Spatially Explicit Epidemiological Simulation System of Influenza A (H1N1) in China

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Abstract—**The outbreak of pandemic influenza A (H1N1) around the world has caused significant economic loss and human death. It is a urgent challenge to improve our response to pandemic influenza A (H1N1) outbreaks, and avoid its epidemic. Computer simulation is a pragmatic and effective methodology for analyses of influenza A (H1N1). A spatially explicit epidemiological simulation system is proposed to study the outbreak and transmission of influenza A (H1N1) in mainland China. In this system, a SEIR epidemic model is developed, and traffic between provinces and four kinds of prevention and control measures are considered. Additionally, Geographic Information System (GIS) tool is incorporated in the system to provide friendly interface for model development, epidemic simulation, and temporal-spatial analysis. Preliminary experimental results have shown the effectiveness of the system.**

Keywords-pandemic influenza A (H1N1); epidemiological simulation system; GIS

I. INTRODUCTION AND MOTIVATION

In March 2009, pandemic influenza A (H1N1) human cases first occurred in Mexico. It spread rapidly to the rest of the world. On 11 June 2009, the World Health Organization (WHO) raised the phase of pandemic alert to level 6. Up to 19 July 2009, influenza A (H1N1) epidemic has reached 142 countries[1]. The outbreak of novel influenza A (H1N1) around the world has lead to tremendous economic loss and threatened people's lives. The latest statistics data from WHO shows that 6770 people have died in the world as of 20 November 2009. World Bank (WB) predicts that it will lead to more than 3000 billion dollar economic loss and obviously affect the world economic recovery [2].

Until now, the most effective means for prevention of influenza epidemic is the injection of vaccinations in the method of government's strategic deployment [3]. Unfortunately, manufacturing and distribution of vaccine have to face a myriad of challenge from technological and socio-political issues [3]. Therefore, proactive planning and strategic deployment of countermeasures are more realistic approach to combat the pandemic influenza A (H1N1) [3]. Computer-based simulation with transmission models is a useful method to predict the epidemic and evaluate the effect of various prevention and control measures. A global structured metapopulation model integrating mobility and transportation data worldwide has been proposed to simulate the spread of influenza A (H1N1) in the world and assess the effect on the whole world epidemic due to people's travel and seasonal transmission [1]. To evaluate the effect of containment measures during the early phase of the epidemic in mainland China, a Monte Carlo model was build [4]. Although, mathematic model can be used to calculate the number of cases, it is not a good tool to visualize and analyze the complicated, spatial-temporal process of an epidemic. Geographic Information System (GIS) provide powerful tools about spatial analysis and display. In this paper, a spatially explicit epidemiological simulation system of pandemic influenza A (H1N1) in China is proposed by integrating GIS and mathematic epidemic model.

II. SIMULATION MODEL

A simulation model is developed to depict the transmission of pandemic influenza A (H1N1) with different prevention and control measures. In the model, there are three spread processing at different scales, including cases importing from abroad, cases flowing among provinces and the spread of influenza A (H1N1) in each province.

A. Travel

Traffic has played an important role in the transmission of influenza A (H1N1) among provinces, it introduces the transmission of A (H1N1) from a province to others. In the model, two travelling methods are considered. Firstly, some cases in each province can travel inter-provincially with different probability; secondly, some regions with international airports have cases importing from abroad. In view of the stochastic of people's transfer, we take advantage of Binomial and multinomial processes to depict their travel (Fig. 1).

The inter-provincial flow of human cases leads to inter-provincial transmission of influenza A (H1N1). A case daily

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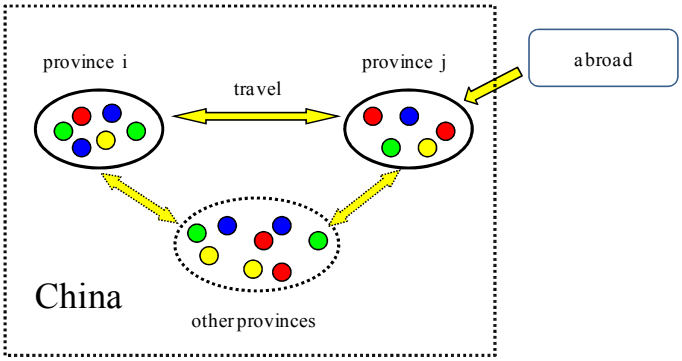

