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Understanding the spatial diffusion process of severe acute respiratory syndrome in Beijing

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Summary *Objectives*: To measure the spatial contagion of severe acute respiratory syndrome (SARS) in Beijing and to test the different epidemic factors of the spread of SARS in different periods.
Methods: A join-count spatial statistic study was conducted and the given hypothetical processes of the spread of SARS in Beijing were tested using various definitions of 'joins'.
Results: The spatial statistics showed that of the six diffusion processes, the highest negative autocorrelation occurred in the doctor-number model (M-5) and the lowest negative autocorrelation was found in the population-amount model (M-3). The results also showed that in the whole 29-day research period, about hour or more days experienced a significant degree of contagion.
Conclusions: Spatial analysis is helpful in understanding the spatial diffusion process of an epidemic. The geographical relationships were important during the early phase of the SARS epidemic in Beijing. The statistic based on the number of doctors was significant and more informative than that of the number of hospitals. It reveals that doctors were important in the spread of SARS in Beijing, and hospitals were not as important as doctors in the contagion period. People are the key to the spread of SARS, but the population density was more significant than the population size, although they were both important throughout the whole period.
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Introduction

Severe acute respiratory syndrome (SARS) is a recently discovered human disease that spread widely from January to June 2003[1]. The spread of SARS was facilitated by the mobility of contemporary society (e.g. through air travel), continuing

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growth of the world population, and the steady rise in the number of highly populated urban areas, especially in Asia. Beijing, the capital of China, faced a SARS outbreak in April 2003.

As Dye and Gay discussed, although molecular biologists have put the finishing touches on the genomic sequence of the new coronavirus responsible for SARS, epidemiologists are still contemplating the answers to questions about how and why the disease has been spreading through populations.[2] Lipsitch et al.[3] and Riley et al.[4] performed quantitative assessments of the epidemic potential of SARS, and the effectiveness of control measures. Donnellym et al. studied the epidemiology of SARS in Hong Kong[5]. Since the route of transmission is one of the most important questions,[6] spatial analysis will help us to understand and control the contagion of a disease. The spatial process reflects interactions between the sites. Additionally, spatial linkages can be constructed to reflect different assumptions about the different possible pathways for the spread of an infectious disease.[7] A join-count spatial statistics study was conducted, and various hypothetical diffusion processes of SARS in Beijing were tested using various definitions of 'joins'.

Materials and methods

Data sources

The first case of SARS in Beijing was discovered in March 2003. As of 27 April, cases had been reported by 18 districts in Beijing (Fig. 1), which included both new actual cases and suspected cases (Fig. 2). We chose the new actual cases each day (i.e. excluding actual cases that were previously reported as suspected cases) as our data focus. For some actual cases that were initially reported as suspected cases, we also used all of the new reports (actual and suspected cases) to test our model. These definitions should reduce the risk of man-made temporal boundaries.

As SARS spread in the hospitals of Hong Kong and Beijing, medical care resources as well as populations are the key factors to determine how the contagion spread. Table 1 shows geographical and demographic information of the districts in Beijing.

Measures of spatial diffusion

A basic property of spatially located data is that sets of values are likely to be related to space. If the values display interdependence over space, the data are spatially autocorrelated. A detailed discussion of spatial autocorrelation has been given by Cliff et al.[7]. In public health, professionals often face the task of investigating the cluster of disease. There are many ways to detect unusual concentrations of health events in space and time (Fig. 3). In epidemiology, spatial dependence may also help us to capture important facets of the realities of processes.[9-11]

Spatial patterns of the spread of SARS provide clues to the process of spreading. The spatial process reflects interactions between the sites. BW join-count statistics was used to measure the spatial autocorrelation of SARS in Beijing. If the district reported a SARS case, it was colour-coded black (B), and if not, the district was colour-coded white (W). When two districts had some defined relations such as a common boundary, they were considered to be linked by a 'join'. A join may link two B districts, two W districts, or one B and one W district. Theses joins were called BB, WW and BW joins, respectively (Fig. 4). We counted the numbers of BB, WW and BW joins in Beijing districts, and compared these results with the expected numbers of BB, WW and BW joins under the null hypothesis, H_0, with no spatial autocorrelation among the districts. There was little difference to choose which of the three statistics should be used as the indicator of autocorrelation, but the results of Cliff and Ord suggest that BW is superior to BB.[9] The standard normal deviation (z scores) was used to test significance. High negative values indicate evidence of clustering, and high positive values indicate evidence of spacing[12] (Fig. 4). Details of the formulae for the BW test, its power and its interpretation are discussed at length by Cliff and Ord.[9]

Although the BW join-count statistic is a simple way to measure the spatial association of data using different 'joins', it can also be used to test hypothetical diffusion processes.[12] It should be noted that the non-free-sampling version of the significance test, which assumes that each district has the same probability of being infected, was used in this study.

