

# Analyzing H7N9 and H5N1 Influenza Cases

Analysis for cases of H7N9 (2013-2014) in China and H5N1 (2010-2017) in Egypt

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## ABSTRACT

There have been a number of cases reported for avian influenza A(H5N1) and A(H7N9) which has infected large number of bird and human species in recent years. It has caused various disease outbreaks in bird populations across the globe. In this analysis, spatial outliers, statistically significant hot spots, cold spots of A(H7N9) reported cases in China between the years 2013 and 2014 were identified by using Anselin Local Moran's I statistic and then hot spot analysis using the Getis-Ord Gi\* statistic was performed to identify clusters of high value and low value of cases. In addition to this, a similar analysis was performed on H5N1 reported cases between 2010 to 2017 in Egypt to identify spatial outliers, statistically significant hot spots, cold spots of A(H5N1) influenza. Results of the analysis revealed that the provinces Shanghai, Zhejiang, Jiangsu, Beijing, Hebei, Guangdong, Hunan were the main areas for the epidemic between 2013 to 2014. The eastern and south east areas of China are key regions for surveillance for future epidemics. For the analysis on Egypt, it was seen that Sharqia, Qalyubia, Beheira, Monufia, Alexandria, Cairo, Ismailia, Minya, Fayum, Benisuef, Giza mainly constituting the central north region in Egypt. These are the areas which can be key regions of surveillance if an outbreak occurs. Through this study we also see that use of GIS in surveillance systems can prove to be very effective and can be very helpful in preventing and controlling future epidemics and also in identifying high-risk areas. It can also be extended to other similar studies and can matter a lot in decision making.

## CCS CONCEPTS

• Applied Computing → Life and Medical Sciences → Health Informatics

## KEYWORDS

H7N9, H5N1, GIS, Anselin Local Moran's, Getis-Ord Gi\* GIS

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## 1. INTRODUCTION

There have been a number of cases reported for avian influenza A(H5N1) and A(H7N9) which has infected large number of bird and human species in recent years. It has caused various disease outbreaks in bird populations across the globe. There have been some devastating effects seen in those infected too. According to an article on Healio, "The mortality rate in documented cases is high for both strains of avian influenza, about 60% for H5N1 and about 30% for H7N9"<sup>3</sup>. These viruses have remained endemic especially in countries like China, Egypt and globally for over two decades. They have continued to remain a problem with frequent outbreaks each year. According to a statement made by WHO, "Influenza viruses constantly undergo genetic changes. It would be a cause for concern, should the H5N1 virus become more easily transmissible among humans"<sup>4</sup>.

## 2. PROBLEM STATEMENT

The aim behind this analysis is to study and highlight regions of impact of H7N9 outbreaks in China. Keeping that in mind and applying it to highlight potential areas of impact for H5N1 outbreaks in Egypt which can later help in forming policies and allocating resources in case of major outbreaks and pandemics. An article by WHO stated that, "H5N1 infection in humans can cause severe disease and has a high mortality rate. If the H5N1 virus were to change and become easily transmissible from person to person while retaining its capacity to cause severe disease, the consequences for public health could be very serious"<sup>4</sup>.

## 3. GOALS AND OBJECTIVES

The main objective of this analysis was to help with policy making and resource allocation and showcase the importance and usefulness of GIS for surveillance if outbreaks occur. Secondary to that would be doing an extensive analysis to investigate the major factors contributing to a region being a potential outbreak site. Lastly, involving other parameters and analyzing patterns of globalization and increased travel and trade to help limit impact at origin of outbreak. As far as this analysis goes, highlight potential areas of impact for H7N9 and H5N1 outbreaks, achieved by first presenting past data relating to both kinds of influenza cases, A(H7N9) and A(H5N1) and second use ArcGIS as a visual representation tool for showcasing analysis done on A(H7N9) for China and then A(H1N5) for Egypt.

## 4. LITERATURE REVIEW

The study done by Wen Dong in Spatial Distribution Characteristics of A(H7N9) Human Infections in China Between 2013 and 2014<sup>1</sup>, uses local spatial autocorrelation analyses, which can detect the autocorrelation of each spatial district and the variation across the area. 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 Gi\* 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.

