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Understanding COVID-19: comparison of spatio-temporal analysis methods used to study epidemic spread patterns in the United States

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Abstract

This article examines three spatiotemporal methods used for analyzing of infectious diseases, with a focus on COVID-19 in the United States. The methods considered include inverse distance weighting (IDW) in-terpolation, retrospective spatiotemporal scan statistics and Bayesian spatiotemporal models. The study co-vers a 12-month period from May 2020 to April 2021, including monthly data from 49 states or regions in the United States. The results show that the spread of COVID-19 pandemic increased rapidly to a high value in winter of 2020, followed by a brief decline that later reverted into another increase. Spatially, the COVID-19 epidemic in the United States exhibited a multi-centre, rapid spread character, with clustering areas rep-resented by states such as New York, North Dakota, Texas and California. By demonstrating the applic-abil-ity and limitations of different analytical tools in investigating the spatiotemporal dynamics of disease out-breaks, this study contributes to the broader field of epidemiology and helps improve strategies for respond-ing to future major public health events.

Introduction

The COVID-19 pandemic, caused by a novel coronavirus, is an acute respiratory infectious disease that began in late 2019 and has since spread globally (Wang Z, Ma W, Zheng X, 2020; Huang J, Gao X, Chen Y, Shi X, 2020). Since its discovery, it has posed a serious threat to human health and life safety, with great impact on global economic and social development and widespread concern in countries around the world and international organizations such as the World Health Organization (WHO) (Liu *et al.*, 2020; Zhang *et al.*, 2020; Zhou *et al.*, 2020). Effective statistical and analytical studies on the development of the pandemic have become an urgent issue for key disciplines such as epidemiology, statistics and geography (Peng *et al.*, 2020; Wang Z, Liu C, Wang Z, 2020). Related studies constitute an important reference value for governments and organizations to respond to similar major public health events in the future.

The development and widespread application of geographic information systems (GIS) technology, combined with geographic modelling methods, converge and have become a key focus of research in the development of major epidemics (Chen *et al.*, 2020; Huang *et al.*, 2022; Wang Q, Wang X, *et al.*, 2020; Zheng *et al.*, 2018). For example, Lv *et al.* (2020) used Crystal Ball and GIS technology (https://www.oracle.com/applications/crystal-ball/) with methods, such as distribution fitting, batch fitting, spatial autocorrelation and mathematical statistics, to analyze the spatiotemporal characteristics of COVID-19 in Hubei Province, one of China's hardest-hit areas, from January 25 to April 8, 2020. Mollalo *et al.* (2020) investigated county-level changes in disease incidence rates in the continental United States (US), compiling a geographic database containing environmental, socio-economic, topographical and demographic variables to explain the spatial variability of disease incidence rates. Anaele *et al.* (2021) used GIS to create a visualization map of COVID-19 mortality rates and explored the geographic relationship between race and COVID-19 mortality rates in various states in the US, including Pennsylvania. In addition to simply combining GIS with infectious diseases, many international scholars focus on combining other analytical methods with GIS to discuss the spatiotemporal distribution of infectious diseases. For example, Liu *et al.* (2020) used exploratory data analysis to explore the spatiotemporal diffusion process of COVID-19 in counties in Henan Province, China and further evaluated the epidemic risk in each county after the Spring Festival based on population flow. Abbasi *et al.* (2022) combined GIS with statistical analysis to analyze the spatiotemporal distribution of the impact of COVID-19 on noise pollution in Tehran, Iran. Khan *et al.* (2021) used machine learning methods such as GIS, decision trees, and support vector machines to predict the development of COVID-19 in India.

Although these studies have provided valuable analyses of the development of COVID-19 outbreaks worldwide in recent years, the advantages of GIS in analyzing the spatiotemporal characteristics of COVID-19 have not been fully utilized, particularly in objective comparisons and applications of methods such as inverse distance weighting (IDW) interpolation, Bayesian spatiotemporal models, and spatiotemporal scan statistics during this pandemic (Li

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et al., 2021; Sun *et al.*, 2021). Therefore, conducting relevant applications of COVID-19 outbreak development by combining multiple spatiotemporal feature analysis methods is of great significance to prevent the spread of infectious diseases and understand the spatiotemporal patterns of future major public health events (Wang J, Tang K, *et al.*, 2020.). Statistical information on COVID-19 available from the Johns Hopkins University throughout the pandemic, with data on confirmed cases, mortality etc. in the US, is comprehensive and has good temporal order, making it a useful resource for observing the development of COVID-19 outbreaks.