Alternative models

Any join-count statistic will depend on the definition of a 'join', and the 'join' reflects some type of hypothetical interaction among the spatial process. For example, a common district boundary join (M-1) reflects the hypothetic SARS spread among the contiguous local districts. Seven alternative joins were used in this study. Models 1 and 2 are based on geographical relationships of the districts
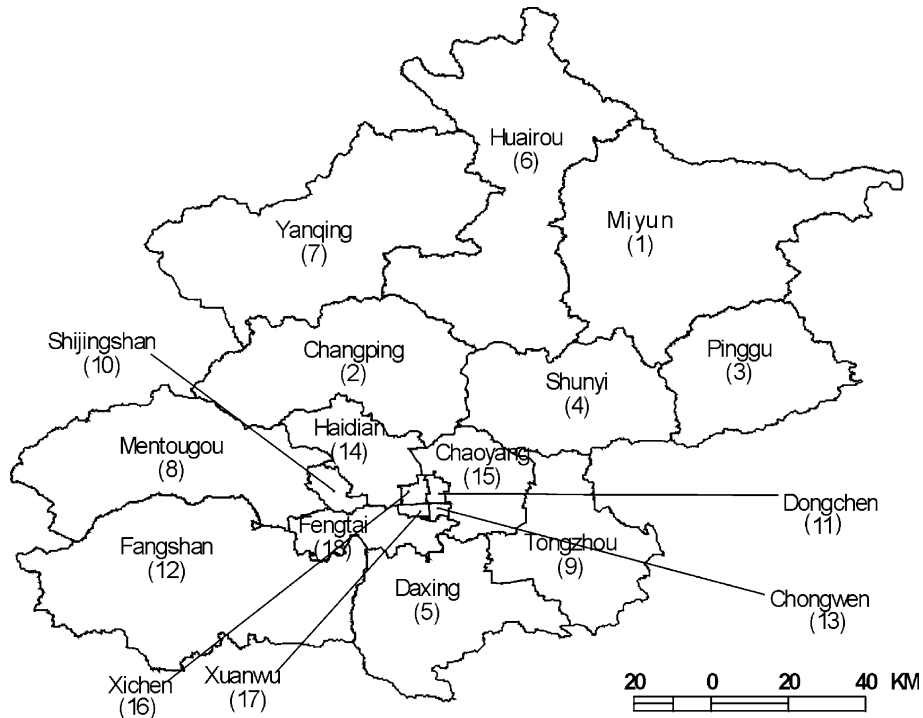
Figure 1   Locations of districts in Beijing. The district ID (in Table 1) is labelled under the name of the districts.

and these are the common methods for studying the spatial relationship. Models 3 and 4 are both based on the population, and they were chosen because people are the key focus of the SARS disease. As SARS spread in the hospitals in Hong Kong and Beijing, Models 5 and 6 were based specifically on the medical care resources. Model 7 was based on the relation of the urban and rural areas, and the model was designed to test the contagion within the urban–rural system.

The local contagion model (M-1) assumes that SARS only spreads among contiguous local districts. Each district joins other districts that have common geographic boundaries. The total number of joins is 42.

