



Each individual in the community can be regarded as a node in the network, and each connection between two individuals is represented by an edge (line) connecting the two nodes. The number of edges emanating from a node i , the number of connections it has, is called the degree of the node i . Therefore, we can measure the total number of connections in the network by the sum of the degrees of all nodes N ($N = N_1 + N_2 + \dots + N_n$), where N_k ($k = 1, 2, \dots, n$) is the number of nodes with degree k . If the total number of nodes is N , then the probability that a randomly chosen individual has k connections is $P(k) = N_k/N$, which is called the degree distribution of the network. Empirical studies have shown that many real networks have scale-free (SF) degree distribution $P(k) \approx k^{-\gamma}$.

and denoted by D and Wachsmuth [20], we have only
 common elements E_k, A_k and I_k are included in the calculation
 of R_0 . In the infection-free state P^0 , the average of
 the average of new infection F and the average of an infection of
 individual V of the common variable V are given by

$$F = \begin{pmatrix} F_{11}^x & F_{12}^x & F_{13}^x \\ F_{21}^x & F_{22}^x & F_{23}^x \\ F_{31}^x & F_{32}^x & F_{33}^x \end{pmatrix},$$

where $F_{11}^x, F_{21}^x, F_{22}^x, F_{23}^x, F_{31}^x, F_{32}^x, F_{33}^x$ are elements of
 matrix,

$$F_{12}^x = \frac{1}{\langle \cdot \rangle} \begin{pmatrix} \beta_1(1) & \beta_2(2) & \dots & \beta_n(n) \\ \beta_1(1) & \beta_2(2) & \dots & \beta_n(n) \\ \vdots & \vdots & \ddots & \vdots \\ \beta_1(1) & \beta_2(2) & \dots & \beta_n(n) \\ \beta_1(1) & \beta_2(2) & \dots & \beta_n(n) \\ \vdots & \vdots & \ddots & \vdots \\ \beta_1(1) & \beta_2(2) & \dots & \beta_n(n) \end{pmatrix}$$

$$F_{13}^x = \frac{2}{\langle \cdot \rangle} \begin{pmatrix} \beta_1(1) & \beta_2(2) & \dots & \beta_n(n) \\ \beta_1(1) & \beta_2(2) & \dots & \beta_n(n) \\ \vdots & \vdots & \ddots & \vdots \\ \beta_1(1) & \beta_2(2) & \dots & \beta_n(n) \\ \beta_1(1) & \beta_2(2) & \dots & \beta_n(n) \\ \vdots & \vdots & \ddots & \vdots \\ \beta_1(1) & \beta_2(2) & \dots & \beta_n(n) \end{pmatrix}$$

=S

and

$$= \begin{pmatrix} -X & 0 & \dots & 0 & 0 & \dots & 0 & 0 & \dots & 0 \\ 0 & -X & \dots & 0 & 0 & \dots & 0 & 0 & \dots & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots & \ddots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \dots & -X & 0 & \dots & 0 & 0 & \dots & 0 \\ l^x & 0 & \dots & 0 & -u_1 & \dots & 0 & 0 & \dots & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots & \ddots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \dots & l^x & 0 & \dots & -u_1 & 0 & \dots & 0 \\ (1-l)x & 0 & \dots & 0 & 0 & \dots & 0 & -u_2 & \dots & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots & \ddots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \dots & (1-l)x & 0 & \dots & 0 & 0 & \dots & -u_2 \end{pmatrix}.$$

Using the concept of new-generation matrix [20], the
 reproduction number $R_0 = \rho(FV^{-1})$, the spectral radius of the matrix FV^{-1} .

To determine the spectral radius of FV^{-1} , we find
 the eigenvalues of V by the following matrix:

We now complete the inductive step of $L(t)$ along the solution of (1)-(5). It is seen that

$$\begin{aligned}
 \dot{L}(t) &= - \frac{1}{2} (C_1^2 + A + \frac{1}{2} L) + 2 \frac{1}{2} (C_1^2 + A + \frac{1}{2} L - VE) \\
 &= (C_1^2 - A) - (C_1^2 - A) \\
 &= 0
 \end{aligned}$$

If $S_k(0) = S_{k0}$, $I_k(0) = I_{k0}$, $E_k(0) = E_{k0}$, $A_k(0) = A_{k0}$, then the final size relation become

$$\ln \frac{S_0}{S_\infty} = \frac{1}{U_1} \left((S_0 - S_\infty) + \frac{1}{U_1} \left(E_0 + \frac{1}{U_1} A_0 \right) + \frac{2}{U_2} I_0 \right)$$

The final size with vaccination

If vaccination follows a binomial distribution, then the final size relation become

$$\ln \frac{S_0}{S_\infty} = \frac{(1-v_1)}{U_1} \left(\bar{A} + \frac{(1-v_2)}{U_1} \bar{I} \right) + \frac{(1-v_2)}{U_1} \bar{E}$$

Conclusions

Network model can capture the main feature of the spread of the H1N1. In this paper, using a network epidemic model for influenza A (H1N1) in China, we calculated the basic reproduction number R_0 and discussed the local and global dynamical behavior of the disease-free equilibrium. The effect of a vaccination scheme was studied and compared. A final size relation was derived for the network epidemic model. The derivation depends on an effective formula for the basic reproduction number of network disease transmission model. The transmission coefficient was estimated through a fitting of the model observed data of the cumulative number of hospitalization. We also gave the estimated value for the basic reproduction number for influenza A (H1N1) in China as $R_0 = 1.6809$.

Parameter was estimated during the period when the vaccination was not applied. For the parameter, we found that $\gamma = 0.85$, which means that 15% of the exposed become infected during the early course of the epidemic. Although vaccination commenced in China in November 2009, we were not able to compare the real data with the model projection due to lack of data.

List of abbreviations used

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Competing interests

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