to identify standard interfaces and infrastructures for the global disease reporting system.

January 2007

Poh C. Lai
Ann S.H. Mak
Conference Chair
Poh C. Lai, University of Hong Kong, China

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GIS Informatics
Exploratory Spatial Analysis Methods in Cancer Prevention and Control

Gerard Rushton
The University of Iowa

Abstract: Improved geocoding practices and population coverage of cancer incidence records, together with linkages to other administrative record systems, permit the development of new methods of exploratory spatial analysis. We illustrate these developments with results from a GIS-based workbench developed by faculty and students at the University of Iowa. The system accesses records from the Iowa Cancer Registry. In using these methods, the privacy of individuals is protected while still permitting results to be available for small geographic areas. Geographic masking techniques are illustrated as are kernel density estimation methods used in the context of Monte Carlo simulations of spatial patterns of selected cancer burdens of breast, colorectal and prostate cancer in Iowa.

Keywords: cancer prevention and control, exploratory spatial analysis

1 The need for maps in cancer prevention and control

The theme of this chapter is the design of cancer maps for cancer control and prevention activities. Abed et al. (2000) describe a framework for developing knowledge for making decisions for comprehensive cancer control and prevention. The decisions these authors have in mind involve local communities setting objectives, planning strategies, implementing them, and finally, determining improvements in health achieved by their activities. Each of these steps is explicitly spatial: where activities are directed, who is affected, and whose health is improved? Location is a critical part of this framework.

As with all chronic diseases, factors that influence the burden of the disease on any population include the behaviors of people, characteristics of environments, and availability and accessibility of health screenings and treatments. Objectives to improve population health, therefore, must iden-
tify spatial differences in these factors and must address strategies to change them in ways that will lead to improved health outcomes. Cancer maps play an important role in this process. Particularly geographic aspects of these tasks are:

- Spatial allocation of resources;
- Identification of areas with higher than expected incidence rates (disease clusters);
- Optimal location of services.

All three tasks require that the maps of the cancer burdens should capture any special demographic characteristics of local populations so that actions for control and prevention relate to population characteristics. None of these tasks should use cancer rates adjusted to standard population characteristics. Yet, these are precisely the characteristics of many cancer maps—see, for example, Pickle et al. 1996; Devesa et al. 1999.

1.1 The limitations of cancer mortality maps

In the short history of mapping cancer, most attention has been given to mapping cancer mortality; for most countries, cancer mortality data are collected routinely.

Since the geocode on a typical death certificate is some politically recognized area—often, in the United States a county—data is available for counties and most maps use counties or aggregates of counties, (Devesa et al. 1999). Mortality maps, however, are not so useful for planning control and prevention interventions because spatial variations in mortality rates can be due to differences in behaviors, in the environment or in local health system characteristics. Yet, untangling risks due to differences in these three factors is precisely what is required before plans to reduce cancer burdens can be established. With the development of cancer registries, however, data is available that allows attempts to be made to separate these influences and to develop interventions that will optimally reduce rates. Cancer maps have a vital role to play by mapping these factors, in addition to mortality.

1.2 The potential contribution of cancer registry data

There are two ways in which cancer registry data can be used for making cancer maps. They can be used to break down the burden of cancer on local populations into component parts. Assumed here is that the cancer registry is population-based; i.e. it accounts for all cases of cancer in a defined population. Although it may rely on health care facilities for much of its
data, it must not be facility based. In most cases, registries are area-based and track down incidences of cancer in its defined population wherever they are diagnosed and treated. The components of interest are first confirmed diagnoses of cancer; the stage of the disease at the time of first diagnosis; the first course of treatment, survival rate, and mortality rate. Other components of cancer are screening rates and treatment rates. Data availability for these components often depends on the comprehensiveness of the health information available for the defined population (see Armstrong 1992).

