

Tracking dynamics of spatial-temporal clustering of infectious diseases

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Abstract

Geographic diffusion of epidemics is the phenomena of dynamic process. Existing spatial statistical methods cannot depict the dynamic patterns of epidemic diffusion. Spatial-temporal clustering methods, such as Ripley's K function and Kulldorff's scan statistics, focus on detecting space-time interactions and identifying the significant disease clusters in time and space. However, the methodology of tracking the temporal progression of disease transmission chain is under noticed. The aims of the study are to propose the methodology of tracking the dynamics of disease clustering in time and space and detecting the changes of clustering diffusion patterns of an epidemic. Residential locations and illness onset weeks of the dengue epidemic in Kaohsiung, 2009, are used as our data to demonstrate the framework of analytical procedure. First, for each space-time pair of dengue cases who are close in time and space, we establish links of space-time pairs and develop an index, called "Common Origin Probability (COP)", for each link to measure the probability of two persons infected from the same origin. An 'origin' means the one who others are infected from. A higher value of a clustering link means higher probability of the two cases not only being close in space and time, but also more likely coming from the same origin. These cases then can be connected as a space-time sub-cluster. Last, we establish the infection chain based on temporal progression of the sub-clusters to identify different diffusion patterns. The proposed method can provide dynamic insights into identifying space-time disease clusters and detect dynamic behaviors of an epidemic. Identifying diffusion patterns could be also beneficial for improving the effectiveness of blocking the transmission chain of epidemic diseases.

Keywords: space-time analysis, dynamic behavior of clustering, diffusion process, infection chain, disease transmission