One Health & Outbreak Surveillance Online Symposium 2021



Tracking Spatial-temporal Transmissibility of Epidemics

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Contents

- Methodological issues in tracking spatial-temporal dynamics of epidemics
 - Understanding clustering evolution in time and space
 - Exploring multivariate epidemiological characteristics
 - Putting geospatial information into estimation of time-varying reproductive numbers (Rt)



1. Understanding clustering evolution in time and space





Space-time kernel density estimation for exploring diffusion process





Occurrence / Disappearance : Life Cycle Growth / Shrink : Change of Severity Split : Source of Infection Merge : Vulnerable Areas





Characterizing diffusion patterns





Step 1: Identifying transmission clusters

The cases, which form a transmission cluster, are considered by not only proximity in time and space with each other but also the transmission relationship, which represents that the neighbors of one case must appear spatially near but later than the case so that these neighbors could be infected by this case.



Defining space-time relationships





Step 2: Differentiating cluster evolution types





Cluster evolution of dengue epidemic in Kaohsiung, 2014







Cluster evolution vs. kernel density





Step 3: Measuring diffusion similarity among townships: Defining 'diffusion zone'



	Time 1	Time 2	Time 3	Time 4	
Region 1	Emerge	Growth	Move	Steady	
Region 2		Growth	Move, Growth	Steady	
Region 3		Emerge	Growth	Move	
Region 4			Growth	Move	



Grouping the regions with similar diffusion patterns





Cluster evolution vs. space-time kernel density





Python Libraries: pySDA

pySDA

a python Suite for Diffusion Analysis (for python 3.5 and above)

Intro

This package currently included the two diffusion analysis algorithms:

- 1. TaPiTaS: A geo-computational algorithm for exploring the structure of diffusion progression in time and space. Scientific Reports. https://www.nature.com/articles/s41598-017-12852-z
- MST-DBSCAN: Characterizing Diffusion Dynamics of Disease Clustering: A Modified Space–Time DBSCAN (MST-DBSCAN) Algorithm. Annals of the American Association of Geographers. https://www.tandfonline.com/doi/full/10.1080/24694452.2017.1407630

Install

You can choose one of the following to install pySDA to your python environment.

https://github.com/wenlab501/pysda



Exploring clustering evolution of COVID-19 outbreaks in Geneva, 2020

THE LANCET Digital Health

COMMENT | VOLUME 2, ISSUE 8, E393-E394, AUGUST 01, 2020

Geospatial digital monitoring of COVID-19 cases at high spatiotemporal resolution

David De Ridder • José Sandoval • Nicolas Vuilleumier • Silvia Stringhini • Hervé Spechbach • Stéphane Joost • et al. Show all authors

Open Access Published: June 16, 2020 DOI: https://doi.org/10.1016/S2589-7500(20)30139-4

Geospatial digital monitoring of COVID-19 cases at high spatiotemporal resolution *Lancet Digital Health*, June 2020



Exploring clustering evolution of COVID-19 outbreaks in Geneva, 2020



https://www.youtube.com/watch?v=U91uJ1FSuuY

Geospatial digital monitoring of COVID-19 cases at high spatiotemporal resolution *Lancet Digital Health*, June 2020



Comparing SaTScan (space-time clusters) vs. Clustering evolution (transmission clusters)



Size and duration of COVID-19 clusters go along with a high SARS-CoV-2 viral load: A spatio-temporal investigation in Vaud state, Switzerland, *Sci Total Environ*. Sep 2021.



2. Exploring multivariate epidemiological characteristics



Epi-Pro: Epidemic Profiler

疫情剖繪分析軟體 NTU GeoMED Suite



NTO GEOWIED Su

https://www.youtube.com/watch?v=CUnZnbLKSTw



Epi-Pro: Epidemic Profile 疫情剖繪分析軟體 **NTU** GeoMED Suite



(for dengue epidemics)

- Developing a standalone open source software called Epidemic Profiler (Epi-Pro)
- Exploring multivariate epidemiological characteristics
- Profiling cluster evolution of epidemics
- Assessing the effectiveness of interventions





https://www.youtube.com/watch?v=CUnZnbLKSTw



3. Putting geospatial information into estimation of time-varying reproductive numbers (Rt)

- The effective reproductive number, denoted as Re or Rt, is the expected number of new infections caused by an infectious individual in a population where some individuals may no longer be susceptible.
- The effective reproductive number Rt is a key epidemic parameter used to assess whether an epidemic is growing, shrinking, or holding steady.



