

## “Spatial Distribution Characteristics of A(H7N9) Human Infections in China Between 2013 and 2014”

This case study is about the Novel avian-origin influenza A(H7N9) virus, and how it has caused a number of disease outbreaks in wild bird populations, domestic poultry and thus caused a problem for human health severely in China. Even though the Chinese Government had tried to take measures for the prevention and control of the human infections being caused due to the virus, the epidemic continued to remain a problem for the public with regular outbreaks each year.

The data for the study regarding confirmed influenza cases was obtained from the WHO website. The data was aggregated at the municipal level and the Spatio-temporal attributes (location and onset date) were used.

The study uses local spatial autocorrelation analyses, which can detect the autocorrelation of each spatial district and the variation across the area [1]. In order to learn about the spatial autocorrelation characteristics of H7N9 between 2013 and 2014, the study uses Anselin Local Moran's I statistic to detect local clusters and outliers of H7N9 human infections and the Getis-Ord  $G_i^*$  statistic to learn about hot spot locations on influenza H7N9 human cases. Both these analyses were conducted using tools provided in the ArcGIS 10.1 software.

### **Cluster and Outlier Analyses**

A set of administrative regions weighted by the respective number of influenza cases, statistically significant hot spots, cold spots and spatial outliers of human infections in China for the specified period were identified using the Anselin Local Moran's I statistic. The statistic provides information about four types of spatial association

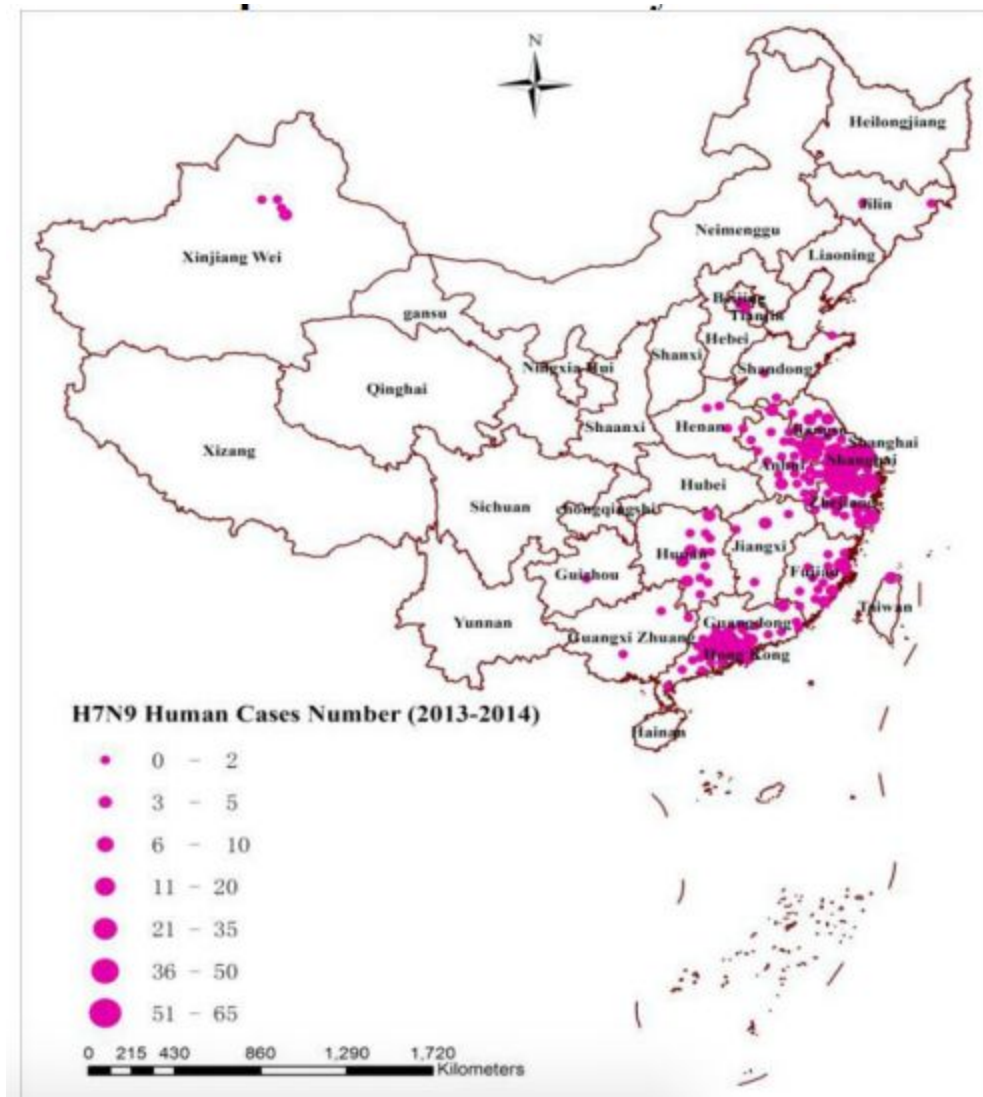
- HH (high values, 0.05 level, above the mean) associated with high neighboring values
- LL (low values, 0.05 level, below the mean), associated with low neighboring values.
- LH (0.05 level) spatial outlier of low values associated with high neighboring values.
- HL (0.05 level) spatial outlier of high values associated with low neighboring values.