The wave contagion model (M-2) assumes that SARS spreads by shortest paths among the districts. Every district will join with another district that has the shortest path linkage. In this study, the path was defined by the distance between the centroids of each district. The total number of joins is 13.
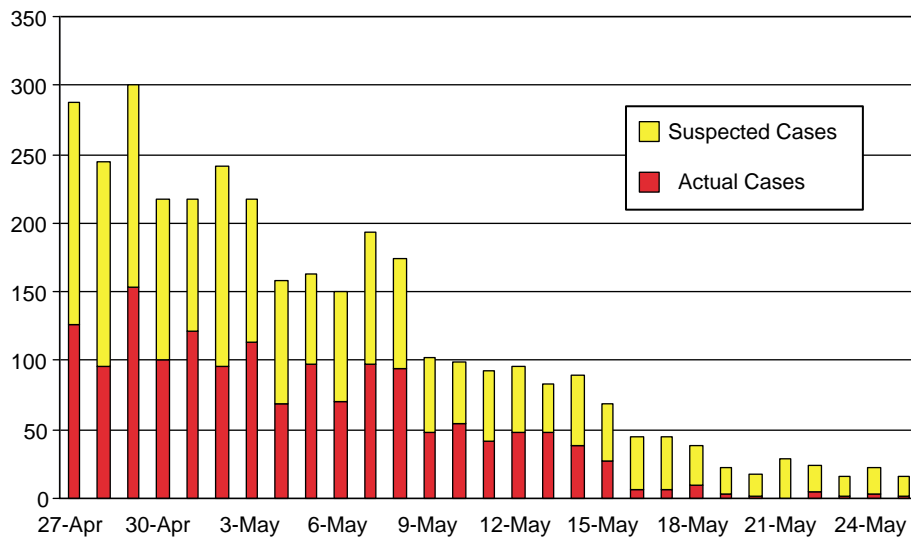

Figure 2   Epidemiological description of the severe acute respiratory syndrome epidemic in Beijing, 2003.

Table 1 Main factor for districts, 2001.

District ID	District name	Land areas (km²)	Permanent population (10,000 people)	Number of hospitals	Number of doctors
1	Miyun	2335.6	41.8	5	997
2	Changping	1430.0	43.6	18	1575
3	Pinggu	1075.0	38.9	7	1099
4	Shunyi	980.0	54.0	14	1414
5	Daxing	1012.0	53.5	14	1319
6	Huairou	2557.0	26.5	10	849
7	Yanqing	1980.0	27.0	5	661
8	Mentougou	1331.3	23.4	5	600
9	Tongzhou	870.0	60.3	13	1583
10	Shijingshan	81.8	33.5	23	2053
11	Dongcheng	24.7	63.0	30	5421
12	Fangshan	1866.7	74.7	6	1185
13	Chongwen	15.9	41.2	7	1796
14	Haidian	426.0	166.9	76	5402
15	Chaoyang	470.8	155.2	113	8419
16	Xicheng	30.0	78.6	24	5931
17	Xuanwu	16.5	56.6	19	3374
18	Fengtai	304.2	83.6	56	3477

Data sources: Beijing Statistical Information Net, http://www.bjstats.gov.cn/english.

The population-amount model (M-3) assumes that SARS spreads down the population size hierarchy from largest to smallest districts, with joins being defined by the population hierarchy. The total number of joins is 17.

The population density model (M-4) assumes that SARS spreads down the population density hierarchy from largest to smallest districts, with joins being defined by the population density hierarchy. The total number of joins is 17.

The doctor-number model (M-5) assumes that SARS spreads down the number of doctors hierarchy from largest to smallest districts, with joins being defined by the number of doctors hierarchy. The total number of joins is 17.

The hospital-number model (M-6) assumes that SARS spreads down the number of hospitals hierarchy from largest to smallest districts, with joins being defined by the number of hospitals hierarchy. The total number of joins is 17.
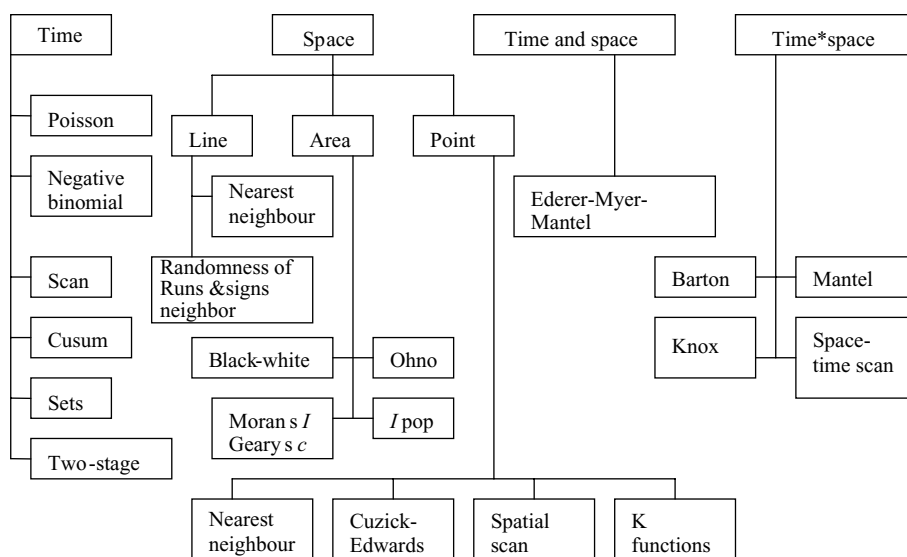