1.3 The role of exploratory spatial analysis

In “exploratory spatial analysis” of cancer, geographic scale and pattern are explored. Each cancer map represents a decision to focus on a defined geographic scale and specific patterns may be revealed—or concealed—by the scale chosen. Figure 1 illustrates this principle using three infant mortality maps of one county in central Iowa. Approximately 20,000 births and 190 infant deaths occurred in this county in the four year period from 1989 through 1992. After geocoding each birth and death to its residential address, the three maps on the right of Figure 1 show the pattern at the scales captured by three, commonly used, administrative areas. A property of these maps is that the variability of the infant mortality rates depends on the size of the areas mapped. The rate for Zipcodes varies from 0 to 20 deaths per thousand births; for census tracts the rate varies from 0 to 36 and for census block groups the rate varies from 0 to 72. The legends for each map—not shown here—must necessarily be adjusted to accommodate these different variances. The sensitivity of the patterns of infant mortality to scale are clear on the left where geographic scales of the three maps are formally defined as spatial filters of 1.2, 0.8, and 0.4 miles respectively—applied in each case to a 0.4 mile grid from which the density estimates were made (see Bithell 1990; Rushton and Lolonis 1996). Again, on the left, patterns are different and depend on scale. We can conclude that patterns depend on scale and actions based on patterns should consider the scales at which the patterns were derived and ask whether the actions contemplated are reliably based on the data that supported them.
Exploratory Spatial Analysis Methods in Cancer Prevention and Control

The ability to control the spatial basis of support for cancer rates is the key idea that geographic information systems bring to the task of providing decision support for cancer prevention and control. A key question we ask is at what geographic scale do significant differences in cancer incidence rates or other measures of cancer exist in any region of interest? A reason for asking this question is so that we can decide the scale at which interventions should be planned. Logical though this question may appear, it has not been the question that has driven the rather large literature of spatial analysis of cancer. Traditionally, cancer maps were based on pre-defined political or administrative units for which cancer data was collected. Starting with regions already defined we made maps and then asked “do we see a pattern.” Such a strategy pre-supposes that spatial variations that occur within the regions mapped do not exist or, if present, are not relevant or important. With GIS, however, we start with geocoded data—at the level of points or small areas—and then we ask “at what geographic scale do we want to view this pattern?” Thus, it is the much smaller literature of spatial analysis of cancer based on data manipulated in a GIS that is the literature most relevant to cancer control and prevention. Cancer maps for this purpose employ density estimation methods. Unlike traditional cancer maps that show cancer statistics based on spatial units of dif-
different sizes, shapes and populations that conceal scale dependent patterns, density estimation techniques are designed to control the spatial basis of support for the spatial pattern of any statistic of interest. These are made possible by developments in the availability of geospatial data, geocoding techniques, and methods of spatial analysis that allow the opportunity to control the size, shapes and population characteristics for the spatial units for which statistics are computed.

1.4 Mapping cancer burdens

The first measure of the cancer burden on a population is the rate of incidence of any particular cancer type adjusted for age and sex of the local population. The first choice to be made is between direct and indirect rate adjustment methods. Direct adjustment of rates is made when rates are to be compared from one area to another to note the rate burden on the population. In such a situation the question being asked is the hypothetical question “if the age-sex structure of the local population was the same as a standard population, what would the overall cancer incidence rate be? These rates are made by multiplying locally observed age-sex defined cancer rates by a common set of weights that sum to one that describe national population characteristics, (see Pickle and White 1995). Indirect adjustment of rates are made when the question being asked is “if the local population were to have cancer incidences at the same rates as a standard population, how much more or less does cancer occur there than in the standard population.” Indirectly adjusted rates are best used when resources are to be allocated to areas based on the impact of the rates on the population of the local area—see Kleinman 1977. The second choice of cancer burden is about the proportion of diagnosed cancer cases that are late stage at the time of their first diagnosis. This can be measured as the proportion of incidences observed in a population that are late stage, or, can be measured as the number in a population adjusted for its age and sex characteristics. The third choice is mortality rates. Illustrations of the different kinds of maps of these three cancer burdens for the Iowa population between 1998 and 2002 can be seen at Beyer et al. 2006. All maps are indirectly age-gender adjusted using national rates of cancer with the rates defined as actual observed number of cancers in the spatial filter area divided by the number expected given the demographic characteristics of people in the filter area. Rates defined in this way reflect the demographic characteristics of the local area. Statistically they are more robust than directly age-gender adjusted rates because they are made by multiplying national rates that are stable by populations in the filter areas which are also stable. The
geographic detail in the indirectly adjusted rate maps is far superior to the geographic detail possible in directly age-sex adjusted maps.