Figure 1. Process of travel

moves from province *i* to province *j* at M_{ij} rate, M_{ij} is calculated by mobility rate between these two provinces.

$$M_{ij} = k * T_i * T_j \tag{1}$$

where T_i and T_j are the traffic of province *i* and *j*. *k* is a parameter [4].

B. Epidemiological Model

Based on a SEIR compartmental model applied in [5], we construct a new SEIR compartmental model (Fig. 2) to describe the transmission process of influenza A (H1N1) spread in each province. In the model, each individual is classified by one of the discrete states such as susceptible (*S*), exposed(*E*), infectious (*I*) and recovered(*R*). The infectious persons are further subdivided into asymptomatic infectious and symptomatic infectious. If a susceptible individual contacts an asymptomatic or symptomatic infectious person, he may be infected at the rate of β or $\gamma\beta$, and then turns into latent state. A latent case will become to an infectious case with the rate of ε, after latent period ($1/\varepsilon$). The proportions of symptomatic and asymptomatic infectious state are $1\text{-}P_a$ and P_a respectively. The recovered rate of infectious persons is μ. Binomial, Poisson and multinomial processes are introduced to describe the discrete nature of individuals for the stochastic evolution of the infection.

Based on the definition of standard incident, as in (2)

$$L_{new} = \theta * I * S / N \tag{2}$$

where L_{new} denotes new latent persons, I is total number of infected people, S is susceptible people, N is the total population of a province, θ is the infected rate whenever a susceptible person contacting a infectious case. In our study, I is so small when compared with N that the value of S / N approximately equals 1. As a result, (2) can be simplified as in (3)

$$L_{new} = \theta * I \tag{3}$$

In our model, infectious cases are divided into symptomatic infectious cases and asymptomatic infectious cases.

$$L_{new} = \beta * Sy(t) + \gamma * \beta * ASy(t) \tag{4}$$

So, we can express evolvement process of influenza A (H1N1) in Fig. 2 as in (5),(6),(7),(8).

$$L(t+1) = L(t) + L_{new} - \varepsilon * L(t) \tag{5}$$

$$Sy(t+1) = Sy(t) + (1 - P_a) * \varepsilon * L(t) - \mu * Sy(t) \tag{6}$$

$$ASy(t+1) = ASy(t) + P_a * \varepsilon * L(t) - \mu * ASy(t) \tag{7}$$

$$R(t+1) = R(t) + \mu * Sy(t) + \mu * ASy(t) \tag{8}$$

where $L(t)$, $Sy(t)$, $ASy(t)$ and $R(t)$ denote case numbers in latent state, symptomatic infectious state, asymptomatic infectious state and recovered state at the *t* day.

C. Prevention and Control Measures

Four countermeasures are designed to prevent and control epidemic of influenza A (H1N1) in the simulation model, including Border Checking (BC), Foreign Immigrants Home-Quarantine (FIHQ), Symptomatic Infectious Person Isolation (SIPI), and Close-Contacts Person Quarantine (CCPQ).

SIPI: symptomatic infectious persons will be quarantined once diagnosed. It is equivalent to divide symptomatic infectious person to two parts: people quarantined will not infect others, and the other part can infect other people by contacting them.

$$L_{new} = \beta * \lambda * Sy(t) + \gamma * \beta * ASy(t) \tag{9}$$

where λ is the intensity value of SIPI.

CCPQ: people who are found to closely contact a symptomatic infectious person will be quarantined for a period of time. When CCPQ is implemented, the formula is

$$L_{new} = \delta * \beta * Sy(t) + \gamma * \beta * ASy(t) \tag{10}$$

where $Sy(t)$ and $ASy(t)$ are symptomatic and asymptomatic infectious person at the t day , δ is the intensity value of CCPQ.