This study employed IDW, spatio-temporal scan statistics and Bayesian spatio-temporal models to conduct a spatio-temporal feature analysis of COVID-19 data, including the number of new cases and cumulative cases, in 49 U.S. states from May 2020 to the end of April 2021. Additionally, a geographically weighted regression (GWR) model was used to examine local spatial non-stationarity. The results show that using different spatio-temporal feature analysis methods is of great reference value for understanding the transmission and control of infectious diseases. They can provide guidance for the decision-making process of public health agencies and policymakers and help improve strategies for responding to future major public health events. Furthermore, this study aimed to contribute to the broader field of epidemiology by demonstrating the applicability and limitations of different analytical tools in investigating the spatio-temporal dynamics of disease outbreaks.

Materials and Methods

Data Sources

This paper obtains authoritative and reliable data from the US Centers for Disease Control and Prevention (CDC, 2022) on the number of new, confirmed and cumulative COVID-19 outbreaks in 49 states in the US. Information from May 2020 to the end of April 2021, derived from the CDC's daily archive of confirmed diagnoses were retrieved from each US state and territory over time.

Research methods

This article employs three analytical methods that are suitable for investigating the spatio-temporal distribution of infectious diseases, including the IDW interpolation method (Islam *et al.*, 2021; Murugesan *et al.*, 2020), retrospective spatio-temporal scan statistics (Hohl *et al.*, 2020; Xu *et al.*, 2021) and Bayesian spatio-temporal model (Jaya *et al.*, 2022).

IDW interpolation

ArcGIS software (ESRI, Redlands, CA, USA) provides many interpolation methods, including the IDW interpolation method, also known as distance reciprocal multiplication. The power parameter controls how the weighting coefficient decreases with the increasing distance from a grid node. For a larger power parameter, closer data points are given a higher weight, while for a smaller power parameter, the weights are evenly distributed among the data points (Jia *et al.*, 2020; Li *et al.*, 2020). Equations 1-3 represent the weighting function involved in the IDW method:

$$W_i = \frac{h_i^{-p}}{\sum_{j=1}^{n} h_j^{-p}} \quad \text{(Eq.1)}$$

$$h_i = \sqrt{(x-x_i)^2 + (y-y_i)^2} \quad \text{(Eq.2)}$$

$$w_i = \frac{[R-h]^2}{\sum_{j=1}^{n}[\frac{R-h}{Rh}]^2} \quad \text{(Eq.3)}$$

where p is an arbitrary positive real number, which usually equals 2; h_i the distance from the discrete point to the interpolation point; x and y the coordinates of the interpolation point; x_i and y_i the coordinates of the discrete point; R the distance from the interpolation point to the farthest point; and n the total number of discrete points.

Retrospective time-scan statistics

The retrospective spatio-temporal scan statistic is a discrete Poisson distribution spatio-temporal model based on the SatScan 9.5 software (Kulldorff, 1997). We constructed a scanning window for the daily confirmed cases in 49 states of the US, with the time scale parameter set to the monthly scale and the spatial scale parameter to 30% of the study area. The expected number of confirmed cases was inferred based on the actual number of confirmed cases and the total population in the area. The logarithm of the likelihood ratio (LLR) was used as the test statistic based on the actual and expected number of confirmed cases inside and outside the scanning window. The p-value indicates the probability of a sample occurrence or observation occurring given the original hypothesis (null hypothesis). This indicator is used in this paper to look at the confidence in the results of the statistics (Chen *et al.,* 2016 Kulldorff, 1997).

The scanning statistic is defined as the maximum likelihood ratio among all possible scanning windows Z, based on the total number of diagnosed patients N (Huang *et al.*, 2022; Li *et al.*, 2016; Yin *et al.*, 2007; Zhang *et al.*, 2012).

$$\frac{L(z)}{L_0} = \frac{\left(\frac{n_Z}{\mu(Z)}\right)^{n_Z}\left(\frac{n_G-n_Z}{\mu(G)-\mu(Z)}\right)^{n_C-n_Z}}{\left(\frac{n_G}{\mu(G)}\right)^{n_C}} \quad \text{(Eq.4)}$$

$$\mu(Z) = \frac{n_G}{m_G} \times m_Z \quad \text{(Eq.5)}$$

where L(z) represents the likelihood function of the scanning window z, and L_0 represents the likelihood function obtained under the null hypothesis; n_z the actual number of diagnoses in scanning window z; M_z the population in scanning window z; and μ(Z) the expected number of diagnoses in scanning window z under the null hypothesis; n_G the total number of diagnoses in all regions G, and m_G the population in all regions G (Yin *et al.*, 2007).

