



Medical Geography Contagious Disease

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Outline

- Disease outbreaks, endemics, epidemics and pandemics
- From Infectious Disease to Contagious Disease
- Contagious Disease
- Spatial Approaches on Infectious Diseases
- Potential Factors
- Case 1: Notifiable Respiratory Infectious Diseases
- Case 2: SARS & H1N1
- Case 3: COVID-19



世界醫師會日內瓦宣言

身為醫業一員: 我鄭重地保證將奉獻一切為人類服務: 病人的健康與福祉將為我的首要顧念; 我將會尊重病人的自主權與尊嚴; 我將堅持對人類生命的最高尊重: 我將不容許有任何年齡、殘疾、信念、族群、性別、國籍、政治立場、 種族、性傾向、社會地 位或其它因素的考量介入我的職責和病人之間; 我將尊重寄託給我的秘密,即便在病人身故之後; 我將秉持良心與尊嚴從事醫業,並遵循優良醫療規範; 我將提升醫業的榮譽及高尚傳統: 我將給予我的師長、同業與學生應有的尊重與感謝: 我將分享我的醫療知識,以增進病人福利和醫療照護的進展; 我將注重自身的健康、福祉與能力,以期提供最高標準的照護; 我將不運用我的醫學知識去違反人權與公民自由,即便受到威脅; 我鄭重地, 自主地並且以我的人格宣誓以上約定。

World Medical Association Declaration of Geneva, 2017

Disease outbreaks, endemics, epidemics and pandemics

- A **disease outbreak** is a rise in disease cases over what is normally expected in a in a defined area, generally over a short period of time, affecting a specific population group.
- A disease is said to be **endemic** when it is consistently present at a low level but limited to a particular region or population.
- An **epidemic** is a disease which spreads rapidly, affecting a large number of people within a community, population or region.
- A **pandemic** is an infectious disease that has spread over multiple countries or continents at the same time affecting a large number of people.

Source: https://www.onehealthpoultry.org/disease-outbreaks-endemics-epidemics-and-pandemics/

From Infectious Disease to Contagious Disease

As the trend of globalization, researchers pay more attention on infectious diseases than ever because of its infection, morbidity, and mortality nature.

Chowell, G. and Rothenberg, R., 2018. Spatial infectious disease epidemiology: on the cusp. *BMC medicine*, *16*, pp.1-5.

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Growth in spatial modeling, 1990–2017 (Web of Science). Search keywords for spatial modeling publications: (spatial model AND infectious diseases) OR (spatial method AND infectious diseases) OR (agent-based model AND infectious diseases) OR (individual-based model AND infectious diseases) OR (metapopulation model AND infectious diseases) OR (microsimulation model AND infectious diseases). Spatial dynamic transmission modeling publications: (microsimulation model AND infectious diseases) OR (agent-based model AND infectious diseases) OR (individual-based model AND infectious diseases) OR (metapopulation Model AND infectious diseases) OR (metapopulatio

From Infectious Disease to Contagious Disease

• So, from a historical perspective, how does it process?



On the cusp of intervention. We are close to a fully integrated approach for early epidemic detection and intervention as evidenced by the burgeoning output of data-driven spatial modeling. Recent events, such as MERS, SARS, Ebola, and influenza, have highlighted the need for coordinated, interactive, and multidisciplinary methods and permit rapid and real-time evaluation and action

Chowell, G. and Rothenberg, R., 2018. Spatial infectious disease epidemiology: on the cusp. *BMC medicine*, *16*, pp.1-5.

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Contagious Disease

A **contagious disease** is an infectious disease that is readily spread (that is, communicated) by transmission of a pathogen through contact (direct or indirect) with an infected person.

The spread of **non-contagious communicable diseases** is changed either very little or not at all by medical isolation of ill persons or medical quarantine for exposed persons.

Thus, a "**contagious disease**" is sometimes defined in practical terms, as a disease for which **isolation** or **quarantine** are useful public health responses.

Negative room pressure is a technique in health care facilities based on aerobiological designs.