BC: checking passenger from abroad at ports of entry.

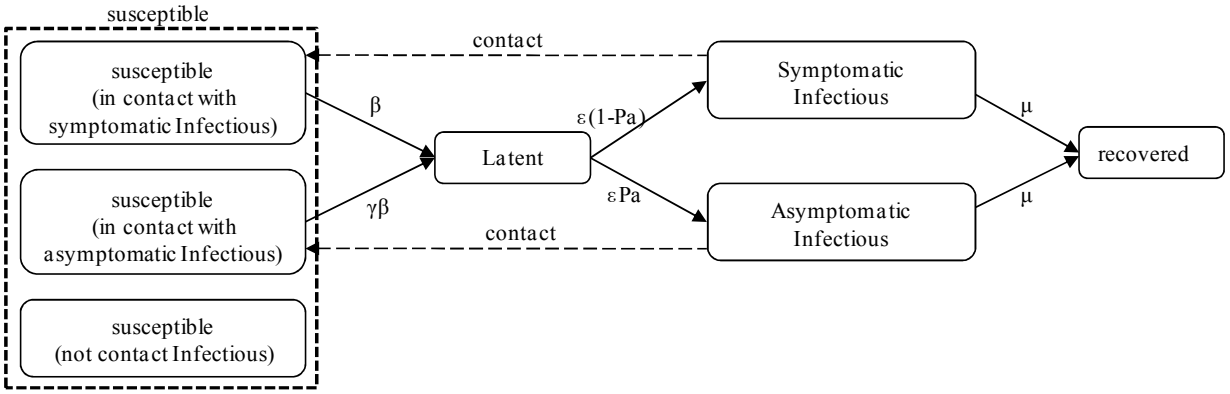

Figure 2. Epidemic model in each province

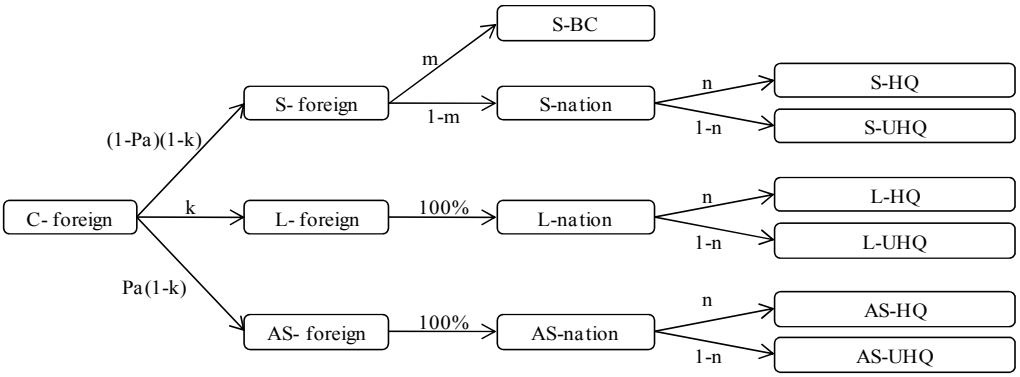

Figure 3. Implement of BC and FIHQ

We suppose that cases(C- foreign) from abroad may be in three state, L-foreign(latent persons from abroad), S-foreign(symptomatic infectious persons from abroad) and AS-foreign (asymptomatic infectious persons from abroad). BC acts on S-foreign, some cases will be checked and isolated with the rate of *m*. Otherwise, L- foreign and AS- foreign will all enter China. Cases who not checked by BC including S-nation, L-nation, AS-nation should isolate themselves at home for a period of time, we design the rate of FIHQ is *n*.

Once he/she is found to be a symptomatic case, he/she will be isolated and can't infect other persons in the country (Fig. 3), *m* is the intensity value of BC.

FIHQ: require persons who come from abroad to stay at home for a period of time (no less than latent period) (Fig. 3), *n* is the intensity value of FIHQ.

The parameters of prevention and control measures can be adjusted on the interface of simulation module. Additionally, cases quarantined by measures will still change their states, their number should be added to total case number. In order to describe the stochastic, we also use random processes.