Figure 3 Methods available for testing clusters in time, space, time and space, and time*space (interaction) (after Carpenter[8]).
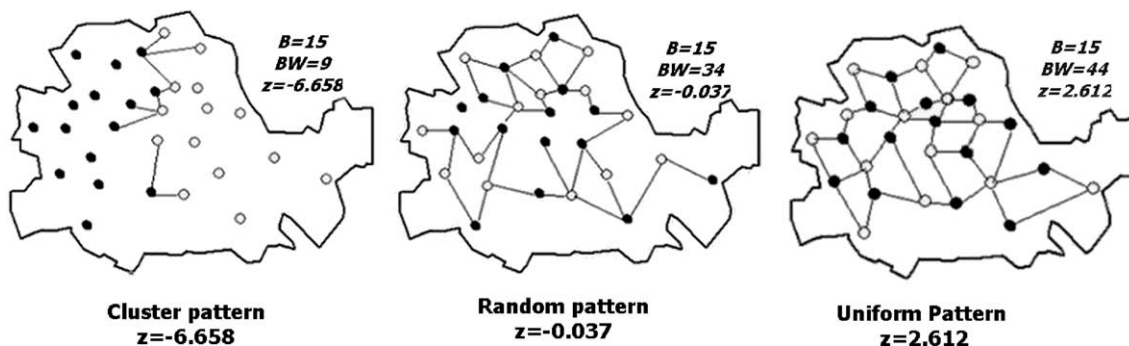
Figure 4 Standard normal deviation for the black-white statistics (BW). Source: Cliff and Ord.[9]

The urban–rural relation model (M-7) assumes that SARS spreads down from urban to rural districts, with joins being defined by the urban–rural relationship. We choose eight (Haidian, Chaoyang, Dongcheng, Xicheng, Chongwen, Xuanwu, Shijingshan and Fengtai) of the total 18 districts as the urban areas and define the relationship based on first and second order contiguous between the urban and rural districts. First order contiguous means that an urban district and a rural district have a common boundary. If a rural district did not have common boundary with an urban district, the second order contiguous was used. Second order contiguous means that a rural district is connected with a urban district through rural districts that have a common boundary with that rural district and urban districts. The total number of joins is 42.

We also used the doctor-population model by defining joins according to doctor-population hierarchy. However, this model was discarded due to poor results.

Results

Table 2 shows the overall results of the diffusion models of SARS in Beijing. As no new cases were reported on 21 May and the BW join count can not be used under this situation, we have compared the BW results of new cases from 27 April to 20 May in Table 2 and Fig. 5. The first six join-count statistics based on new cases or total new reports had a similar pattern during the various periods except for the population-amount model (M-3). The doctor-number model (M-5) had the highest negative autocorrelation, and the population-amount model (M-3) had the lowest negative autocorrelation. Unlike the first six models, the urban–rural model had a positive value for the standard normal deviation but had a negative value based on all new

reports; this requires further study. Table 2 also shows that throughout the study period, a significant degree of contagion was experienced for 4 or more days except for the population-amount model (M-3).

As a direct comparison was not justified,[11] the seven graphs in Fig. 5 compare the same spread process over time and the same time based on different models. In Fig. 5, the red dashed lines, (for interpretation of the reference to colour in this legend, the reader is referred to the web version of this article) indicate the significance threshold ($P=0.05$). The x-axis is the temporal for SARS, and the y-axis is the negative z value of the join-count statistic. Model 7 is an exception as its y-axis is the positive z value. The greater the degree of spatial autocorrelation (contagion), the larger (negative) the z score for BW joins. Comparison of temporal variety suggests that besides the population-amount model (M-3) and urban–rural model (M-7), the whole trends of spatial autocorrelation of the new cases (blue line, (For interpretation of the reference to colour in this legend, the reader is referred to the web

Table 2 Spatial autocorrelation of alternative join model.