Crowdsource/VGI Mobile Apps

Digital Contact Tracing

- COVID-19 Contact Tracing
- COVID-19 Data Visualization and Exploratory Data Analysis

Infectious Diseases Modelling

- Clustering
- Maximum Entropy Modelling (Maxent) Approach
- Susceptible-Infectious-Recovered (SIR) Model

Hotspot and Coldspot Analysis

Saran, S., Singh, P., Kumar, V. and Chauhan, P., 2020. Review of geospatial technology for infectious disease surveillance: use case on COVID-19. *Journal of the Indian Society of Remote Sensing*, 48, pp.1121-1138.

Crowdsource/VGI Mobile Apps:

- **Definition:** Crowdsourcing is the practice of turning to a body of people to obtain needed knowledge, goods or services.
- These entities rely on the internet, social media and purposebuilt platforms to elicit and receive the knowledge, goods or services they're seeking.

https://www.techtarget.com/searchcio/definition/crowdsourcing

Crowdsource/VGI Mobile Apps:

Benefits and challenges of crowdsourcing:

 Crowdsourcing can give entities access to a wider set of expertise at a faster pace and at a lower cost than traditional routes. On the other hand, those entities can't guarantee that the crowd they reach has the expertise, experience or resources to deliver what they need nor whether they're reaching the best sources to deliver the best possible outcome.

https://www.techtarget.com/searchcio/definition/crowdsourcing

Digital Contact Tracing

 During the COVID-19, most countries developed a/ several contact tracing apps for epidemic surveillance and monitoring tools.



Budd, J., Miller, B.S., Manning, E.M., Lampos, V., Zhuang, M., Edelstein, M., Rees, G., Emery, V.C., Stevens, M.M., Keegan, N. and Short, M.J., 2020. Digital technologies in the public-health response to COVID-19. *Nature medicine*, *26*(8), pp.1183-1192.

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Digital Contact Tracing

 How does the contact tracing app work?



Proximity-detecting contact-tracing apps use Bluetooth signals emitting from nearby devices to record contact events. Centralized apps share information about contacts and contact events with a central server. The centralized TraceTogether app⁷² uploads information when a user reports testing positive for COVID-19. Some centralized Bluetooth-enabled contact-tracing apps upload the contact graph for all users¹⁴⁸. Decentralized apps, such as SwissCovid¹⁴⁹, upload only an anonymous identifier of the user who reports testing positive for COVID-19. This identifier is then broadcast to all users of the app, which compares the identifier with on-phone contact-event records.

Budd, J., Miller, B.S., Manning, E.M., Lampos, V., Zhuang, M., Edelstein, M., Rees, G., Emery, V.C., Stevens, M.M., Keegan, N. and Short, M.J., 2020. Digital technologies in the public-health response to COVID-19. *Nature medicine*, *26*(8), pp.1183-1192.

Digital Contact Tracing

 The usage of contact tracing app throughout the world?



Mobile subscriptions per 100 people (blue; International Telecoms Union¹⁵⁰, 2018) and reported COVID-19 cases by country (red; WHO¹⁵¹, 8 June 2020). COVID-19 is a global pandemic, yet some countries may be better resourced than others to respond with digital health interventions. There may be intracountry inequalities in mobile subscription rates. Case detection and reporting practices differ among countries, with variable under-reporting of true cumulative case counts.

Budd, J., Miller, B.S., Manning, E.M., Lampos, V., Zhuang, M., Edelstein, M., Rees, G., Emery, V.C., Stevens, M.M., Keegan, N. and Short, M.J., 2020. Digital technologies in the public-health response to COVID-19. *Nature medicine*, *26*(8), pp.1183-1192.

Digital Contact Tracing

 The position of different epidemic surveillance tools.



Digital data are created by the public, both at the population level and at the individual level, for epidemiological intelligence and public-health interventions, and for the support of clinical case management. They are also informed by conventional surveillance via laboratory and clinical notification. This feeds into public-health decision-making and communication with the public through digital channels. Other relevant sources of information include ..., Rees. G., Emery, V.C., Stevens M.M., Keegan, N., and Short, M.J., 2020. Digital technologies in the public-health

Budd, J., Miller, B.S., Manning, E.M., Lampos, V., Zhuang, M., Edelstein, M response to COVID-19. *Nature medicine*, *26*(8), pp.1183-1192.