III. SIMULATION SYSTEM

A. System Frame

The system is developed by C# （with ArcGIS Engine）. It provides a friendly user interface to show spatial-temporal pattern during the influenza epidemic progress in China. Graphical interface is provided to data import, parameters setting, visualization and analysis. So, it is a convenient and intuitive system to study epidemiology of influenza in China using modeling and simulation. Additionally, we apply stochastic process to describe the natural pattern of people's travel and development of a case.

It consists of four modules, namely Master-program module, Data-import module, Simulation module, Spatial-temporal-analyses module (Fig. 4).

Master-program module: it is a basic platform organizing other module. It contains operation interface, map-display window and tools of thematic map manipulation, so that it can manage data and show simulation result by thematic map.

Data-import module: it takes charge of importing data for simulation. A visual interface is designed to display the content of imported data so that user can confirm whether the data are needed or not, which will help to reduce operational error.

Simulation module: it is the core of the simulation system. It contains epidemic model, parameters setting and storage of simulation results. The simulation course of transmission is accomplished there. User-friendly interface is provided to set parameters, which is used to set coefficients of epidemic model and intensity values of containment.

Spatial-temporal-analyses module: it is a toolbox to deal with simulation result by GIS.

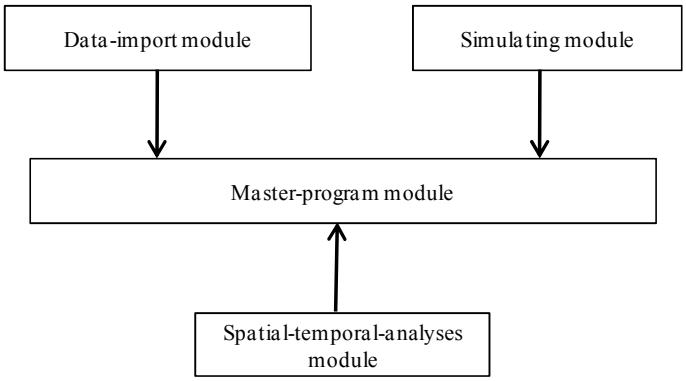

Figure 4. Frame of the simulation system

B. Assistant Analysis Tool

The system provides some tools which are spatial-temporal analysis tools to deal with and analyze simulation results. Spatial-temporal tools contains temporal-evolution tool which can analyses expanding of epidemic in the time dimension and spatial-distribution tool used to analyses epidemic distribution in spatial scale. This assistant analysis tools are developed by taking advantage of ArcGIS engine, and it implements map exhibit, map query and human-computer interaction (Fig. 5, Fig. 6).

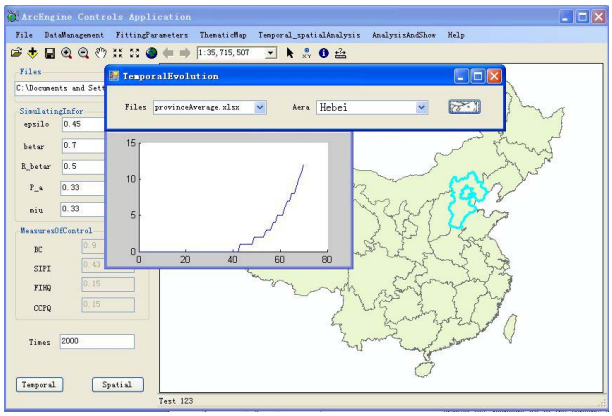

Figure 5. Interface of temporal-evolution tool

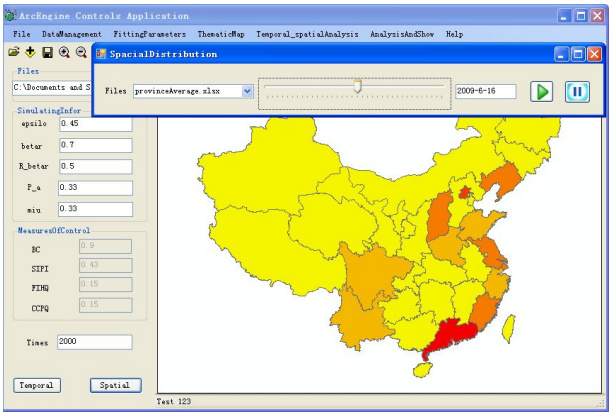

Figure 6. Interface of spatial-distribution tool

IV. Preliminary Simlulation Experiments

We simulate transmission process of influenza A (H1N1) from 11 May to 30 June, 2009, (a period of 70 days time).