Time-varying reproductive numbers (Rt)

Canada's *Rt* has remained below 1 for six weeks, indicating the epidemic has remained out of a growth pattern at the national level



" This means that the epidemic has remained out of a growth pattern nationally. However, Rt may still be at or above one in some areas. "

Source: Public Health Agency of Canada



Temporal Transmission Dynamics



$$p^{ij} = \frac{g(\hat{t}^{ij})}{\sum_{k \neq i} g(\hat{t}^{ik})}$$

$$R_t = \int_{x=t}^{\infty} \frac{\hat{b}_x g(x-t)}{\int_{a=0}^{\infty} \hat{b}_{x-a} g(a) da} dx$$

g(a) stands for the distribution of the generation interval, which is used as a weighting function for representing transmission potential at time interval a.



- At the individual level, a generation interval is defined as the time between when a person becomes infected and when that person infects another person.
- The intrinsic generation-interval distribution describes the expected time distribution of infectious contacts made by a primary case.



Comparisons of the transmission likelihood

(Dengue epidemic in Tainan, 2015)



generation-interval





Spatially adjusted reproductive numbers



Individual transmission distance :

$$D^{j} = \sum_{i \neq j, t^{i} > t^{j}} \frac{\hat{d}^{ij} p^{ij}}{\sum_{i \neq j, t^{i} > t^{j}} p^{ij}} = \sum_{i \neq j, t^{i} > t^{j}} \frac{\hat{d}^{ij} p^{ij}}{R^{j}}$$



Estimated time-varying reproductive numbers





Visualizing spatial distributions of individual reproductive numbers

(Dengue epidemic in Tainan, 2015)





COVID-19 Outbreaks in Taiwan, 2021

Daily new confirmed COVID-19 cases

7-day rolling average. Due to limited testing, the number of confirmed cases is lower than the true number of infections.



https://ourworldindata.org/



COVID-19

cases

Estimating spatial-temporal transmissibility of COVID-19 (COVID-19 Outbreaks in Taiwan, 2021)

Township-level transmission likelihood







Estimating spatial-temporal transmissibility of COVID-19 (COVID-19 Outbreaks in Taiwan, 2021)

Township-level transmission links





Developing R package: EpiTrans Estimation of epidemic transmissibility in time and space

devtools::install_github("wenlab501/EpiTrans")

library(EpiTrans)	Aa 名稱	■ 說明
EniTranslibnany()	CreatePoints	創建sf點圖層
	CreateBaseMap	創建底圖tmap地圖
	bnd_modify	重設邊界
	plot_points	點座標分布(Rj可當大小顏色屬性;t可當顏色屬性)
	■ plot_grid	點分布六角形圖(Rj可當顏色深淺屬性)
	■ plot_hex	點分布六角形圖(Rj可當顏色深淺屬性)
	plot_kde	點分布熱區圖
	plot_polygons	行政區病例面量圖
	■ plot_Rt	Rt曲線(隨時間)
	■ plot_epi	流行病學曲線(直方圖)
	animate.points	點分布座標位置動畫(Rj可當大小屬性)
	animate.grid	點分布六角形動畫(Rj可當顏色深淺屬性)
	animate_polygons	行政區病例面量圖動畫
	■ plot_trans	人與人傳播關係圖
	🗎 plot_Tij	行政區間傳播關係地圖



Concluding remarks

Methodological issues in epidemic dynamics

- Clustering evolution
- Multivariate epidemiological characteristics
- Spatial transmissibility: Spatial version of reproductive numbers
- Software/Packages development
 - pySDA: python Suite for Diffusion Analysis (python library)
 - Epi-Pro: Epidemic Profiler (standalone app)
 - EpiTrans: Estimating Epidemic Transmissibility (R package)



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Thank you for listening.

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