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Infectious Diseases Modelling - Clustering

 Proximity Effect: the further distance has a lower impact on pandemic.

Pei, S., Kandula, S., Cascante Vega, J., Yang, W., Foerster, S., Thompson, C., Baumgartner, J., Ahuja, S.D., Blaney, K., Varma, J.K. and Long, T., 2022. Contact tracing reveals community transmission of COVID-19 in New York City. *Nature Communications*, *13*(1), p.6307.

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a, **b** The exposures and transmission events across ZIP codes in NYC identified from contact tracing data. Arrows indicate direction of exposure (from index cases to reported close contacts) and transmission (from index infections to infected contacts). Arrow thickness indicates the number of exposures and transmission events. ZIP code area color represents the cumulative number of confirmed cases during the study period (yellow to red—low to high). To better visualize, exposure links with less than 30 events and transmission links with <2 events are not shown on the maps. For cross-ZIP code transmission events, the distributions of index infections and infected contacts across ZIP code areas are presented in **c** and **d**. **e** The distribution of distance between home ZIP codes of index infections and infected contacts in cross-ZIP code transmission events. The population weighted centroids for ZIP code areas were used to compute the distance.

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Infectious Diseases Modelling -Clustering

 After understanding the proximity effect, we need to have some statistical analyses to prove it.

Tesema, G.A., Tessema, Z.T. and Tamirat, K.S., 2020. Decomposition and Spatio-temporal analysis of health care access challenges among reproductive age women in Ethiopia, 2005-2016. *BMC Health Services Research*, *20*, pp.1-23.



Infectious Diseases Modelling - Clustering

- From a proximity effect to formulating a cluster.
- Useful tool: SaTScan

Tesema, G.A., Tessema, Z.T. and Tamirat, K.S., 2020. Decomposition and Spatio-temporal analysis of health care access challenges among reproductive age women in Ethiopia, 2005-2016. *BMC Health Services Research*, *20*, pp.1-23.



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- Infectious Diseases Modelling Maximum Entropy Modelling (Maxent) Approach
- Recent studies on geographical mapping of pathogens causing disease transmission, machine learning-based maximum entropy method (Maxent) (Elith et al. 2011; Phillips 2010) is applied on spatial records of COVID-19 with a set of 19 bioclimatic environmental variables from WorldClim (Poggio et al. 2018; Ramírez Villegas and Bueno Cabrera 2009) to analyse their favourable environmental conditions, required in maintaining its population.
- The Maxent principle is to estimate the target probability distribution by applying the maximum entropy to distribution which is most spread or closest.

Saran, S., Singh, P., Kumar, V. and Chauhan, P., 2020. Review of geospatial technology for infectious disease surveillance: use case on COVID-19. Journal of the Indian Society of Remote Sensing, 48, pp.1121-1138.

Infectious **Diseases Modelling** -Maximum Entropy **Modelling** (Maxent) Approach

Saran, S., Singh, P., Kumar, V. and Chauhan, P., 2020. Review of geospatial technology for infectious disease surveillance: use case on COVID-19. *Journal of the Indian Society of Remote Sensing*, 48, pp.1121-1138.



Predicted suitability of Betacoronavirus using data till March, 2020

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Susceptible-Infectious-Recovered (SIR) Model

- Epidemiology deals with the study of pattern and occurrence of diseases in space and time associated with other factors such as environment demography, and the translation of epidemiology into mathematical equations to describe the spread of infectious diseases is known as mathematical epidemiology (Allen et al. 2008; Rayner and Bender 1980).
- The mathematical epidemiology model is implemented to understand the transmission dynamics of communicable diseases by categorizing population into susceptible, infectious, and recovered compartments.
- The first basic model, known as Susceptible-Infectious-Recovered (SIR) model, was proposed by Kermack and McKendrick (1991) to describe the transmission of epidemic diseases from individual to individual.

Saran, S., Singh, P., Kumar, V. and Chauhan, P., 2020. Review of geospatial technology for infectious disease surveillance: use case on COVID-19. Journal of the Indian Society of Remote Sensing, 48, pp.1121-1138.