A. Parameter Setting

We obtained parameter values of the SEIR compartmental model, based on relevant research [1, 5] and the parameters are $1/\varepsilon$=2.2, $1/\gamma$=2, $1/\mu$=3, P_a=0.33, R_0 =1.75. The value of β is calculated by (11).

$$\beta = R_0 * \mu * (1 - P_a + \gamma * P_a)^{-1} \tag{11}$$

As a result, β=0.7. In our preliminary experiments, the same values of above-mentioned parameters are used for all the provinces.

B. Travel Calculation

Railway is the most important vehicle for people's travel from a province to another one. So, in this system, we use (1) to calculate M_{ij} by treating railway traffic of province i and province j as T_i and T_j.

These railway traffics of provinces come from the statistic data in 2007 [4]. Exporting cases from a province to others generated in the method of multinomial distribution in the light of coefficient of provinces.

According to the data of influenza A(H1N1) transmission in China, four provinces (Beijing, Shanghai, Guangdong and Fujian) have cases importing from abroad every day, its average number is 0.4 or 0.2, additionally, there is one case in Sichuan province at 11 May, so we design there is 1 case in Sichuan province, at the start of simulation. In the system, Poisson distribution is used to generate case number importing from abroad every day.

C. Results and Discussion

Experiments have been conducted to evaluate the impact of countermeasures (Fig.7). We compare simulation accumulative cases with statistical accumulative cases [6]. Especially, stochastic process usually generates some extream data, which often lead some simulation result very high or low. In order to keep simulation result stabile, we calculate the average values without the maximal and minimal simulation values of 5%.

Three configurations with different values of measures (Tab.I) show that different intensity of measures affect simulation result significantly. The simulation case data will increase faster than reported case data in the case with little countermeasure intensity (Fig.7A), on the other side, the

TABLE I. Values of Prevention and Control Measures

Configuration	*m (BC)*	*λ (SIPI)*	*n (FIHQ)*	*δ (CCPQ)*
A	0	0	0.15	0.15
B	0.90	0.43	0.15	0.15
C	0.90	0.90	0.15	0.15

strongest countermeasure intensity will lead to rise slowly (Fig.7C).

We find that simulation result with values of measures m=0.9, λ=0.43, n=0.15, δ=0.15, is similar to reported data in the transformation trend of total case number (Fig.7B). Based on this group of parameter values, we compared the simulation data with reported data from two date times, calculated their differences and discussed the reasons which lead to these differences. Especially, the simulation data (blue lines) is an average value (along with 90% confidence interval) (Fig. 8, Fig.9, Fig.10, Fig.11).