Bayesian spatio-temporal models

The Bayesian spatio-temporal model is a special statistical model for spatio-temporal data, which considers both temporal and spatial correlation of the data and quantifies uncertainty as a probability distribution emphasizing the spatio-temporal correlation features of COVID-19 transmission (Hu *et al.*, 2018; Rehman *et al.*, 2018). Here, the prior distribution and likelihood function are composed of factors that describe the distribution of variables in different times and spaces to compute the posterior distribution, *i.e.* inference of the probability distribution of unknown parameters in consideration of the known data. This paper references the Gaussian Process (GP) in the Bayesian spatio-temporal model analysed by the R software model, which is mathematically represented by the following equation:

$$\log(p_{it}/P) = N_i + M_t + C_{it} + \alpha \qquad \text{(Eq.6)}$$

where P represents the total number of confirmed cases; p_{it} the number of confirmed cases in region i at time t: N_i the spatial effect; M_t the temporal effect, C_{it} the spatio-temporal interaction effect; and α the mean number of new COVID-19 infections in the US during the study period.

Results

Overview of the study area

The US consists of 50 states and the District of Columbia. Its geographical location borders Canada in the North, Mexico to the South and the Atlantic and Pacific oceans to the East and West, respectively (Nevitte *et al.*, 2017). This study was carried out in the 49 states that make up contiguous US, excluding Alaska and Hawaii. In 2020, the US experienced a significant outbreak of COVID-19, prompting swift action by federal, state and local governments to implement measures, such as social distancing, mask mandates and vaccination campaigns to slow the spread of the virus. Despite initial challenges, the country made progress in controlling the pandemic through a combination of public health initiatives and individual efforts (Cuadros *et al.*, 2021; Pei *et al.*, 2021; Wadhera *et al.*, 2021). Understanding the varying spatio-temporal distribution of the pandemic in different states can provide valuable insights into effective pandemic response strategies. Figure 1 provides an overview of the administrative divisions of the study area.

Spatio-temporal characterisation based on GIS

Conducted preliminary A GIS analysis was first conducted to explore the state-level differences with regard to confirmed COVID-19 cases across the US from May 2020 to April 2021. The total population (Figure 2) and the cumulative confirmed cases (Figure 3) of each state during the study period were visualized using a hierarchical tree diagram. The results show that there were significant differences with respect to the cumulative, confirmed cases among states, especially in New York, Texas and Indiana, where the pandemic has hit the hardest. Combining the population distribution with the number and distribution of cases, we found a certain correlation. Texas and the eastern region of the U.S. are densely populated, with a higher number of cumulative confirmed cases and a considerable spatial distribution. To further examine the non-stationarity of local space, we introduced a geographically weighted regression (GWR) model to explore the spatial correlation between the cumulative confirmed cases and the population (Figure 4). The results indicated a positive relationship between

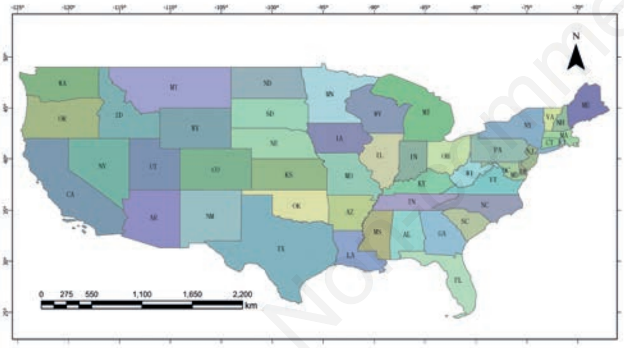

Figure 1. Administrative divisions of the study area in the contiguous United States.

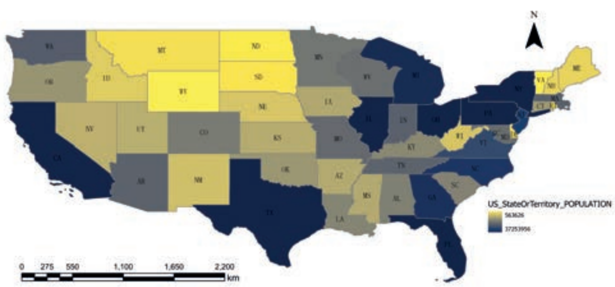

Figure 2. Actual population in in the contiguous United States during the study period.