 The SIR model is a set of nonlinear ordinary differential equations, which is mathematically defined as follows:

•
$$\frac{dS}{dt} = \mu(N+S) - \beta SI$$

•
$$\frac{dI}{dt} = \beta SI - \gamma I - \mu I$$

• $\frac{dR}{dt} = \gamma I - \mu R$

Saran, S., Singh, P., Kumar, V. and Chauhan, P., 2020. Review of geospatial technology for infectious disease surveillance: use case on COVID-19. Journal of the Indian Society of Remote Sensing, 48, pp.1121-1138.

- S is the class of susceptible individuals who are not yet contracted to disease,
- I is the class of infectious people who are now infected with disease and become infectious to infect others,
- *R* is class of recovered individuals who have recovered now and are removed from class *S*,
- N is a total population size, N = S + I + R, and t is time in days or weeks
- β is the contact rate of infected person with suspected person per day,
- \mathbf{I}_{γ} is the infectious period and average infectious period is $\frac{1}{\gamma}$
- μ is the per capita death rate which is adjusted by birth rate μN .





Saran, S., Singh, P., Kumar, V. and Chauhan, P., 2020. Review of geospatial technology for infectious disease surveillance: use case on COVID-19. Journal of the Indian Society of Remote Sensing, 48, pp.1121-1138.

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- There are many other compartment models derived from the basic epidemic model, (SIR), with more compartments and transitions:
 - (1) Susceptible-Exposed-Infectious-Recovered (SEIR) (Li and Muldowney 1995)
 - (2) Susceptible-Infectious-Exposed-Recovered-Dead (SEIRD) (Piccolomiini and Zama 20s20)
 - (3) Susceptible-Infectious-Exposed-Recovered-Susceptible (SEIRS) (Liu and Zhang 2011)
 - (4) Susceptible-Infectious-Quarantine-Recovered (SIQR) (Erdem et al. 2017), etc.

Saran, S., Singh, P., Kumar, V. and Chauhan, P., 2020. Review of geospatial technology for infectious disease surveillance: use case on COVID-19. Journal of the Indian Society of Remote Sensing, 48, pp.1121-1138.

 Hotspot and Coldspot Analysis







https://www.sfgate.com/news/editorspicks/article/San-Francisco-covid-peak-holiday-surge-15884563.php# Chun-Hsiang Chan (2023)

Potential Factors



Pei, S., Kandula, S., Cascante Vega, J., Yang, W., Foerster, S., Thompson, C., Baumgartner, J., Ahuja, S.D., Blaney, K., Varma, J.K. and Long, T., 2022. Contact tracing reveals community transmission of COVID-19 in New York City. *Nature Communications*, *13*(1), p.6307. Incidence rate ratios (exponentiated coefficients) for non-household within-ZIP code transmission and cross-ZIP code transmission are shown for 12 covariates in **a** and **b**, respectively (Deviance information criterion, DIC = 6342 for **a** and DIC = 12,644 for **b**). Coefficients were estimated using a Poisson generalized linear mixed model controlling for spatial-temporal autocorrelations. We used the log-transformed population as the offset in the regression model. Covariates were standardized and are shown on the y-axis. The incidence rate ratio quantifies the multiplicative change in the number of transmission events per each covariate increase of one standard deviation, controlling for other covariates. The violin plots show the distributions of incidence rate ratios. Black dots and horizontal black lines highlight the median estimates and 95% CIs. Distributions in **a** and **b** were obtained using n = 20,000 MCMC samples of the posterior estimates.

Potential Factors

Table 2 Responsible bioclimatic variables in suitability modelling

From: Review of Geospatial Technology for Infectious Disease Surveillance: Use Case on COVID-19

Bioclimatic variables	Percent contribution
Mean temperature of coldest quarter	22.3
Precipitation of wettest month	14
Mean diurnal range	13.2
Isothermality	8.8
Annual mean temperature	8.2
Max temperature of warmest month	5.9
Precipitation of coldest quarter	5
Precipitation of wettest quarter	4.2
Annual precipitation	3.2
Precipitation of driest quarter	2.6
Mean temperature of driest quarter	2.6
Mean temperature of wettest quarter	2.4
Precipitation seasonality	2.4
Temperature seasonality	1.6
Precipitation of warmest quarter	1.4
Mean temperature of warmest quarter	1.1
Temperature annual range	0.7
Precipitation of driest month	0.5
Min temperature of coldest month	0.1

Saran, S., Singh, P., Kumar, V. and Chauhan, P., 2020. Review of geospatial technology for infectious disease surveillance: use case on COVID-19. Journal of the Indian Society of Remote Sensing, 48, pp.1121-1138.

