# $SIS$-$SEIQR$ **Adaptive Network Model for Pandemic Influenza**

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*Abstract:* This paper aims to present an $SIS$-$SEIQR$ network model for pandemic influenza. We propose a network algorithm to generate an adaptive social network with dynamic hub nodes to capture the disease transmission in a human community. Effects of visiting probability on the spread of the disease are investigated. The results indicate that high visiting probability increases the transmission rate of the disease.

*Key–Words:* Adaptive network, Homogeneous network, Heterogenous network, $SIS$-$SEIQR$ epidemic model, Pandemic influenza.

## 1 Introduction

Many countries around the world have continuously announced about new human cases of an influenza A(H1N1) virus infection. Geographic spread of the H1N1 virus continues to evolve. The greatest number of cases is in Mexico, the United States, and Canada. There are also reports of cases in Europe, Asia, and in Latin America [3]. The influenza situation in Thailand was worrisome, after 470 people fell ill and two died in January, 2011 [4]. Currently, such outbreaks are taking place only in North America. The WHO is now keeping the pandemic alert level at phase 5. Whenever community-level transmission occurs in more than 1 WHO region, the pandemic alert level will increase to phase 6. In Thailand for the moment, there is no tool available for simulating and forecasting the spread of influenza.

Over the last three decades, a number of works on influenza modeling have been done [1, 2, 5, 8]. It has been recognized that mathematical model solely may cause the uncertainty in prediction of the spreading and public health responses. Recently, many researchers have proposed epidemic models involving a network of nodes in a discrete space domain [6, 7, 9, 10, 11, 12]. The existing epidemic network models just consider the disease spread only among the people in a contact range. In fact, the disease frequently spreads from the public places to population. Thus, the epidemic network model taking into account the features of public places in the community can capture the spread of the disease in biological network.

This paper proposes an algorithm for generating a complex network and presents a numerical study for the spreading of $SIS$-$SEIQR$ infections in complex networks. The rest of the paper is organized as follows. The network algorithm is presented in section 2, followed by the network characteristics in section 3. Section 4 deals with the $SIS$-$SEIQR$ network model, and discussion and conclusion are given in section 5.

## 2 Network Algorithm

To mimic the social activities, we propose a network algorithm to generate an adaptive social network for studying the $SIS$-$SEIQR$ disease transmission. There are two types of networks in this study consisting of a number of ordinary nodes (people) and may or may not have dynamic hub nodes (public places) with connecting links within a unit square region.

Let $N$ and $N_h$ be the total number of nodes and hub nodes in the network; $R_{min}$, $R_s$, $R_{homin}$, $R_h$ and $R_{hmin}$ be the minimum distance between any two ordinary nodes, the neighborhood contact radius of each ordinary node, the minimum distance between hub nodes and any ordinary nodes, the hub radius, and the minimum distance between any two hub nodes, respectively; $(x_r, y_r)$ be a random coordinate in $[0,1] \times [0,1]$; $P(x,y)$ be the positions of any node and $d_{ij}$ be the distance between any node $i$ and $j$.

**Step 1 Generating hub nodes**
    If ($N_h = 0$ ), go to Step 2.

  **Step 1.1** Set a position of the first hub node $(i = 1)$,

$$P_i(x,y) \leftarrow P(x_r, y_r)$$

attach the node to the network
set $i = i + 1$.

**Step 1.2** Select randomly a new position $P(x_r, y_r)$ .

**Step 1.3** $P_i(x, y) \leftarrow P(x_r, y_r)$.

**Step 1.4** If $(0 < d_{ij} < R_{hmin}$ for $j = 1, ..., i)$, goto Step 1.2.

**Step 1.5** Attach the hub node to the network and set $i = i + 1$.

**Step 1.6** Repeat Step 1.2 to Step 1.5 until all hub nodes are generated.

**Step 2  Generating ordinary nodes**

**Step 2.1** Set a position of the first ordinary node $(i = N_h + 1)$,
$P_i(x, y) \leftarrow P(x_r, y_r)$.

**Step 2.2** If $(N_h = 0)$,
attach the node to the network
else
if $(0 < d_{ij} < R_{homin}$ for $j = 1, ..., i)$,
goto Step 2.1
else attach the node to the network
set $i = i + 1$.