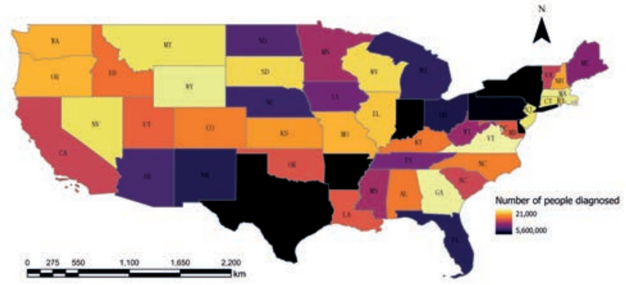

Figure 3. Cumulative number of diagnoses in the study area for the 12-month period from May 2020 to April 2021.

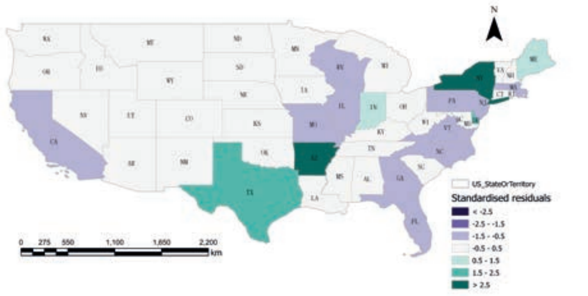

Figure 4. The geographically weighted regression model examines the spatial non-stationarity between the number of confirmed diagnoses and the population in the study area.

cumulative confirmed cases and population, which was consistent with our inference that high population density is a risk factor for the spread of infectious diseases and that controlling the spread of the virus in densely populated areas is critical to controlling the overall spread of the virus. However, the larger standard deviation results for areas with concentrated populations, such as New York State and Arizona, suggested that the local spatial non-stationarity of the model was pronounced in that the effect of population on the number of confirmed cases can only explain part of this relationship. Thus, there may be also other factors that influence the spread of infectious diseases, such as climate, policy and population mobility.

Spatio-temporal feature analysis based on IDW

To visualize the spatial distribution of the COVID-19 epidemic in the US and to study its spatial and temporal spread on a monthly scale, with the data were smoothed and interpolated using IDW on to generate a spatial and temporal distribution map (Figure 5), depicting the inverse distance weighted interpolation of new COVID-19 cases generated by month. Each month exhibited distinctive temporal and spatial features indicating low to high spatio-temporal clustering of COVID-19. The analysis of temporal characteristics showed that from May 2020 to January 2021, there were widespread clusters observed across cities, with cluster centres primarily located in the Southeast of the country. However, from February to March 2021, a large number of low spatio-temporal clusters emerged, with the monthly new case numbers even returning to levels seen in the initial stages of the study. This is consistent with the policies adopted to coexist with COVID-19 in 2020, but it was not until the signing of the American COVID Relief Bill on 27 December 2020 and the subsequent emergency approval of the Pfizer vaccine that COVID-19 cases decreased in March and April 2021, thus leading to effective control of the pandemic. However, the lifting of epidemic prevention and control measures in April 2021 led to a surge in new COVID-19 cases (Jackson *et al.*, 2021). By analysing the spatio-temporal distribution patterns in Figure 5, it can be seen that the clustering areas are mainly located in populous and densely populated regions such as Texas, California, Florida and New York, with large spatial clustering ranges, whereas the spatial clustering ranges in other states were relatively small. This is consistent with the results reported previously.

Spatio-temporal characteristics based on scan statistics

In this study, we used a retrospective spatiotemporal scan method to investigate the spatial clustering distribution of COVID-19 confirmed cases. Markov Chain Monte Carlo (MCMC) algorithm simulations were used to generate 999 simulated datasets and the scan windows with the highest degree of anomaly determined based on the ranking of real data in the simulated datasets, and the calculated *P*-values (Costa *et al.*, 2014). The results of the