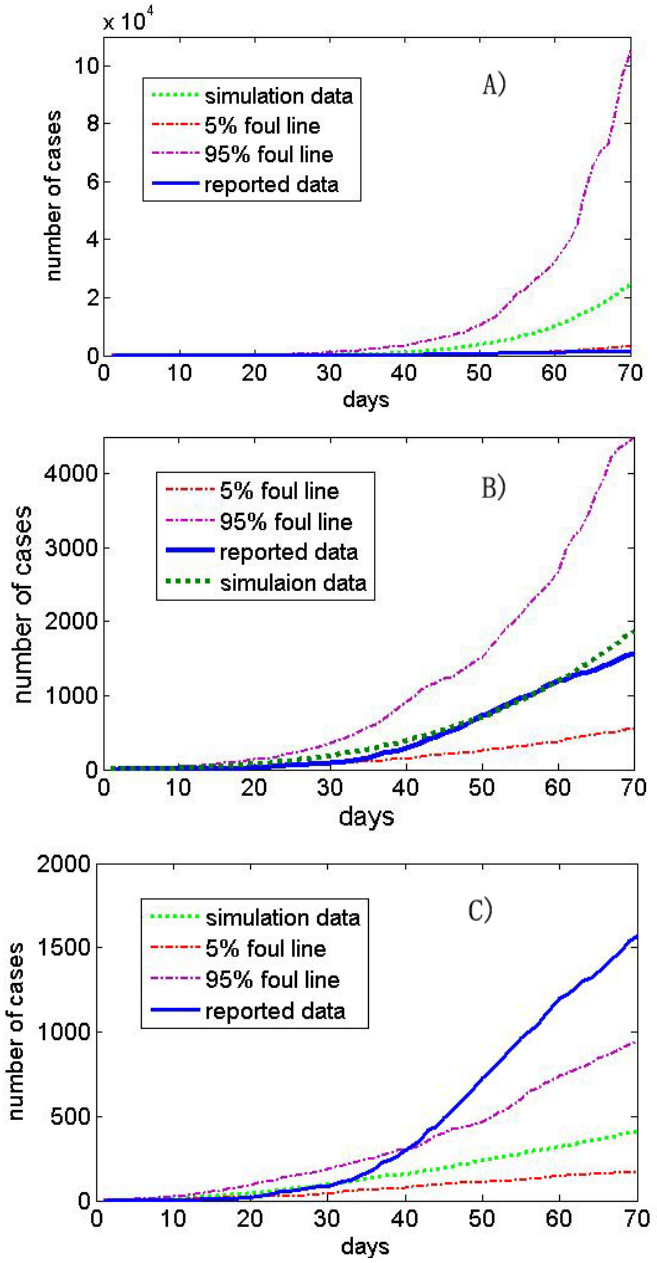

Figure 7. Simulation data with different prevention and control measures. The blue solid line represents the reported data, the green dashed expresses simulation average values. The other two lines denote 5% and 95% confidence lines of simulation result

Fig.8 and Fig.9 showed that, influenza A (H1N1) outbreaks occurred in Beijing, Guangdong, Shanghai, Hainan and Sichuan, both in the simulation result and reported data on 31 May. Besides, reported data shows that some other provinces also have cases, but there is no one in the simulation results. Fig.10 and Fig.11 show that provinces with influenza A(H1N1) cases mainly lie east part of China, and the number of provinces with cases both in simulation data and reported data reach 18. The result shows that transmission trend of influenza A(H1N1) in the simulation result in 31provinces is consistent with the reported data.

Some problems exist in the speed of influenza A(H1N1) transmission among 31 provinces. The speed of transmission of pandemic influenza A (H1N1) from simulations is slower than that from reported data speed. Two aspects can verify this difference. On one hand, the total number of provinces with cases is different between simulation result and reported data. On the other hand, the total number of cases in each province is different. These problems may be caused by values of M_{ij}, they don't ideally describe the transmission of influenza A(H1N1) among 31 provinces, because we only take railway travel into account to calculate values of M_{ij}, maybe other factors also affect people's travel among provinces (e.g. airline flight, bus).