**Step 2.3** Select randomly a new position $P(x_r, y_r)$.

**Step 2.4** $P_i(x, y) \leftarrow P(x_r, y_r)$.

**Step 2.5** For $j = 1, i$
If $(j > N_h)$
If $(0 < d_{ij} < R_{min})$, goto Step 2.3.
else
If $(0 < d_{ij} < R_{homin})$, goto Step 2.3.

**Step 2.6** Attach the ordinary node to the network and set $i = i + 1$.

**Step 2.7** Repeat Step 2.3 to Step 2.6 until all ordinary nodes are generated.

**Step 3  Determining neighborhood $\mathcal{N}_i$**
For $i = 1, N$
For $j = 1, N$
If $(i \leq N_h$ and $i \neq j)$
If $(j \leq N_h$ and $d_{ij} < R_h)$
add node $j$ to neighborhood $\mathcal{N}_i$ of the hub node $i$
else
If $(j > N_h$ and $d_{ij} < R_s)$
add node $j$ to neighborhood $\mathcal{N}_i$ of the ordinary node $i$.

# 3   The Network Characteristics

Using our network algorithm to generate a network in a unit square region and setting $N_h = 0$ (no hub node)

and $R_s \leq \sqrt{2}$, we have a local network. If $R_s \approx \sqrt{2}$, it is a homogenous network. Otherwise, it is a heterogenous network. For the homogenous network, every node has $N - 1$ edges and each node connects to one of the other $N - 1$ nodes. For $N_h > 0$, $R_s \ll \sqrt{2}$ and the degree of hub node varies in time, we have a network with adaptive hub nodes and we call it an adaptive network.

The topologies and properties of the network depend on the network parameters including the number of nodes and contact radius. Figure 1 presents topologies of a part of the heterogenous network with 4 different contact radii.



(a)                              (b)
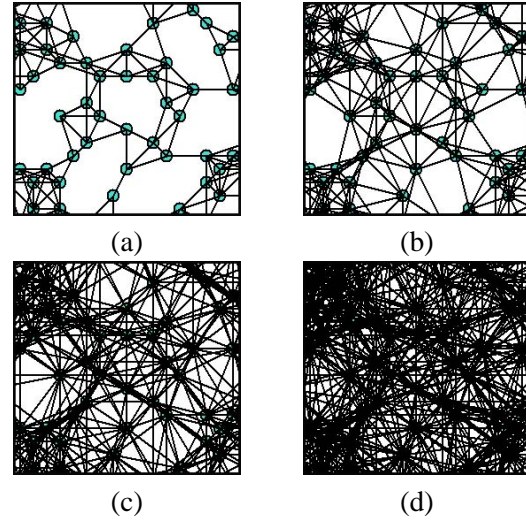
(c)                              (d)

Figure 1: Topologies of a part of the heterogeneous network with 4 different contact radii (a) $R_s = 0.05$, (b) $R_s = 0.07$, (c) $R_s = 0.09$ and (d) $R_s = 0.11$

An increase of contact radius increases the number of edges $(|E|)$ , the average degree $(\bar{k})$, the clustering coefficient $(C)$ but decreases the average vertex-vertex distance $(\bar{d})$ as shown in Figure 2 and Table 1.

Table 1: Properties of the local network for different contact radii $R_s$

| $R_s$ | 0.05 | 0.07 | 0.09 | 0.11 | $\sqrt{2}$ |
|---|---|---|---|---|---|
| $|E|$ | 3625 | 6879 | 11279 | 17460 | 499500 |
| $\bar{k}$ | 7 | 14 | 23 | 35 | 999 |
| $\bar{d}$ | 9.687 | 6.688 | 5.131 | 4.162 | 1 |
| $C$ | 0.497 | 0.559 | 0.584 | 0.604 | 1 |