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. It was 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 in humans seemed more often in spring and winter between 2013 and 2014 according to the cases that were collected. After this cluster and outlier analysis were performed for both the years, in parallel to it hotspot analysis was also performed and the results were found to be consistent.

Another study done on finding priority areas for surveillance and prevention of avian influenza during the water-bird migration season in Pakistan<sup>2</sup> involved reporting Avian influenza viruses may be introduced into domestic poultry through migratory wild birds, particularly from Pakistan. A subset of Asian water bird census data was reviewed. A retrospective case-series analysis of previous outbreaks (2006-2008) of influenza A virus, subtype H5N1 was performed, which revealed that 64% of outbreaks, reported to Office International des Epizooties, the World Organization for Animal Health, occurred during the migratory period. This paper introduces another parameter (bird migration) which can further spread the outbreak, hence this is something which aligns with the overall objectives of this analysis and study too.

## 5. METHODOLOGY

### 5.1 Data Collection and Processing

Information about the reported influenza cases for A(H7N9) and A(H5N1) was obtained from the WHO and other reputed national authorities. The data was found from the ArcGIS online search tool. Data was imported from there<sup>5</sup>. The data consisted of 31030 reported cases globally. For A(H7N9), a total of 975 reported cases between 2013 and 2014 were selected. The cases spatio-temporal attributes including the location (latitude, longitude) and reported date were used. In addition to this a Chinese province boundary depicting map was added as a layer to help in visualizing the affected regions. For A(H5N1), a total of 2555 reported cases in Egypt between 2010 and 2017 were selected.

Here also the cases spatio temporal attributes including the location (latitude, longitude) and reported date were used. In addition to that an Egyptian province boundary depicting map was added as a layer to help in visualizing the affected regions and regions of surveillance in case of outbreaks. ArcGIS Pro software was used to perform the analysis and visualize the results.

### 5.2 Methods Used

In order to understand the autocorrelation characteristics of H7N9 (2013-2014) and H5N1 (2010-2017), in this study the Anselin Local Moran's I statistic was used to detect clusters and outliers of reported sum of cases and Getis-Ord Gi\* was used to find the locations of hotspots of the cases. This was conducted using ArcGIS Pro Software.

#### 5.2.1 Cluster and Outlier Analysis

Statistically significant hot spots, cold spots, and spatial outliers of A(H7N9) cases in China and A(H5N1) cases in Egypt during the study period were identified by using the Anselin Local Moran's I statistic<sup>1</sup>. The statistic provides information about four types of spatial association.

(1) HH (high values, 0.05 level, above the mean) associated with high neighboring values. (2) LL (low values, 0.05 level, below the mean), associated with low neighboring values. (3) LH (0.05 level) spatial outlier of low values associated with high neighboring values. (4) HL (0.05 level) spatial outlier of high values associated with low neighboring values<sup>1</sup>.

The first two cases represent local spatial clustering of a similar number of A(H7N9) or A(H5N1) reported cases. The last two cases are examples of spatial outliers that point to locations that are different from their neighbors.

#### 5.2.2 Hotspot Analysis

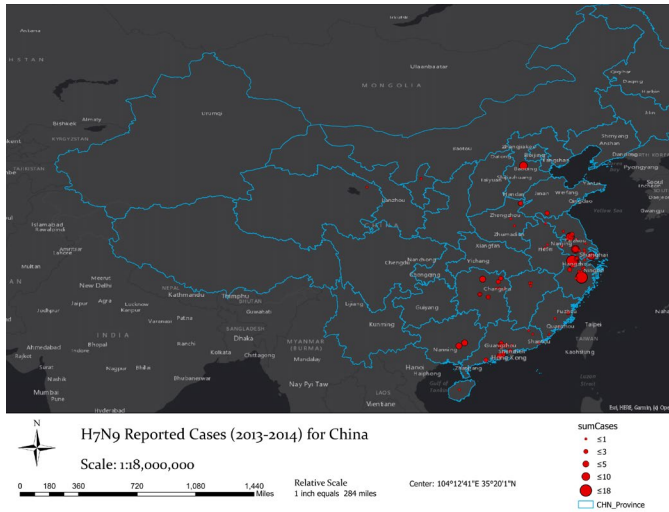
Statistically significant spatial clusters of high and low values (hot and cold spots) were identified using the Getis-Ord Gi\* statistic. The Getis-Ord Gi\* returns a Z-score which indicates the degree of a location surrounding by areas with similar number of cases. The Z-scores >1.96 represent statistically significant hot spots at the 95% confidence level, while those <-1.96 are statistically significant cold spots at the 95% confidence level<sup>1</sup>.