The first two cases represent local spatial clustering of a similar number of influenza A(H7N9) human cases. The last two cases are examples of spatial outliers that point to locations that are different from their neighbors.

### **Hot Spot Analysis**

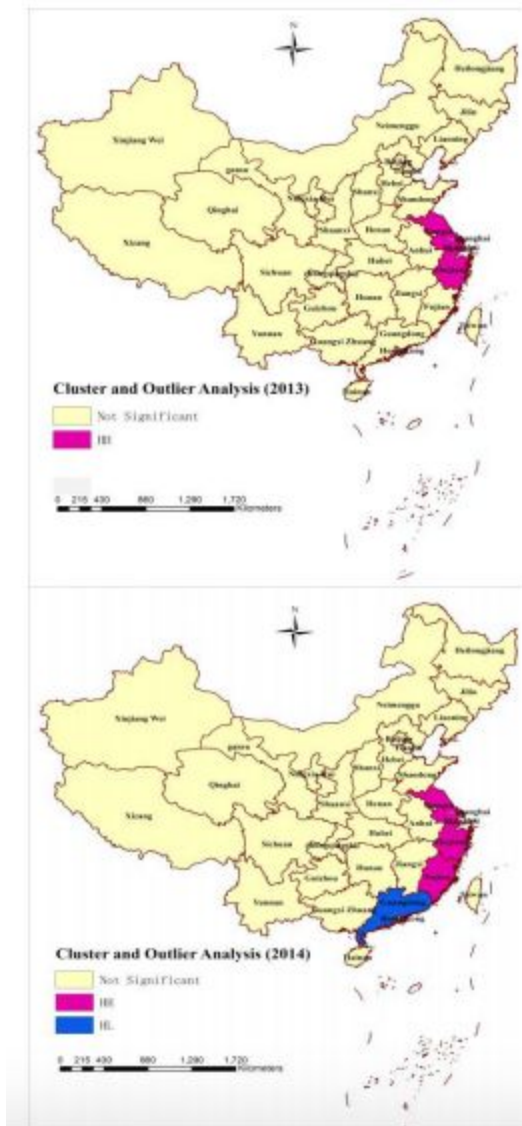
A set of administrative regions weighted by the respective number of influenza cases, statistically significant spatial clusters of high and low values (hot and cold spots) were identified using the Getis-Ord  $G_i^*$  statistic. This gives us a Z-score which indicates the degree of a location surrounding by areas with similar case numbers. For a z-score  $>1.96$ , it's represented as statistically significant hotspots at the 95% confidence level, and cold spots for  $<-1.96$  at the

95% confidence level. Majority of the regions fell in the statistically insignificant middle categories, showing no similarity in cases between adjacent areas. [1]