The homogeneous network with $R_s \approx \sqrt{2}$ is a small-world network. Its clustering coefficient $(C)$ is highest, $C = 1$. To investigate the effect of contact radius on the degree distribution of the local network, we use four values of contact radii. Figure 3 plots
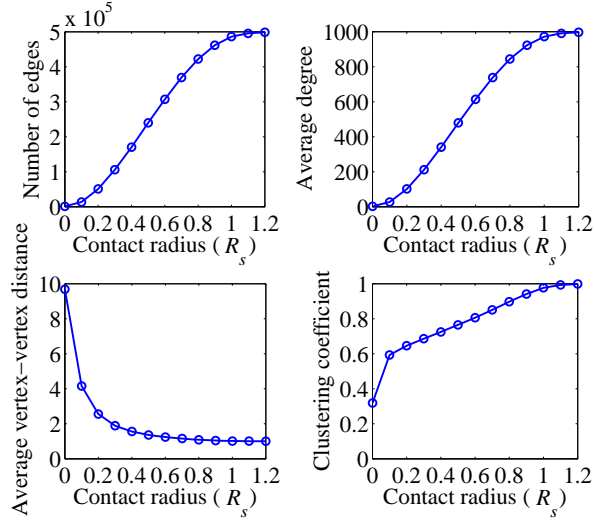
Figure 2: Dependence of the network properties with contact radius for the local network.

an average fraction of nodes of degree $k$, denoted by $P(k)$, versus degree $k$. It shows the effect of contact radius on the degree distribution. The result indicates that contact radius has significant effect on the degree distribution of the network. High contact radius gives high degree of nodes but reduces peak value of $P(k)$.
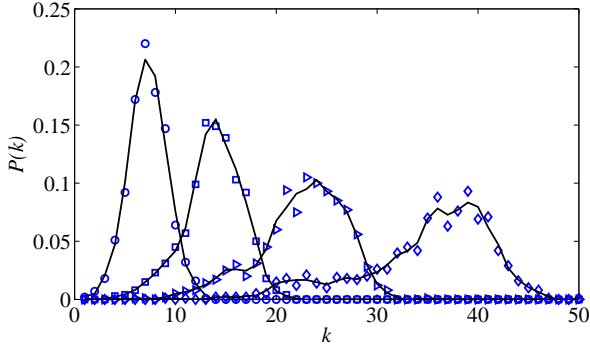


Figure 3: The degree distribution of the heterogeneous network with four contact radii $R_s$ of 0.05, 0.07, 0.09 and 0.11 (from the left to the right curves).

To study how the disease spreads in the population network, we use the adaptive network with 1000 nodes comprising a number of ordinary nodes $N_p$ and a few number of hub nodes $N_h$. In real situation, people in a different group may visit public places in a different time, we then apply the visiting probability $p$ of the ordinary nodes to determine the change of the node-hub links of network over the time. Figure 4 presents topologies of the adaptive network with the hub radius $R_h$ of 0.25, the contact radius $R_s$ of 0.07

and the visiting probability $p$ of 0.5 at four different times including 0, 5, 10 and 15 days. The use of the visiting probability results in the change of the connection over time time between hub nodes and surrounding nodes.

## 4  The $SIS$-$SEIQR$ Network Model

We here consider the pandemic influenza A (H1N1) on the adaptive network with dynamic 9 hub nodes, contact radius $R_s$ of 0.07 and hub radius $R_h$ of 0.25 based on the flow diagram in Figure 5 corresponding to the following $SIS$-$SEIQR$ epidemic model.
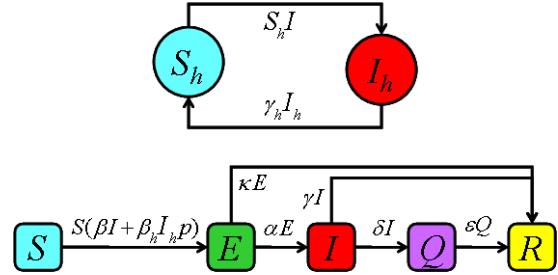


Figure 5: A flow diagram of transmission dynamic of $SIS - SEIQR$.