## 6. RESULTS

### 6.1 Descriptive Statistics Analysis

Here, information about the collected and processed data for H7N9 cases in China and H5N1 cases in Egypt has been displayed with a map showing the spatial distribution of the affected regions. A Chinese and an Egyptian Chinese province boundary depicting map layers are added to help in visualizing the affected regions.

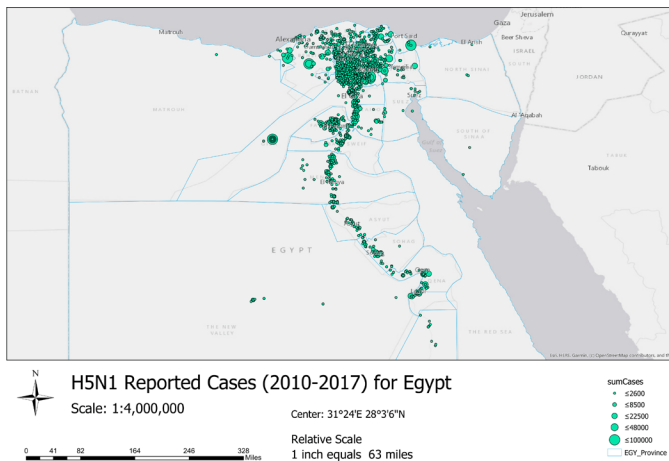
Following is a figure displaying the A(H7N9) affected regions for the outbreak of 2013-2014 cases.



**Figure 1: H7N9 reported cases for China (2013 – 2014) having 975 reported cases.**

Figure 1 provides us with an impression of how spatially distributed the reported cases were in China during the outbreak for the study period. The eastern and south east coast seem to be the most affected areas because of the H7N9 spread. Out of the reported cases, Zhejiang (193), Shanghai (97), Jiangsu (81), Guangdong (347) constituted 74% of the cases (718/975).

Following is a figure displaying the A(H5N1) affected regions for the outbreak of 2010-2017 cases in Egypt.

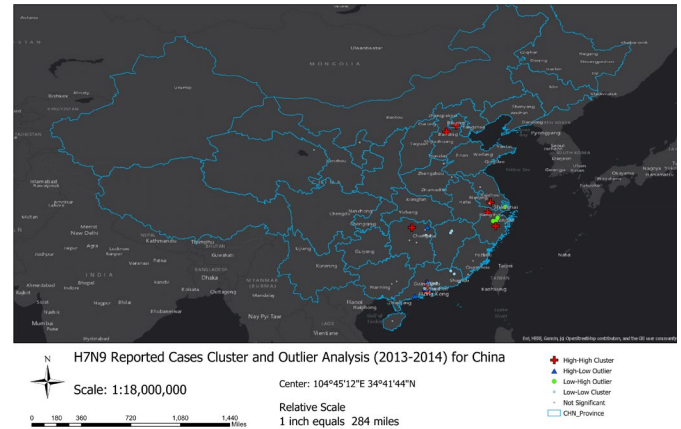


**Figure 2: H5N1 reported cases for Egypt (2010 – 2017) having 2555 reported cases.**

Figure 2 provides us with an impression of how spatially distributed the reported cases were in Egypt during the outbreak for the study period. The central north region seems to have the most affected areas because of the H5N1 cases reported. Out of the reported cases, Sharqia, Qalyubia, Beheira, Monufia, Alexandria, Cairo, Ismailia, Minya constituted 88% of the cases.