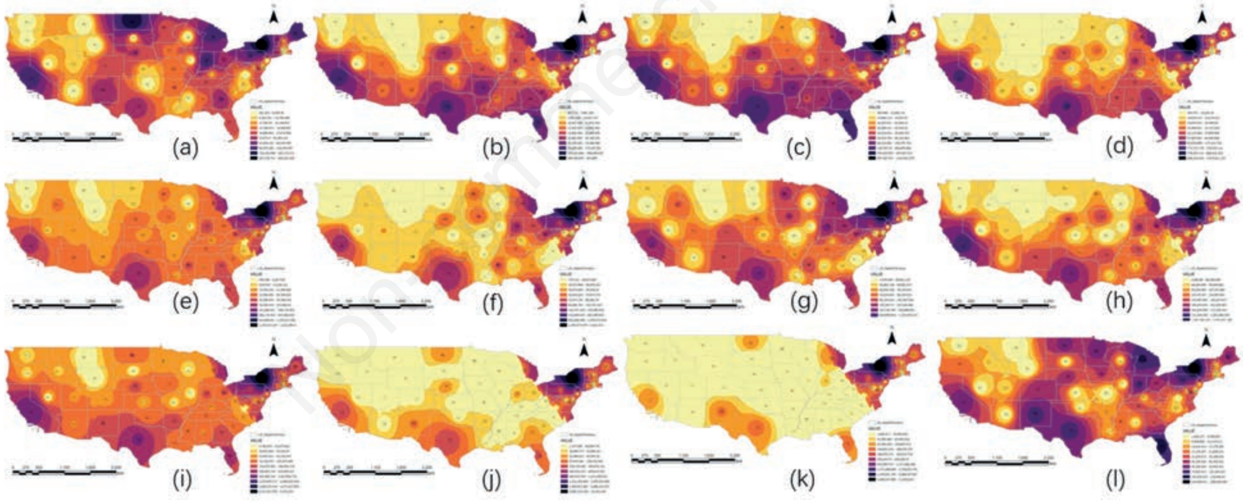

Figure 5. Month-scale analysis of the spatio-temporal aggregation and distribution of the COVID-19 out-break in the United States using inverse distance weighting interpolation. Study period: 2020/05-2021/04); (a)-(l) indicate the month-by-month results for the study period.

Table 1. The spatiotemporal aggregation of confirmed COVID-19 cases in the United States May 2020 to April 2021.

Cluster	Time	No. of states	Gathering radius (km)	No. of cases (actual)	No. of cases (exp.)	LLR	RR	P
1	2020/5/1-2020/8/30	1	0	404,276	15,909.52	935013.04	27.55	0.001
2	2020/5/1-2020/8/30	1	0	219,767	4,899.21	325683.95	46.87	0.001
3	2020/5/1/-2020/8/30	12	1030.15	517,524	154,034.71	277612.11	3.63	0.001
4	2020/5/1-2020/8/28	10	817.59	680,846	395,342.77	93591.53	1.84	0.001

Results obtained with SatScan; LLR, logarithm of the likelihood ratio; RR, relative risk; P, level of statistical significance.

retrospective spatiotemporal scan, including the number of clusters, time period, actual and expected number of confirmed cases, relative risk (RR), LLR and *P*-values are shown in Table 1 that says that these clusters were concentrated in the first half of the study period. The scan results were visualized using ArcGIS software, as shown in Figure 6, which shows that there were mainly four spatial clusters during the study period. The cluster areas in New York and Texas were very small, indicating a high degree of spatial clustering that cannot be expressed on the map. The cluster areas 3 and 4, on the other hand, involved 12 and 10 states, respectively, with large cluster areas, indicating a lower degree of spatial clustering. The *P*-values met the requirements, and thus, these results are considered acceptable.

Spatio-temporal characteristics based on Bayesian spatio-temporal model

This study employed the GP model in the Bayesian spatiotemporal analysis to investigate the COVID-19 outbreak in the US incorporating the influence of population size on the infection rate. Table 2 presents the detailed model parameters of the Bayesian spatiotemporal model. We obtained the monthly mean infection rate αn(n=Jan, Feb...) by dummy variable differentiation of the month-scale information.

As shown in Table 2, all GP regression coefficients of the selected monthly sample data were significantly different from zero at the 95% significance level, and the spatial effect (N_i) is markedly greater than the temporal effect (M_t). Based on the spatiotemporal distribution characteristics of the COVID-19 outbreak under study, we conclude that spatial aggregation has a great impact on the spread of COVID-19 in the US. The trend plots of the parameter trajectories obtained from the MCMC algorithm used in the GP model indicate that the outbreak had undergone significant growth and fluctuations at the spatiotemporal scale during the study period, as illustrated in Figure 7. Furthermore, the average spatial decay (phi) reached 0.9795. Combined with the density plot (Figure 8), a significant and continuous spread of COVID-19 in the study area, consistent with the relaxed epidemic control policies in the US, is indicated (Wei *et al.*, 2009; Zhu *et al.*, 2013).