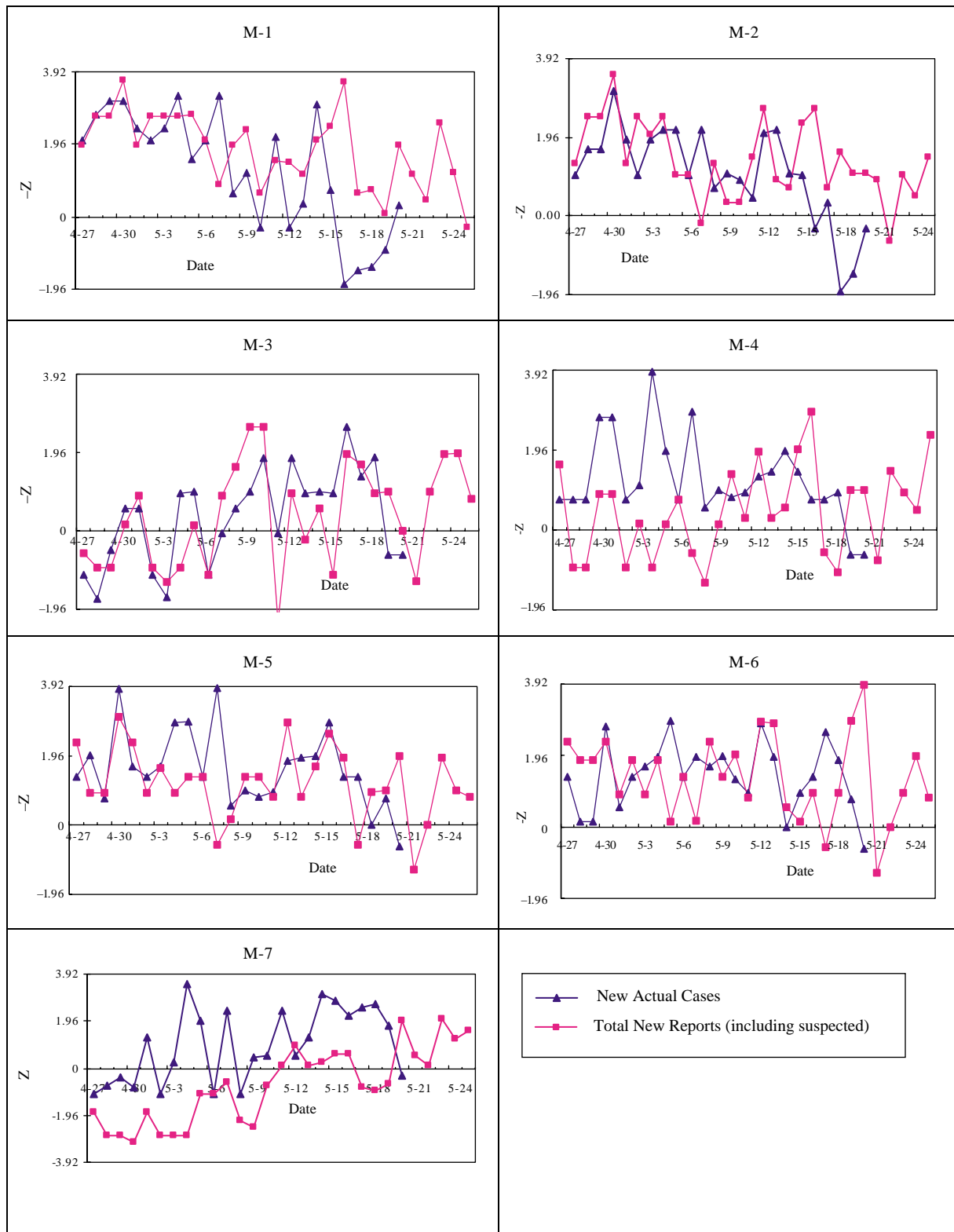| Join model	Mean z score of BW		Days with significant (0.05) level	
	New cases	Total new reports	New cases	Total new reports
M-5	−1.60	−1.11	6	5
M-6	−1.40	−1.34	4	8
M-1	−1.27	−1.80	12	12
M-4	−1.24	−0.45	4	2
M-2	−1.06	−1.38	6	9
M-3	−0.35	−0.34	1	2
M-7	0.96	−0.73	9	8