## 6.2 Cluster and Outlier Analysis – A(H7N9)

In order to identify spatial clusters of regions with high or low values of A(H7N9) reported cases and detect spatial outliers of H7N9 outbreaks in China, cluster and outlier analyses from (2013-2014) were conducted by the Anselin Local Moran's I statistic.



**Figure 3: H7N9 Reported Cases Cluster and Outlier Analysis (2013-2014) for China.**

In 2013-2014, statistically significant (0.05 level) spatial clusters of high values (HH) of influenza A(H7N9) cases were observed in three regions including Jiangsu, Zhejiang and Shanghai and a statistically significant (0.05 level) spatial outlier in Guangdong (HL) was observed, indicating an uneven spatial distribution.

## 6.3 Hotspot Analysis - A(H7N9)

In order to identify statistically significant spatial clusters of high values of influenza A(H7N9) reported cases (hot spots) and low values of influenza A(H7N9) reported cases (cold spots), hot spot analysis of influenza A(H7N9) cases in 2013 and 2014 was carried out by the Getis-Ord Gi\* statistic.

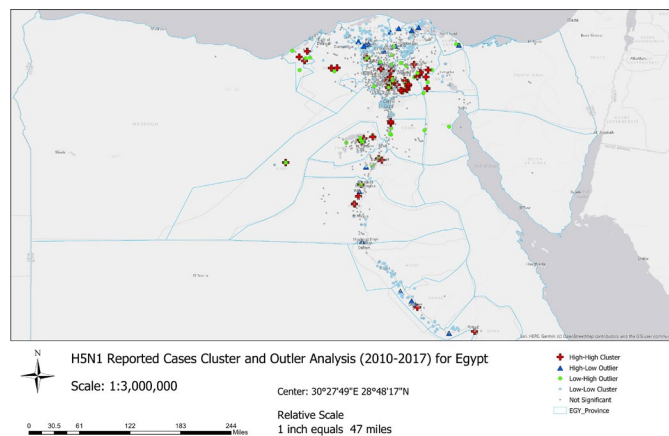


**Figure 4: H7N9 Reported Cases Hotspot Analysis (2013-2014) for China.**

The results in Figure 3 illustrated statistically significant (at the 0.05 level) clusters of regions with high or low values of A(H7N9) reported cases. From 2013-2014, four hot spot areas of A(H7N9) infected regions were detected basically consistent with the results of cluster and outlier analysis in this study.

#### 6.4 Cluster and Outlier Analysis – A(H5N1)

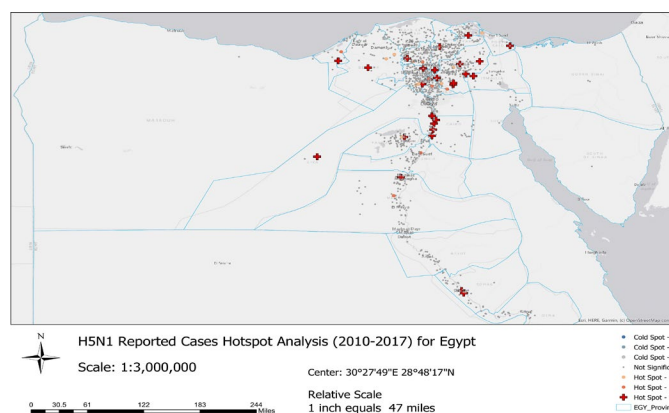
In order to identify spatial clusters of regions with high or low values of A(H5N1) reported cases and detect spatial outliers of H5N1 outbreaks in Egypt, cluster and outlier analyses from (2010-2017) were conducted by the Anselin Local Moran's I statistic.



**Figure 5: H5N1 Reported Cases Cluster and Outlier Analysis (2010-2017) for Egypt.**

In 2010-2017, statistically significant (0.05 level) spatial clusters of high values (HH) of A(H5N1) cases were observed in the northern central region of Egypt. And statistically significant (0.05 level) spatial outliers were found near to the northern coast of Egypt for the study period considered.