To further enhance the spatiotemporal analysis of the study, a Bayesian spatiotemporal model was used for visualization. By collecting and preprocessing epidemic data, a spatially 'discretized' epidemic dataset was interpolated to generate a continuous spatiotemporal distribution of the epidemic over time (Figure 9).

This approach can further enhance the understanding and predictive ability of spatiotemporal distribution patterns of the epidemic, while also reducing the interpolation errors caused by data sparsity and spatial heterogeneity.

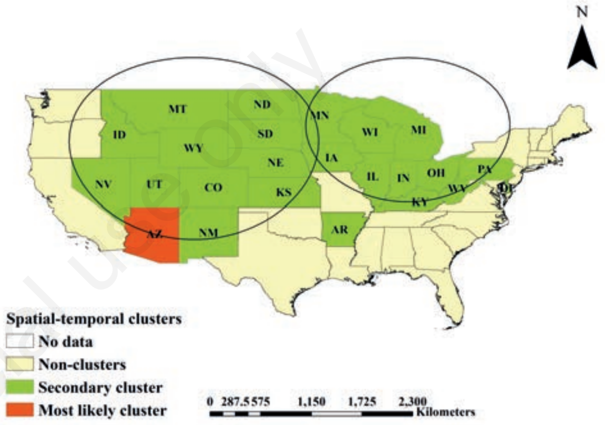

Figure 6. Spatio-temporal clustering expression analysis of the diagnostic population in the United States based on spatio-temporal scanning.

Table 2. Parameters of Bayesian spatio-temporal model.

Parameter	Mean	Median	SD	Low 2.5p	Up 97.5p
Intercept	368.3304	368.2973	4.6730	359.0652	377.6753
αYear	0.0002	0.0002	0.0001	-0.0001	0.0004
αMay	-0.6308	-0.6463	13.7848	-27.9090	25.9325
αJun	114.3268	114.3385	13.9664	86.5946	140.1974
αJul	238.3949	238.1554	10.0705	219.3352	258.8064
αAug	-88.3141	-88.4465	10.0546	-107.4919	-68.7793
αSept	-153.1744	-153.4090	14.3685	-118.2386	-124.5395
αOct	-91.0310	-91.1373	14.1379	-118.2386	-124.5395
αNov	-51.3767	-51.4433	14.1082	-78.9892	-23.5206
αDec	42.4249	42.4533	13.7232	15.9347	70.2759
αJan	-0.1034	-0.1031	0.0302	-0.1628	-0.0455
αFeb	-0.1495	-0.1490	0.0334	-0.2168	-0.0861
αMar	-104.0984	-103.9917	14.0846	-132.2393	-76.7544
αApr	-56.0540	-55.9964	14.4099	-84.9446	-28.0474
M_t (sig2eps)	0.0051	0.0051	0.0001	0.0050	0.0053
N_i (sig2eta)	130197.2478	130108.9568	2295.2961	125866.7190	134688.4308
C_{it} (phi)	0.9795	0.7271	0.9023	0.0763	3.3525

The α-suffix represents the average number of confirmed cases at the corresponding month; N_i, the spatial effect; M_t, the temporal effect; C_{it}, the spatio-temporal interaction effect.

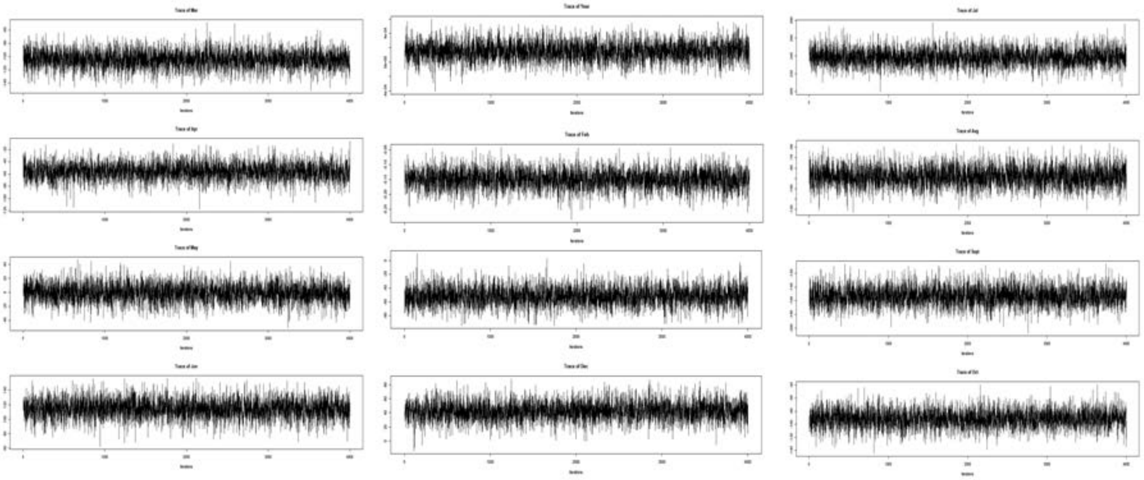

Figure 7. Parameter trajectory variation diagram of Markov chain Monte Carlo methodology.