 Here, we share a representative paper to perform it...

Li, X., Chen, D., Zhang, Y., Xue, X., Zhang, S., Chen, M., Liu, X. and Ding, G., 2021. Analysis of spatial-temporal distribution of notifiable respiratory infectious diseases in Shandong Province, China during 2005-2014. *BMC public health*, *21*(1), p.1597.



1684 Accesses 6 Citations Metrics

- Aim: This study aimed to determine the spatiotemporal distribution and epidemic characteristics of notifiable respiratory infectious diseases.
- Data: Time series was firstly performed to describe the temporal distribution feature of notifiable respiratory infectious diseases during 2005-2014 in Shandong Province.

Table 1 The incidence of each notifiable respiratory infectious disease in Shandong Province during the study period

From: Analysis of spatial-temporal distribution of notifiable respiratory infectious diseases in Shandong Province, China during 2005-2014

Disease	Time-period	Number of cases	Average annual incidence rate (/10 ⁵)
Influenza A (H1N1)	2009.5–2014.12	4755	1.008
Measles	2005.1-2014.12	25,994	2.772
Tuberculosis	2005.1-2014.12	34,3161	36.450
Meningococcal meningitis	2005.1-2014.12	242	0.026
Pertussis	2005.1-2014.12	1606	0.170
Scarlet fever	2005.1-2014.12	22,554	2.366
Influenza	2005.1-2014.12	23,874	2.496
Mumps	2005.1-2014.12	105,305	11.065
Rubella	2005.1-2014.12	10,014	1.069



Monthly incidence of notifiable respiratory infectious diseases from 2005 to 2014 in Shandong Province



The average annual incidence rate of notifiable respiratory infectious diseases by the natural breaks (Jenks) method from 2005 to 2014 in Shandong Province. The Shandong map was created with ArcGIS software based on the public geographical data downloaded from Resource and Environment Science and Data Center Institute of Congraphica Sciences and Natural Resources Research. CAS (https://www.resda.cm/)



The LISA cluster maps of notifiable respiratory infectious diseases during 2005–2014 in Shandong Province. The Shandong map was created with GeoDa software based on the public geographical data downloaded from Resource and Environment Science and Data Center, Institute of Geographic Sciences and Natural Resources Research, CAS (<u>https://www.resdc.cn/</u>)

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Spatial-temporal clusters of notifiable respiratory infectious diseases during 2005–2014 in Shandong Province. The Shandong map was created with ArcGIS software based on the public geographical data downloaded from Resource and Environment Science and Data Center, Institute of Geographic Sciences and Natural Resources Research, CAS (<u>https://www.resdc.cn/</u>)

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 Our study revealed that different notifiable respiratory infectious diseases display different trends. Our study confirmed the spatial autocorrelation of notifiable respiratory infectious diseases, and spatial-temporal clusters with high risk of notifiable respiratory infectious diseases in Shandong Province.

Case 2: SARS & H1N1

Brockmann, D. and Helbing, D., 2013. The hidden geometry of complex, network-driven contagion phenomena. *science*, *342*(6164), pp.1337-1342.