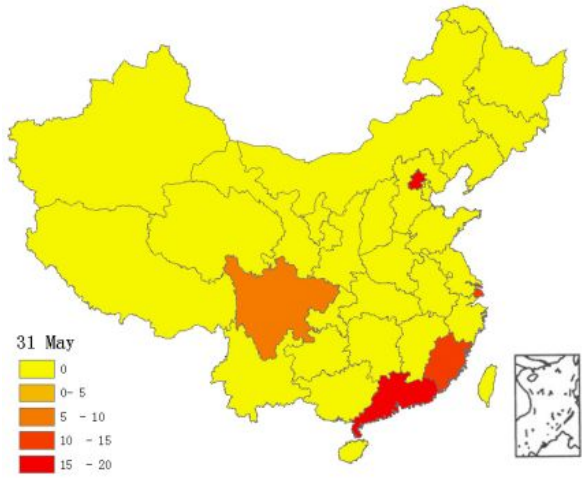

Figure 8. Spatial distribution of cases of simulation data on 31 May

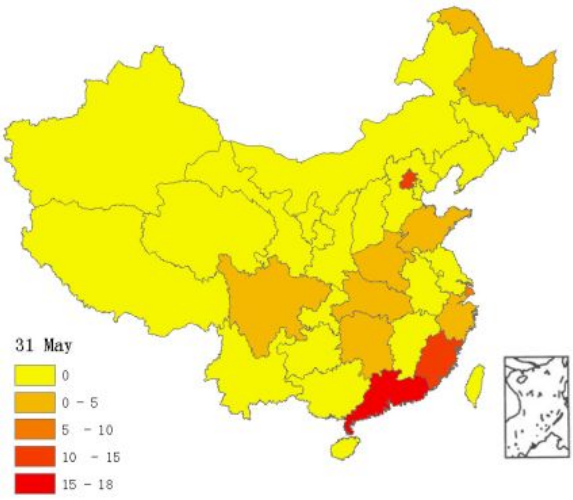

Figure 9. Spatial distribution of cases of reported data on 31 May

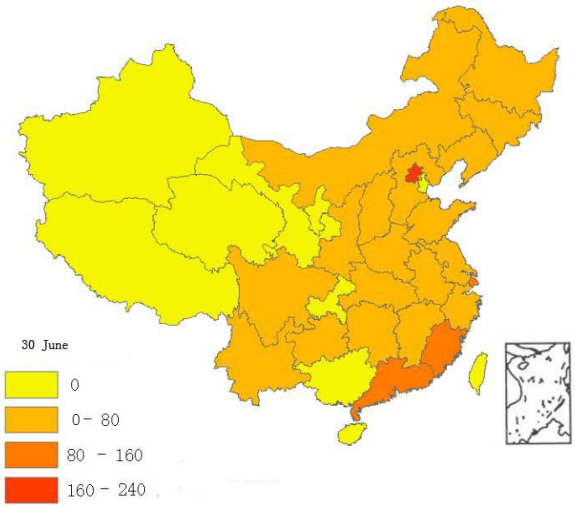

Figure 10. Spatial distribution of cases of simulation data on 30 June

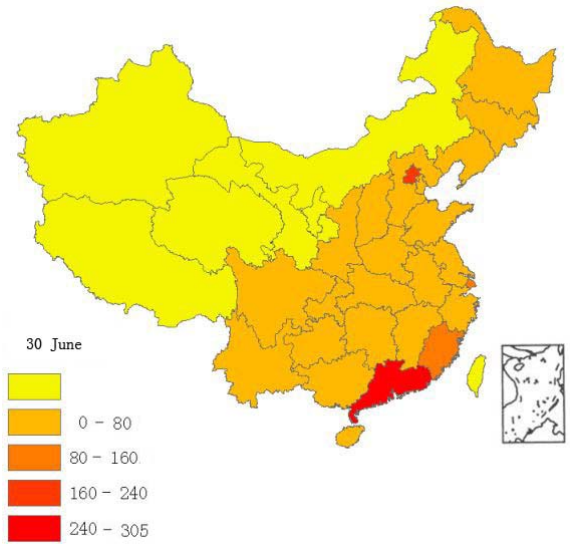

Figure 11. Spatial distribution of cases of reported data on 30 June

V. CONCLUSION

A spatially explicit epidemiological simulation system is proposed for modeling, simulation, and temporal-spatial analysis of pandemic influenza A (H1N1). Experiments have proved the validity of the simulation system, and the temporal-spatial analysis tools developed based on ArcGIS Engine can display the simulation result through maps visually and intuitively. The moving trend of all influenza A(H1N1) cases from the simulation results is similar to reported statistic data, the distribution of infected provinces is reasonable. However, some problems still exist and lead to some warp in simulating result. It is mainly attributed to the travel parameters between two provinces, as a result of geography factors not taken into account. In the future, we will pay more attention to improving the travel simulation method in the model.

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