I illustrate the control of scale with design of a map of late stage colorectal cancer rates in Iowa for the period 1993 through 1997. The approximate population of Iowa in 2000 was 2,800,000. The number of new incidences of colorectal cancer in Iowa for a four year period was 8,403 cases. All were geocoded either to their street address, or, in a few cases where the street address could not be matched to the geographic base files to the centroid of their Zip code; there are 940 Zip code areas in Iowa. Using a regular grid of four miles, we applied the “sliding window” method of Weinstock (1981) for estimating the late-stage rate at each node of this regular grid. For the area surrounding each node on this grid, the rate of late stage diagnosis is the ratio of the number of late stage colorectal cancers to the total number of colorectal cancers within the filter area (or kernel). In Figure 2 we illustrate the grid points from which the late stage colorectal cancer rates were constructed. On the right, the rates are illustrated as average values for the closest eight neighbors to each grid point, using an inverse distance weighting algorithm. In Figure 3 we change the scale of the patterns by using progressively larger spatial filters from ten miles radius to fifteen miles radius. In this illustration, we are mapping the rate with which women diagnosed with early stage breast cancer selected breast conserving surgery (lumpectomy with radiation) rather than the more radical surgery—mastectomy. As is to be expected on all disease rate maps, as the geographic scale of the map decreases (larger spatial filters), details in the pattern—many of which are spurious because the rates are based on small numbers—drop out and a more persistent regional pattern emerges which is best seen on the fifteen mile filter map. The named places on these maps had radiation facilities at the time of this data—early 1990s.

Fig. 2. Late stage colorectal cancer (number late stage per thousand cases of colorectal cancer diagnosed) interpolated from computed values on the regular grid (left)
Fig. 3. Number of women selecting lumpectomy with radiation per 1000 cases of localized breast cancer, Iowa, 1991-1996; map on the left used 10 mile spatial filter; map on the right used 15 mile filter.

The maps illustrate the tendency for women who live far from radiation facilities to not choose this recommended surgical therapy over the traditional more radical surgery of mastectomy. Recent research confirms that this tendency is a national phenomenon (Nattinger et al. 2001; Schroen et al. 2005). The critical choice in such spatial filtering of disease data are selection of the size of the grid and the size of the filter (Silverman 1986). The grid size is the less important choice since providing the grid is detailed enough geographically to provide the level of resolution desired in the output, further detail in the grid will add no further value to the map. Changing the size of the spatial filter, as illustrated in Figure 3, will affect the pattern because the differences in rates that typically occur within the size of the filter will be averaged or smoothed and some of the variability in the geographic pattern will disappear.

The geographic detail of a disease density map does depend on the level of spatial aggregation of the data used. Figure 4 illustrates late-stage colorectal cancer rates for the case (left map) where input data consists of approximately 940 Zip code areas in Iowa compared with (right map) where input data is individually geocoded cancer cases. Note that there are differences between these maps, particularly along the edges of the study area; but the geographic patterns are also quite similar. We conclude that, at this geographic scale—15 mile radius filters—considerable geographic detail is preserved by using the spatially aggregated data. This is important since geocoded data of individuals is often not made available by cancer registries in North America to researchers or to public health personnel because of privacy laws and commitments to maintaining the confidentiality of data records (CDC 2003; Olson et al. 2006). The improved geographic detail may also be compared with Figure 5 where area-based disease maps are based on the same data aggregated by county.
Fig. 4. Comparison of spatially filtered maps (15 mile filters) using geocoded cancer data at two different levels of spatial resolution. Rates of late-stage colorectal cancer at first diagnosis 1993-1997. The map on the left is made from spatially aggregated data which used Zipcode centroids as geocodes. The map on the right used address-matched geocodes. The same cancer incidence data is used on both maps.

Fig. 5. Percent of colorectal patients with late stage tumors at time of first diagnosis, Iowa, 1993 - 1997

1.5 Adaptive spatial filters

Further geographic detail may be achieved by adapting the size of the spatial filter to the density of the disease data.

In Figure 6 the map on the left aggregates the cancer cases in order of their distance from the grid point until at least 100 cases are found. The map on the right of this figure shows percent late-stage colorectal cancer rates based on a 24 mile filter. The spatially adaptive filter provides more geographic detail in areas of high population density where the numbers of cancer cases within any given size spatial filter area is large enough to support a reliable estimate of the late-stage rate—Tiwari and Rushton 2004; Talbot et al. 2000. The spatial detail provided by such maps should not be confused with the apparent geographic detail on maps that are
smoothed using rates for administrative or political entities (Kafadar 1996). Such maps use spatial smoothing functions based on centroids of areas. Examples can be seen in two recently published cancer atlases which superficially may appear to be similar to the mapping method proposed here—Tyczynski et al. 2006; Pukkala et al. 1987. In these atlases, rates are computed for political areas (counties in Ohio; municipal areas in Finland)—first-level data smoothing--and then the smoothed cancer rate surface is produced by a floating spatial filter producing a weighted average of the rates in surrounding counties—second-level data smoothing. This double smoothing of data and then rates, we believe, should be avoided. In kernel density estimation the data for numerator and denominator are collected for the spatially adaptive area and then the rate is computed and attributed to the grid point from which the kernel is measured. This method for controlling the change of support (see Haining 2003, p 129) is theoretically more valid than the gross spatial smoothing functions so commonly used. Spatial interpolations are made only locally; that is, between closely spaced grid points.