Fig. 1. Complexity in global, network-driven contagion phenomena. (A) The global mobility network (GMN). Gray lines represent passenger flows along direct connections between 4069 airports worldwide. Geographic regions are distinguished by color [classified according to network modularity maximization (39)]. (B) Temporal snapshot of a simulated global pandemic with initial outbreak location (OL) in Hong Kong (HKG). The simulation is based on the metapopulation model defined by Eq. 3 with parameters $R_0 = 1.5$, $\beta = 0.285$ day⁻¹, $\gamma = 2.8 \times 10^{-3}$ day⁻¹, $\varepsilon = 10^{-6}$. Red symbols depict locations with epidemic arrival times in the time window 105 days $\leq T_a \leq 110$ days. Because of the multiscale structure of the underlying network, the spatial distribution of disease prevalence (i.e., the fraction of infected individuals) lacks geometric coherence. No clear wavefront is visible, and based on this dynamic state, the OL cannot be easily deduced. (**C**) For the same simulation as in (B), the panel depicts arrival times T_a as a function of geographic distance D_g from the OL [nodes are colored according to geographic region as in (A)] for each of the 4069 nodes in the network. On a

global scale, T_a weakly correlates with geographic distance D_g ($R^2 = 0.34$). A linear fit yields an average global spreading speed of $v_g = 331$ km/day (see also fig. S7). Using D_g and v_g to estimate arrival times for specific locations, however, does not work well owing to the strong variability of the arrival times for a given geographic distance. The red horizontal bar corresponds to the arrival time window shown in (B). (**D**) Arrival times versus geographic distance from the source (Mexico) for the 2009 H1N1 pandemic. Symbols represent 140 affected countries, and symbol size quantifies total traffic per country. Arrival times are defined as the date of the first confirmed case in a given country after the initial outbreak on 17 March 2009. As in the simulated scenario, arrival time and geographic distance are only weakly correlated ($R^2 = 0.0394$). (**E**) In analogy to (D), the panel depicts the arrival times versus geographic distance from the source (China) of the 2003 SARS epidemic for 29 affected countries worldwide. Arrival times are taken from WHO published data (2). As in (C) and (D), arrival time correlates weakly with geographic distance.

Case 2: SARS & H1N1



Fig. 2. Understanding global contagion phenomena using effective distance. (**A**) The structure of the shortest path tree (in gray) from Hong Kong (central node). Radial distance represents effective distance D_{eff} as defined by Eqs. 4 and 5. Nodes are colored according to the same scheme as in Fig. 1A. (**B**) The sequence (from left to right) of panels depicts the time course of a simulated model disease with initial outbreak in Hong Kong (HKG), for the same parameter set as used in Fig. 1B. Prevalence is reflected by the redness of the symbols. Each panel compares the state of the system in the conventional geographic representation (bottom) with the effective distance representation (top). The complex spatial pattern in the conventional view is equivalent to a homoge-

neous wave that propagates outwards at constant effective speed in the effective distance representation. (**C**) Epidemic arrival time T_a versus effective distance D_{eff} for the same simulated epidemic as in (B). In contrast to geographic distance (Fig. 1C), effective distance correlates strongly with arrival time ($R^2 = 0.973$), i.e., effective distance is an excellent predictor of arrival times. (**D** and **E**) Linear relationship between effective distance and arrival time for the 2009 H1N1 pandemic (D) and the 2003 SARS epidemic (E). The arrival time data are the same as in Fig. 1, D and E. The effective distance was computed from the projected global mobility network between countries. As in the model system, we observe a strong correlation between arrival time and effective distance.

Brockmann, D. and Helbing, D., 2013. The hidden geometry of complex, network-driven contagion phenomena. *science*, *342*(6164), pp.1337-1342.

• The ordinary hot spot analysis is based on the equation of Getis-Ord Gi* Statistic as follows.

$$G_{i}^{*} = \frac{\sum_{j=1}^{n} w_{i,j} x_{j} - \overline{X} \sum_{j=1}^{n} w_{i,j}}{S \sqrt{\frac{\left[n \sum_{j=1}^{n} w_{i,j}^{2} - \left(\sum_{j=1}^{n} w_{i,j}\right)^{2}\right]}{n-1}}}$$

• Where x_j is the attribute value for village j, $w_{i,j}$ is the spatial weight between villages i and j, n is equal to the total number of villages.