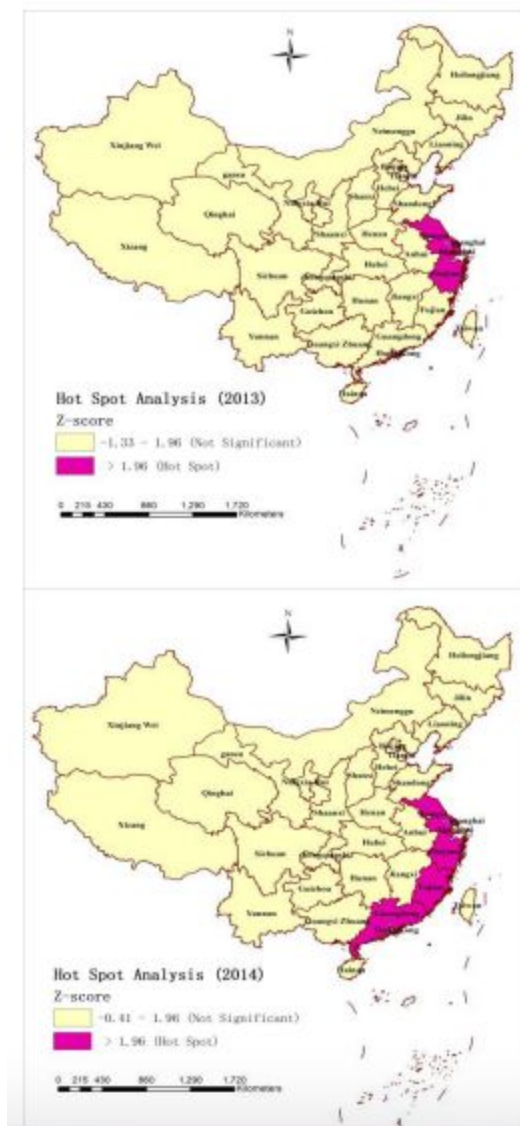


(Figure 1)

After processing the collected data in GIS, a map displaying the spatial distribution of influenza A(H7N9) human cases was created with a Chinese digital topographic map as the base. (Figure 1). It can be seen that there were 18 provinces and municipalities involving human infections in China during the study period. The eastern and southeast area seemed to be the high incidence areas. Furthermore, from the view of cases onset time, H7N9 outbreaks 240 in humans seemed more often in spring and winter between 2013 and 2014 according to the cases that were collected. [1]



(Fig 2)



(Fig 3)

As specified earlier, after using the Anselin Local Moran's  $I$  statistic it was seen that in 2013, statistically significant (0.05 level) spatial clusters of high values (HH) were 241 observed in three regions including Jiangsu, Zhejiang, and Shanghai; in 2014, however, the "HH" pattern regions were Jiangsu, Zhejiang, and Fujian, and a new statistically significant (0.05 level) spatial outlier in Guangdong (HL) was observed, indicating an uneven spatial distribution in A(H7N9) human infections (Figure 2). [1]

(Figure 2) indicated that the areas that belonged to the "HH" type had a positive spatial autocorrelation from 2013 to 2014, where high values of case number were surrounded by neighbors with high values. Furthermore, the areas that belonged to the "HL" type exhibited a negative spatial autocorrelation, i.e. (regions with high values of case number surrounded by neighbors with low values) forming the hot spots.

Also, when we look at (Figure 3), which uses the Getis-Ord  $G_i^*$  statistic, in 2013, three hot spot areas of A(H7N9) human infections were detected in Jiangsu (Zscore=4.2691), Zhejiang (Z-score=4.1694) and Shanghai (Zscore=5.4639); however, in 2014 hot spot areas were changed to Jiangsu (Z-score=1.9990), Zhejiang (Z-score=3.6497), Fujian (Zscore=1.9618) and Guangdong (Z-score=3.9114), which were basically consistent with the results of cluster and outlier analysis in this study. [1]

To sum it up, using GIS in combination with local spatial autocorrelation analysis in epidemiological surveillance systems can be very helpful in preventing and controlling future epidemics and also in identifying high-risk areas. It can also be extended to other disease studies and can matter a lot in the process of decision making.

Note:

- Anselin Local Moran's I and Getis-Ord  $G_i^*$  [cluster and outlier analysis, and hotspot analysis] can both be used using ArcGIS.
- I plan to learn more about these techniques and try to use at least one of them in my final project depending on the use case chosen. I plan to learn about more techniques relating to hotspot analysis as I had previously mentioned in earlier case studies and incorporate them into my project.

Reference(s):

[1] Dong, W. (2018). Spatial Distribution Characteristics of A(H7N9) Human Infections in China Between 2013 and 2014. *Proceedings of the 3rd International Conference on Intelligent Information Processing - ICIIP 18*. doi: 10.1145/3232116.3232675