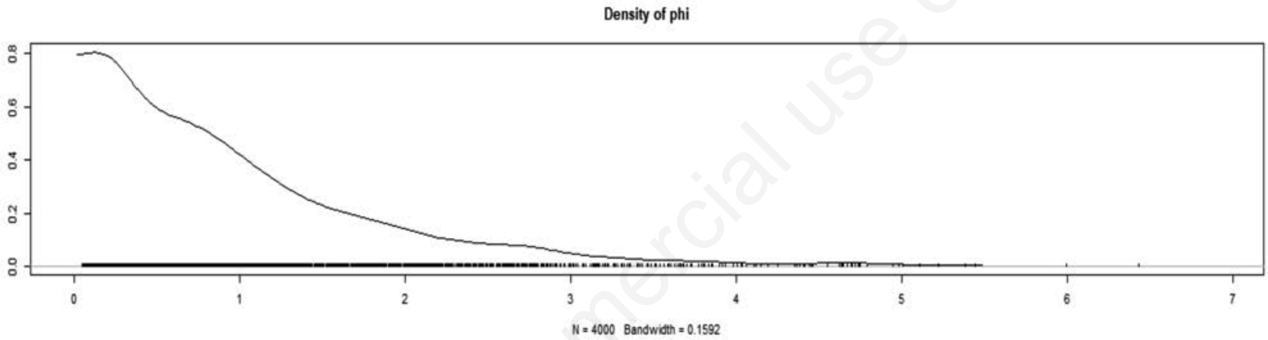

Figure 8. Decay parameter diagram of the average spatial decay (phi) space.

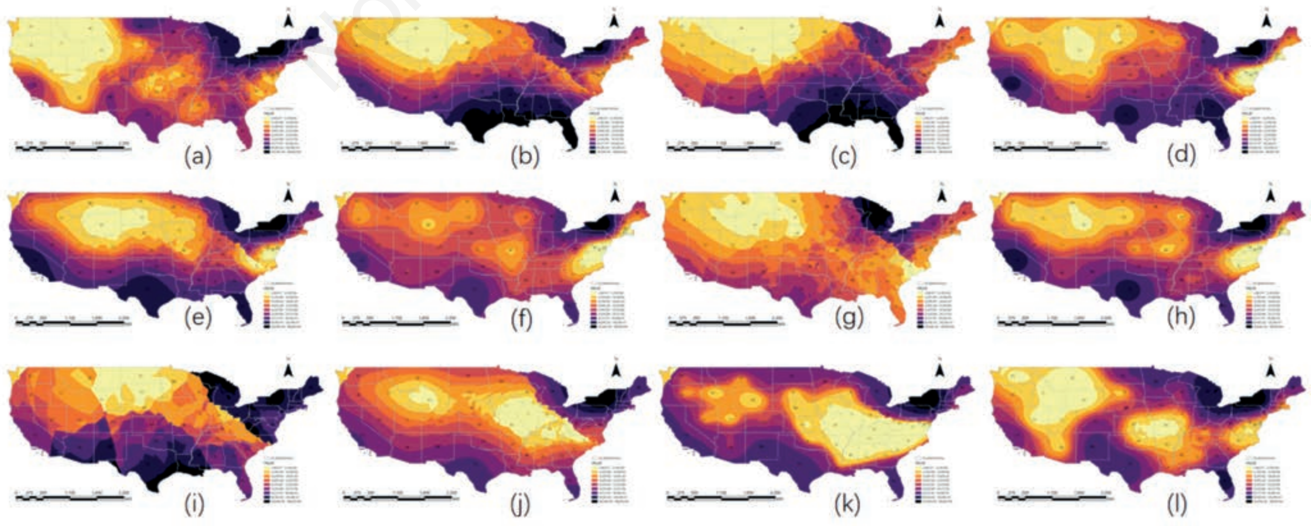

Figure 9. The spatial visualisation results for Bayesian spatio-temporal models. Study period: 2020/05-2021/04); (a)-(l) indicate the month-by-month results for the study period.