#### 6.5 Hotspot Analysis - A(H5N1)



**Figure 6: H5N1 Reported Cases Hotspot Analysis (2010-2017) for Egypt.**

In order to identify statistically significant spatial clusters of high values of A(H5N1) reported (hot spots) and low values of influenza A(H5N1) reported cases (cold spots), hot spot analysis of influenza A(H5N1) cases between 2010 and 2017 was carried out by the Getis-Ord  $G_i^*$  statistic.

The results in Figure 6 illustrated statistically significant (at the 0.05 level) clusters of regions with high or low values of A(H5N1) reported cases. From 2010-2014, hotspot areas of A(H5N1) infected regions were detected basically consistent with the results of cluster and outlier analysis in this study, comprising mainly in the northern central region of Egypt.

### 7. DISCUSSION

In this analysis, spatial outliers, statistically significant hot spots, cold spots of A(H7N9) reported cases in China between the years 2013 and 2014 were identified by using Anselin Local Moran's I statistic and then hot spot analysis using the Getis-Ord  $G_i^*$  statistic was performed to identify clusters of high value and low value of cases. In addition to this, a similar analysis was performed on H5N1 reported cases between 2010 to 2017 in Egypt to identify spatial outliers, statistically significant hot spots, cold spots of A(H5N1) influenza. Results of the analysis revealed that the provinces Shanghai, Zhejiang, Jiangsu, Guangdong, Hunan were the main areas for the epidemic between 2013 to 2014. The eastern and south east areas of China are key regions for surveillance for future epidemics. For the analysis on Egypt, it was seen that Sharqia, Qalyubia, Beheira, Monufia, Cairo, Ismailia, Minya mainly constituting the central north region in Egypt. These are the areas which can be key regions of surveillance if an outbreak occurs.

### 8. CONCLUSION

This kind of analysis can be useful to mark down high-risk areas especially for such epidemics which have the ability to become pandemics.

Through this study we also see that use of GIS in surveillance systems can prove to be very effective and can be very helpful in preventing and controlling future epidemics and also in identifying high-risk areas. It can also be extended to other similar studies and can matter a lot in decision making.

In addition to this when it comes to future work, analyzing data related to bird migration would also prove essential in finding more relevant results. Also, to align to our overall objective of involving other parameters and analyzing patterns of globalization and increased travel and trade to help limit impact at origin of outbreak would be the next step.

### 9. REFERENCES

- [1] Wen Dong. 2018. Spatial Distribution Characteristics of A(H7N9) Human Infections in China Between 2013 and 2014. In Proceedings of the 3rd International Conference on Intelligent Information Processing (ICIIP '18). ACM, New York, NY, USA, 238-242. DOI: <https://doi.org/10.1145/3232116.3232675>
- [2] Tariq Abbas, Hendrik Wilking, Christoph Staubach, Mario Ziller, and Franz Josef Conraths. 2011. Priority areas for surveillance and prevention of avian

influenza during the water-bird migration season in Pakistan. *Geospatial health* 6, 1 (January 2011), 107. DOI:<http://dx.doi.org/10.4081/gh.2011.162>

- [3] August 2013 Donald Kaye *Infectious Disease News*. Avian influenza: A comparison of A(H5N1) and A(H7N9). Retrieved October 16, 2019 from <https://www.healio.com/infectious-disease/news/print/infectious-disease-news/{bfb26f60-bf2a-4db7-9359-b6ba04dc4c4f}/avian-influenza-a-comparison-of-ah5n1-and-ah7n9>
- [4] Anon. 2012. FAQs: H5N1 influenza. (March 2012). Retrieved October 16, 2019 from [https://www.who.int/influenza/human\\_animal\\_interface/avian\\_influenza/h5n1\\_research/faqs/en/](https://www.who.int/influenza/human_animal_interface/avian_influenza/h5n1_research/faqs/en/)
- [5] Anon. Retrieved October 16, 2019 from <https://ritarcgis.maps.arcgis.com/home/item.html?id=7042aa5dedad4bae81aa9cdec47cc6c>