Model for hub nodes:

$$\begin{aligned}
\frac{dS_h}{dt} &= -S_h I + \gamma_h I_h, \\
\frac{dI_h}{dt} &= S_h I - \gamma_h I_h,
\end{aligned} \tag{1}$$

Model for ordinary nodes:

$$\begin{aligned}
\frac{dS}{dt} &= -S(\beta I + \beta_h I_h p), \\
\frac{dE}{dt} &= S(\beta I + \beta_h I_h p) - (\alpha + \kappa)E, \\
\frac{dI}{dt} &= \alpha E - (\gamma + \delta)I, \\
\frac{dQ}{dt} &= \delta I - \varepsilon Q, \\
\frac{dR}{dt} &= \kappa E + \gamma I + \varepsilon Q,
\end{aligned} \tag{2}$$

where the parameters $\beta$, $\beta_h$, $\alpha$, $\gamma$, $\delta$ and $\varepsilon$ are nonnegative constants described in Table 2. The letters $S$, $E$, $I$, $Q$ and $R$ represent the numbers of susceptible, exposed, infected and recovered individuals of ordinary nodes whereas $S_h$ and $I_h$ represent numbers of susceptible and infected individuals of hub nodes.
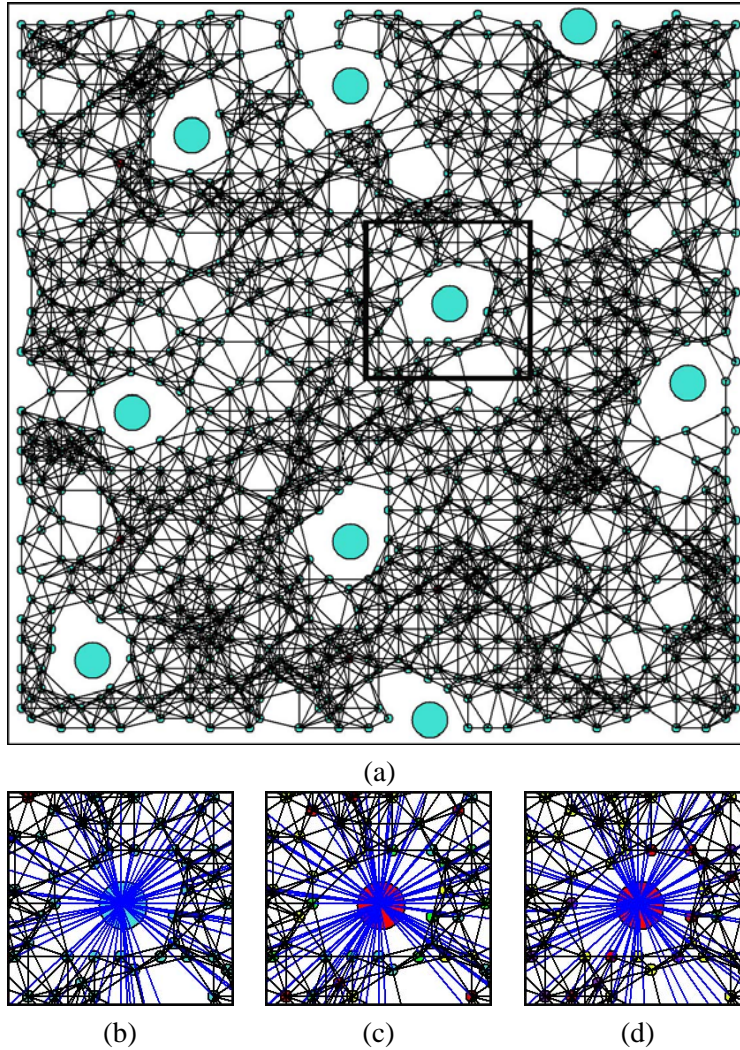
(a)



(b)    (c)    (d)

Figure 4: Topology of a part of the adaptive network ($N_h = 9$) corresponding to the neighborhood contact radius $R_s$ of 0.07, the hub radius $R_h$ of 0.25 and the visiting probability $p$ of 0.5 at four different times: (a) $t = 0$ day, (b) $t = 5$ days, (c) $t = 10$ days, (d) $t = 15$ days.