Fig. 6. Adaptive spatial filter--left map uses closest 100 cases to define the filter area from each grid point on a three mile grid; right uses a 24 mile filter area. Number of late stage colorectal cancer cases per thousand cases at first diagnosis, Iowa, 1993 – 1997

1.6 Adjusting for rate variability due to small numbers

The issue of reliability of rates is important. With traditional spatial density maps that use fixed size spatial filters, some local rates are based on a large amount of information while other local rates are based on little information. A Monte Carlo procedure can be used to evaluate the statistical significance of rates observed at any grid point. For this procedure we use random re-labeling of the known cancer locations so that the total number of late-stage cases in the study area is equal to the observed number of such cases. Thus the null hypothesis being tested is that the rate of late-
stage colorectal cancer for this time period was uniform across the state of Iowa. We computed 1,000 simulated maps of late-stage colorectal cancer based on the probability that each colorectal cancer incident case is late-stage according to the statewide rate. For each of these simulated maps we compute the rate of late stage at each grid location. We then compute the proportion of the simulated rate maps at each grid location that are smaller than the observed late-stage rate. This is known as a p-value (probability value) map. Figure 7 illustrates these proportions for the colorectal cancer map shown in Figure 6. Because this method of measuring reliability involves multiple tests of the hypothesis that the observed rate is greater than the rate of the null hypothesis, these proportions are not equivalent to conventional significance rates—for a discussion of true maps of significance, see Kulldorff 1997 and 1998. This is a well-known feature of the work of Openshaw et al. (1987) where a similar approach was first used. Further details of this test procedure are provided in Rushton et al. 1996.

Fig. 7. P-value map showing results of Monte Carlo test of hypothesis that no areas are significantly different from the state wide rate of late-stage colorectal cancer, Iowa, 1993-1997

2 Conclusions

Different measures of the cancer burden can be mapped at reasonably local geographic scales. These maps can be used by both health professionals and the public to guide policy making, decision making, and action. The spatial basis of support for cancer statistics that are mapped needs more research and experimentation. Spatial density estimation techniques have
been comparatively neglected in favor of inferior spatial analysis approaches that have focused on given, often inappropriate, spatial units. The drawbacks of current mapping approaches are well-known. Rates for areas with different population sizes differ in their reliability and many statistical methods and spatial smoothing methods are used to compensate and adjust for these problems. These mapping approaches do not convey clearly the geography of the cancer burden to local communities in a form that satisfies the needs of the public. Better methods exist but they have not been used with currently available geo-spatial population data and geocoded cancer registry data largely because software to make such maps is not available for general registry use. There are three essential properties of more useful mapping methods:

1. Rates mapped should be based on control of the population basis that supports them;
2. The spatial basis of this population support will typically vary in size of area so that the geographic detail that can be validly observed will typically vary across the map;
3. The user of a cancer map should be able, for any location on the map, know the size of the area and the size of the population that supports the rate as well as full details of the rates mapped consistent with full privacy protection of the cancer data.

No currently available cancer map has these three essential properties and no software tool exists to produce such a map.

An outline of the directions for research in this area can be made, based on three principles that we accept to be true:

* The deficiencies of current area-based methods for representing the spatial patterns of disease will increasingly be recognized and demands for more useful representations will grow;
* The availability of finely geocoded disease data will grow although access to such data will be increasingly tightly controlled through data sharing agreements and legal regulations, (see Rushton et al. 2006);
* The availability of demographic data for very small areas will grow as modern censuses tabulate data for flexible, GIS controlled, areas and as algorithms are developed for more intelligent disaggregating of demographic data to custom-defined areas, (see Cai et al. 2006; Mennis 2003; Mugglin et al. 2000).