Figure 5   Spatial diffusion of the severe acute respiratory syndrome epidemic in Beijing.

version of this article)) are declining with the epidemic. Fig. 5 also shows that in different SARS processes, the dominated diffusion model is also changed.

Discussion

The spatial process reflects interactions between the sites. Fig. 4 shows that almost all the significant

negative spatial autocorrelation (contagion) appeared before 15 May, and this means that the trend of contagion changed since that date. Fig. 2 supports this finding, and shows a change in the number of cases reported from 27 cases on 15 May to just seven cases on 16 May. The new case reports and total reports had similar trends in every model with some exceptions in Models 4 and 7.

Model l (joins based on common geographic boundaries) and Model 2 (joins based on shortest path linkages) show that the geographical relationship was important during the early phase of SARS in Beijing. These two models show that some of the infections may have been determined by the spatial structure of Beijing. Fig. 1 illustrates that the districts of Beijing have a tessellation-like distribution, so joins based on common geographic boundaries would be similar to joins based on shortest path linkages.

Both Models 3 and 4 are based on the populations in the districts. The people are the key to the spread of SARS, but the population density (M-4) is more significant than the population size. A higher population density means that there are more chances of interaction among the people, and this will increase the risk of contagion.

As SARS spread in the hospitals of Hong Kong, Guangdong and Beijing,[13,14] Models 5 (doctor numbers) and 6 (hospital numbers) were used to test this diffusion model. The results suggest a visible diffusion model dominated by the medical resources, and this is accordant to some other research.[13,14] The result demonstrated that doctors were important to the spread of SARS in Beijing, and this may explain why doctors faced more risks in SARS diffusion. The hospital model showed that hospitals were not more important than doctors in the contagion period, and both were important throughout the whole period. This comparison was very interesting because hospitals were deemed to be one of the biggest sources of contagion for some time. More research should have been conducted before we concluded that hospitals were the root of the diffusion.

Model 7 assumes that SARS spreads down from urban to rural districts. Unlike the other six models, Model 7 indicated that after the peak of SARS in Beijing, there was a uniform pattern of infection in the urban and rural areas. There are two reasons for this. Firstly, differences such as population densities, lifestyles and outside connections between the urban and rural areas are important factors in the spread of SARS. Secondly, the spatial structure of urban and rural regions in Beijing likes concentric circles.

Due to a lack of early SARS case reports in Beijing, the whole epidemic and endemic periods were not analysed. The graph of SARS cases in Beijing (Fig. 2) and the pattern of spatial contagion (Fig. 5) are not symmetric over time. Only two models based on geographical relationships (M-1 and M-2) show the same pattern as the change in SARS contagion.

Conclusions

As a new epidemic disease, SARS spread exclusively through individual contact. The spatial behaviour of people is one of the keys to understanding the spatial diffusion of SARS. Spatial analysis focuses on the spatial characteristic of the object and can help us to discover how the disease spread through different areas and populations.

Differences between the seven models suggest that the spatial contagion of SARS in Beijing was affected by the population density and medical care resources. However, the main factors causing this diffusion were different in different periods of the epidemic.

Due to a delay in data collection, the research does not include the whole process of SARS diffusion in Beijing, and the beginning of the SARS outbreak in Beijing may have included more information about the spatial diffusion. The BW join-count statistics only considered the spatial interaction between the districts and did not include the temporal facts. In fact, this method could be developed to a spatiotemporal model,[10,11] but case reports or earlier data would be required.

Another way to improve the research would be to select finer spatial statistic units. The spatial units used in this study were the city districts by which the municipal governments reported SARS cases daily to the public. However, as we can tell from Table 1, the areas, the populations and the medical care resources are significantly different between the districts. Therefore, the results could have been better if the spatial units had been chosen more carefully.

Acknowledgements

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