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Pribadi, D.O., Saifullah, K., Putra, A.S., Nurdin, M. and Rustiadi, E., 2021. Spatial analysis of COVID-19 outbreak to assess the effectiveness of social restriction policy in dealing with the pandemic in Jakarta. Spatial and Spatio-temporal Epidemiology, 39, p.100454.

$$\bar{X} = \frac{\sum_{j=1}^{n} x_j}{n}$$
$$S = \sqrt{\frac{\sum_{j=1}^{n} x_j^2}{n} - (\bar{X})^2}$$

 The G^{*}_i statistic produces hot spot z-score and p-value of a region showing clusters with high and low value spatially.

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Pribadi, D.O., Saifullah, K., Putra, A.S., Nurdin, M. and Rustiadi, E., 2021. Spatial analysis of COVID-19 outbreak to assess the effectiveness of social restriction policy in dealing with the pandemic in Jakarta. Spatial and Spatio-temporal Epidemiology, 39, p.100454.

- The time variable was included in the spatial weight, thus, we have 3-dimensional spatiotemporal weight where x (latitude) and y (longitude) axes represent the centroid of the region (village) while z axes represents time.
- These three axes form a unit called bin as a spatiotemporal weight variable, and every bin has a close relationship with its neighboring bin spatially and temporally.



Pribadi, D.O., Saifullah, K., Putra, A.S., Nurdin, M. and Rustiadi, E., 2021. Spatial analysis of COVID-19 outbreak to assess the effectiveness of social restriction policy in dealing with the pandemic in Jakarta. Spatial and Spatio-temporal Epidemiology, 39, p.100454.

• By replacing spatial weight $(w_{i,j})$ with bin, ...

$$G_{i}^{*} = \frac{\sum_{j=1}^{n} b_{i,j,t} x_{j} - \overline{X} \sum_{j=1}^{n} b_{i,j,t}}{S \sqrt{\frac{\left[n \sum_{j=1}^{n} b_{i,j,t}^{2} - \left(\sum_{j=1}^{n} b_{i,j,t}\right)^{2}\right]}{n-1}}}$$

where $b_{i,j,t}$ (bin) is the spatial relationship between villages *i* and *j* at a certain period of related time.

Pribadi, D.O., Saifullah, K., Putra, A.S., Nurdin, M. and Rustiadi, E., 2021. Spatial analysis of COVID-19 outbreak to assess the effectiveness of social restriction policy in dealing with the pandemic in Jakarta. Spatial and Spatio-temporal Epidemiology, 39, p.100454.

 The result of the emerging hot spot (a) from 25th March to 12th April 2020 and (b) from 25th March to 28th April 2020 (note: number of villages is written in the bracket).



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 Spatial distribution of emerging spacetime clusters of COVID-19 risk at the village-level (a) from 25th March to 12th April 2020 and (b) from 25th March to 28th April 2020 (note: number of villages is written in the bracket).

Pribadi, D.O., Saifullah, K., Putra, A.S., Nurdin, M. and Rustiadi, E., 2021. Spatial analysis of COVID-19 outbreak to assess the effectiveness of social restriction policy in dealing with the pandemic in Jakarta. *Spatial and Spatiotemporal Epidemiology*, 39, p.100454.



 Priority areas of COVID-19 surveillance based on the dynamic of hot spot clusters of cases and the dynamic of transmission risk (a) from 25th March to 12th April 2020 and (b) from 25th March to 28th April 2020 (note: number of villages is written in the bracket).

Pribadi, D.O., Saifullah, K., Putra, A.S., Nurdin, M. and Rustiadi, E., 2021. Spatial analysis of COVID-19 outbreak to assess the effectiveness of social restriction policy in dealing with the pandemic in Jakarta. Spatial and Spatio-temporal Epidemiology, 39, p.100454.







Pribadi, D.O., Saifullah, K., Putra, A.S., Nurdin, M. and Rustiadi, E., 2021. Spatial analysis of COVID-19 outbreak to assess the effectiveness of social restriction policy in dealing with the pandemic in Jakarta. *Spatial and Spatio-temporal Epidemiology*, *39*, p.100454.



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Discussion

• For the next pandemic, if you are the president or the minister of Ministry of Health and Welfare. How will you do?

• As a geographer, what kinds of methods will you use for epidemic surveillance?



The End

Thank you for your attention!

Email: chchan@ntnu.edu.tw Web: toodou.github.io