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References

Environmental Risk Factor Diagnosis for Epidemics

Jin-feng Wang

State Key Laboratory of Resources and Environmental Information System, Institute of Geographical Sciences and Nature Resources Research, Chinese Academy of Sciences

Abstract: There is evidence to suggest that the rapidly changing physical environment and modified human behaviors have disrupted the long-term established equilibrium of the chemical composition between human and the Earth environment. We have noticed that environmentally related endemic is increasingly persistent in poorer areas and occurring in rapidly developing regions. This chapter describes two models developed respectively to diagnose the risk of environmentally related diseases and to simulate the spatio-temporal spread of communicable diseases. In the first model, we used birth defects to show the diagnosis of an endemic by (i) detecting risk areas, (ii) identifying risk factors, and (iii) discriminating interaction between these risk factors. Here, a spatial unit is considered a pan within which multiple environmental factors are combined to exert impacts on the human which may lead to either positive or negative health consequences. We were able to show that a diagnosis of environmental risks to population health discloses the locations at risks and the potential contribution of environment factors to the disease. In the second case, we used SARS to show the modeling of a communicable disease by (i) inversing epidemic parameters, (ii) recognizing spatial exposure, (iii) detecting determinants of spread, and (iv) simulating epidemic scenarios under various environmental and control strategies. We were able to demonstrate spatial and temporal scenarios of the disease through the modeling of communicable epidemic spread.

Keywords: environmentally related diseases, spatio-temporal simulation, spatio-temporal modeling
1 Introduction

The modern society is characterized by rapidly changing physical environment and modified human behaviors which disrupt the long-term established equilibrium of the chemical composition between human and the earth environment. Increasingly, we have noticed that environmentally related endemic is persistent in poor areas and occurs in rapidly developing regions.

The causal factors and determinants of a disease are critical in its control and intervention. These factors could be in different levels, from micro gene, physiological, chemical or biological abnormality, to the macro media or geographical environment. Such factors at different levels could exist in a cause-effect chain or separately and independently impact the human bodies and causing diseases.

A GIS coupled with spatial analysis and spatial statistics offers powerful tools in exploring macro patterns and factors. The macro-level examination could suggest proxies on the visible surface of some obscured micro agents along the cause-effect chain to uncover the real and direct causes of a disease. Spatial analysis tools are now available to explore environmentally related diseases. The causal factors \( X \) could be investigated through cases, or a response variable \( y \) in the mathematical nomenclature, such as spatial pattern alignment between cases \( y \) and the proposed causes \( X \); spatial ANOVA of \( y \) and \( x \); and time series of \( X \). This chapter looks at our efforts in employing spatial analysis tools in diagnosing environmental risk factors for diseases.

2 Inversion Epidemic Parameters

We started by exploring the inversion epidemic model which is stated simply as

\[
\Theta = g^{-1}(Y)
\]

Eqn. (1)

where \( Y \) denotes reported cases of infections, \( \Theta \) stands for epidemic parameters, \( g \) is a mechanistic equation of the variable \( Y \), and \( -1 \) denotes an inverse transformation. The epidemic parameters reflect the essential features of an epidemic which correspond either to a unique cause or is a complete consequence of several factors.

Two approaches can be employed to derive the parameters: (i) a field survey which needs a huge amount of data collection work, and (ii) a
model reversion. If the mechanistic model of a disease is known, then only a few cases must have the parameters reverted, because we know that

\[ Y = \text{mechanism} \otimes \text{epidemic parameters} \quad \text{Eqn. (2)} \]

where \( \otimes \) denotes a combination in a broad sense between components on both sides of the symbol. When the first two items in Eqn (2) are known, the epidemic parameters can then be estimated.

We used the 2003 SARS data of Beijing to illustrate the philosophy (Wang et al. 2006). A communicable disease spreads in time in a mechanism described by a time varying parameter following the SEIR model:

\[
\begin{align*}
S & \xrightarrow{\ell(t)} E & g & \xrightarrow{a} I & R \\
\end{align*}
\]

where \( E(t) \), \( I(t) \) and \( R(t) \) are respectively the number of exposed, infectious and removed individuals at time \( t \). \( S \) denotes the population susceptible to the disease. \( I(t) \), the average number of contacts per infectious person, depends on time because the control effort changes over time. \( g \) is the rate at which the exposed (latent) individuals become infectious while \( a \) is the rate at which the infectious individuals are removed (recovered or isolated). The basic reproduction number for this model is given by \( R_0 = \ell(0)/a \approx (b+c)/a \) and the eventual reproduction number is approximated by \( R_0 \approx b/a \).