Table 2: Model parameters and descriptions

| Parameter | Descriptions |
|---|---|
| $\beta$ | Transmission rate of ordinary nodes |
| $\beta_h$ | Transmission rate of hub nodes |
| $p$ | Visiting probability |
| $\alpha$ | Transfer rate at which $E$ becomes $I$ |
| $\gamma$ | Transfer rate at which $I$ becomes $R$ |
| $\delta$ | Transfer rate at which $I$ becomes $Q$ |
| $\varepsilon$ | Transfer rate at which $Q$ becomes $R$ |

To examine of the effect of the visiting probability on the disease spread, four values of $p$ are investigated. Figure 6 shows the effect of the visiting probability on the disease spread on the adaptive network with $\beta$ of 0.05, $\beta_h$ of 0.002 and $R_h$ of 0.25. The results indicate that the network with the higher visiting probability gives larger number of exposed, infected and quarantine individuals. Additionally, the higher of the visiting probability leads to the higher transmission rate and the shorter period of transmission. An increase of $p$ from 0.2 to 0.8 reduces the period of transmission from 32 days to 18 days.

## 5    Discussion and Conclusion

We propose an algorithm to generate adaptive social network for studying the $SIS\text{-}SEIQR$ pandemic influenza. The network characteristics and properties are presented. We simulate the pandemic influenza on the $SIS\text{-}SEIQR$ adaptive network with 9 dynamic hub nodes. The results show that the visiting proba-

(a) $p = 0.20$

(b) $p = 0.40$

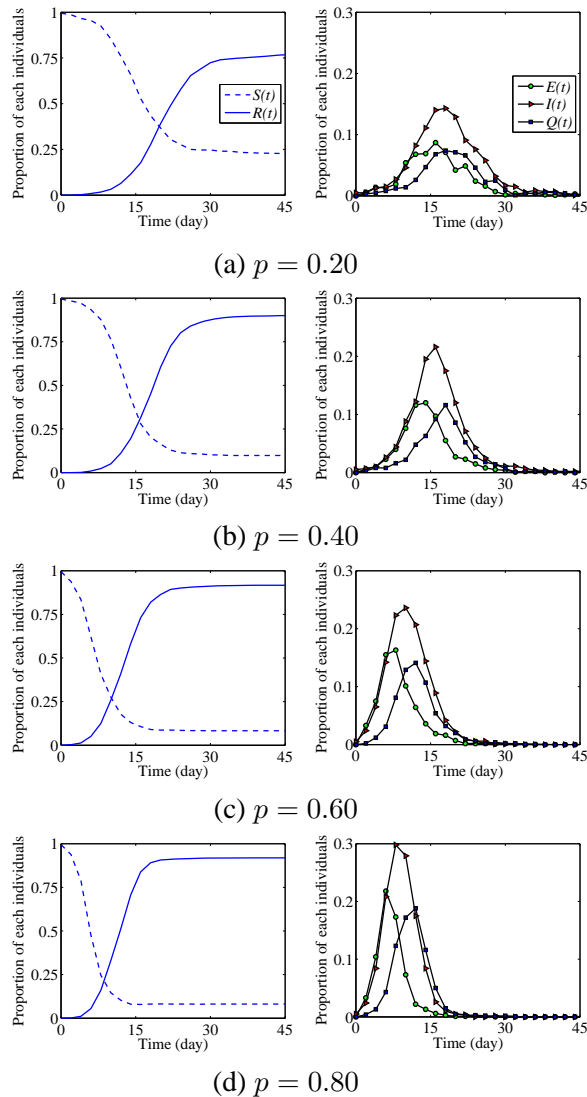(c) $p = 0.60$

(d) $p = 0.80$

Figure 6: Effect of visiting probability $p$ on the disease spread in the adaptive network with $R_s = 0.07$ and $R_h = 0.25$.

bility has significant effects on disease transmission. This implies that to control the spread of the disease when the pandemic influenza occurs, the public places such as theater and school would be closed or epidemiologist would suggest the risk people avoid visiting the public places.

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