As can be seen from Figure 9, the COVID-19 epidemic has generally spread from the Midwest to the periphery of the contiguous US. The spatial pattern of the epidemic changed over time from being relatively concentrated in a few states to being “multipolar”; the interpolated results for each state show that epidemic-prone areas such as Texas, New York, California and Florida remained active over time, and new epidemic areas such as Michigan and Los Angeles continued to emerge, which is consistent with the development of the epidemic in real time in the US.

Discussion

By comparing the results, we can see that each of the three methods has its advantages and disadvantages when applied to the spatiotemporal analysis of COVID-19 in the study area. IDW interpolation can to some extent compensate for the spatial discontinuity caused by the scale of the data source and, combined with continuous temporal analysis, it can provide intuitive information on the spatiotemporal distribution of the pandemic. The spatiotemporal scan statistics method can intuitively reflect the spatiotemporal clustering of epidemic development within a certain range, but the analysis is greatly affected by the provided geographic data, as shown in the results of this study where the maximum values of spatial clustering were observed in New York and Texas, making it difficult to accurately visualize the situation spatially. The Bayesian spatiotemporal model can reflect the effect and direction of current response measures. For example, our obtained phi density value is close to 1, which indicates incomplete convergence. This result is consistent with the loose epidemic prevention and control policy in the US and indicates that the pandemic still had a large diffuse nature at the end of our study period. However, the Bayesian spatiotemporal model can only reflect the epidemic situation overall and cannot accurately reflect local specific situations. Therefore, we combined spatial visualization with the obtained dataset for spatial interpolation to effectively address this issue.

Through analyzing the application of various spatiotemporal analysis methods with respect to COVID-19 spread, we can summarize their applicability and effectiveness. The Bayesian spatiotemporal model is suitable for macroscopic overall control of epidemic trends in the early and middle stages of the pandemic, and for rational policy adjustment and resource allocation. Under the premise of complete and accurate geographic data, the retrospective spatiotemporal scan statistics method is suitable for the later stage of epidemic spread. It is also suitable for reviewing and analyzing the complete spatiotemporal development process of infectious disease spread. IDW can effectively compensate for the spatial discontinuity of data sources, and can be used to observe the specific situation of epidemic dissemination from a macroscopic perspective, providing intuitive understanding of the spatiotemporal development of the pandemic to the general public.

In summary, under incomplete geographic data and accuracy, appropriate spatiotemporal analysis methods can be selected according to different stages of epidemic development and different research purposes, in order to obtain more comprehensive and accurate spatiotemporal distribution information of the pandemic. This information can provide a scientific basis for public health policy making, resource allocation, and epidemic prevention and control, and has important reference value for future similar public health events.

Conclusions

The global COVID-19 pandemic has been effectively controlled, but combining GIS spatial-temporal analysis methods to analyze its transmission from a geographical perspective can help provide scientific basis for future responses to similar major public health events. This article explores three such methods, namely IDW interpolation, retrospective spatial-temporal scan statistics and Bayesian spatial-temporal models, applied to the spatial-temporal development of COVID-19 outbreaks in the contiguous US over 12 months, from May 2020 to April 2021. The research results show that by combining the three spatial methods to observe the research area comprehensively, four main spatial clusters were found: i) in eastern US, mainly New York State; ii) in southern US, mainly Texas; iii) in western US, mainly California; and iv) in south-eastern coastal area, mainly Florida. These regions are densely populated and are well developed economically. The GWR analysis showed that there is a degree of correlation between population and the number of confirmed cases, but the influence of the total population on the number of confirmed cases was limited and there may be other factors that influence the spread of COVID-19, such as climate, policy and population mobility.

In terms of time, from May to August 2020, the US had many low-level spatial clusters and during this period, the national epidemic spread widely showing multiple clusters. In the middle period of the study, especially from November 2020 to January 2021, with the arrival of winter, the epidemic in the research area reached a high level and continued to be high until March 2021 before showing a significant decline. However, during the same period, epidemic prevention and control policies were lifted, which led to another surge in April 2021.

A comparison of the three research methods has important implications with respect to the understanding the spatial-temporal distribution of the pandemic from multiple perspectives based on geographical analysis. However, it should be noted that although the spatial-temporal analysis methods used in this study would have an important application value in epidemic research, there are still some limitations, such as data source uncertainty and spatial discontinuity. Therefore, in actual research, it is necessary to carefully screen and process all data and verify and supplement them to ensure the accuracy and reliability of the research results.

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