We fitted the model to the case incidence data of Beijing over the period between 19 April and 21 June in 2003 to obtain these parameter estimates: \( a = 0.252, \ b = 0.008, \ c = 0.588, \ d = 0.368, \ e = 54 \) and \( g = 0.200 \).

Figure 1 shows a fitted curve for the number of infected individuals and a fitted curve for the transmission rate showing a very rapid decline over the period between 20 April and 30 April. The average incubation period was \( 1/g \) or about 5 days and the average infection period was \( 1/a \) or about 4 days. Our estimate of the basic reproduction number was 2.37. The eventual reproduction number, achieved at around 11 June, was found to be 0.1, indicating a dramatic reduction in the reproduction number. The total size or cases of the epidemic for estimating the epidemic parameters using the model was 2522.

The difference between the curve of the estimated infection rate and those of similar diseases confirmed that the model can disclose, to a certain extent, the strength of intervention if there was no abrupt change of other factors during the epidemic.
Following a similar argument for Eqn. (2), we regarded that

\[ \text{Estimated } Y = \text{Observed } Y + \text{Residual} \quad \text{Eqn. (3)} \]

Then, the residual is actually a factor which has not been included in the mechanism model.

### 3 Pattern Alignment

We also employed the spatial pattern alignment model to explore environmentally related diseases with some degree of success. The model is simply stated as

\[ \text{Pattern } Y = \text{Pattern } X \quad \text{Eqn. (4)} \]

where \( Y \) denotes cases of an infection and \( X \) the factors.

Birth defects, defined as "any anomaly, functional or structural, that is present in infancy or later in life (ICBDMS)", are a major cause of infant mortality and a leading cause of disability in China. The left side of Figure 2 illustrates the neural tube birth defect (NTD) prevalence in China; the right side of Figure 2 shows the NTD in Heshun County of the Shaanxi province, which is the location of our pilot study.
Fig. 2. Neural tube birth defect (NTD) prevalence in China

NTD is believed to be caused by a multitude of factors including hereditary, crude and artificially polluted environment, nutritional deficiency, and social, economic and behavioral factors (Figure 3). However, the risk factors associated with heredity and/or environment are very difficult to single out from our analysis. An exhaustive survey of each of the factors in the study area is possible but too expensive and time consuming to undertake.

We used the pattern alignment method to justify roles of the geological environment and the genetic factor in NTD within the study area (Wu et al. 2004). The NTD ratio was calculated according to birth defect registers from the hospital records and field investigations in villages over a four year period in 1998-2001. The ratio was adjusted by the Bayesian model to reduce variation in the records of a small probability event by borrowing strengths of its neighbors (Haining 2002). The Getis G* statistics (Getis and Ord 1992) was used to detect spatial hotspots of the ratios in different distance scales. Two typical clustering phenomena were found present in the study area.
Fig. 3. Causes of birth defects

Fig. 4. Two scales of hotspots of NTD prevalence
The upper left display of Figure 4 unveiled spatial clusters at a distance of around 6.5 km, which corresponded with the average distance separation of 6.31-9.17 km among villages in the Heshun County. This average distance of social contact indicated very little mixing of inhabitants between villages further apart which would infer that hereditary might have a role in inducing NTD within the study area.

A macro belt pattern emerged when the scanning radius was increased to 19-30 km, as seen in the lower right display of Figure 4. This pattern matches almost perfectly with the geological and soil patterns of the study area shown in Figure 5. Accordingly, we could infer that the geological circumstance might also be a risk factor to NTD occurrence within the study area.

![Fig. 5. Lithozone and soil distribution in Heshun County](image)

The results of our spatial pattern alignment exercise have provided clues that NTD was likely an environmentally related disease. Such findings from the two spatial scales could be used to suggest further actions be taken, such as the conduct of more physical, chemical and even molecular laboratory tests.

4 Spatial Regression

To explore further the relationship between NTD and the geological structures of Heshun County (Li et al. 2006), we tried a spatial regression model as defined below:

\[ Y = f(X) \quad \text{Eqn. (5)} \]

where Y denotes the response variable; X the causal variable; and \( f \) a statistical function between Y and X. \( f \) could be a spatial linear regression function such as SAR, MA and CAR (Anselin 1988; Haining 2003); or a nonlinear function such as neural network, genetic algorithm and Bayesian network; or ANOVA; or just a scatter plot of Y and X. A significant statis-