Vaccination Deployment in Protection against Influenza A (H1N1) Infection

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Abstract

Vaccination is an effective way to control epidemic spreading by adjusting the composite structure of susceptible, infected and vaccinated populations. Three vaccine deployment factors can affect the H1N1 infection dynamics, they are: (1) total amount of vaccine, (2) vaccine releasing time, and (3) vaccine distribution method. Yet the impact of these deployment factors still remain to be systematically understood. In our study we develop an SIV (susceptible, infected and vaccinated) model that incorporates 6 age-grouped populations, and a survey-based contact matrix. We parameterize this model with current H1N1 influenza parameters. The developed SIV infection equations for each group enable us to simulate both within- and between-group epidemic spreading dynamics. Under different vaccination deployment settings, we observe that enough vaccine availability can lower the final percentage of infected population. Releasing vaccine before infection stage transition can improve the dynamical infection process. Vaccination by infection force can improve the efficacy of vaccine deployment.

1 Introduction

The outbreak of swine-origin influenza A (H1N1) in the main region of the world led the World Health Organization (WHO) to declare an influenza pandemic on June 11, 2009 [3]. Influenza virus can be transmitted among population communities, geographical regions and countries through human contact activities. The fast spreading of virus infection can cause intense pandemic outbreaks all over the world. Thus it is critical important to stop or restrain infection propagation. Presently one of the effective epidemics intervention strategies is population vaccination. Here, the vaccination means the health people can be immunized by injecting vaccine dose and hence will not be infected by epidemics virus. In the view of the number of infections, the core problem of vaccination is how immunize a fractal of host population in order to prevent a virus infection from becoming a epidemic outbreak in the whole population.

In the past, several virus infection model based on the assumption of population's homogeneous infection has been proposed, such as SIS/SIR models [4] [7] [8] [5]. These models are designed by assuming that the probability of virus infection is identical for each member of host population and the infection rate can be represented by reproductive number R_0, defined as the number of secondary infections caused by a single infectious case in a completely susceptible population [4]. However, most of these model cannot adapted well to discuss the roles of human demographical features and contact relationship play in epidemic spreading dynamics.

In real vaccination practice, the deployment of vaccines for a pandemic virus might be limited by several operational factors, they are (1)vaccine availability, such as, how many doses of vaccine are required and when vaccines are available to start to be released, (2) vaccine distribution, such as what is the distribution priority for individuals with different demographical features or contact frequency.

In addition, prior to and during the vaccine deployment process, the composite structure of infected population are dynamically evolved as a result of virus spreading. These vaccine deployment factors and infection dynamics will change the landscape of epidemic spreading and should be considered in order to schedule an effective vaccine deployment plan.

To address this question mentioned above, we developed an age-structured infection model to describe the H1N1 virus spreading during 2009. We use this model to observe the infection dynamics under different vaccination settings, such as the amount of available vaccine, vaccine releasing time and the vaccine distribution methods. Based on the results of our simulations, we analyze the impact of each vaccination deployment factors on infection dynamics, which can provide an solid foundation for design an optimal vaccination deployment plan in real practice.

The remainder of this paper is organized as follows: Section 2 provide a survey of existing work in epidemic vaccination. Section 3 states the problem to be dealt in this paper. Section 4 presents detailed epidemic infection model. Section 5 is about the vaccination deployment strategies. Section 6 provides simulation experiment and results analysis. Section 7 conclude the whole paper and highlight the major

contribution of this paper.

2 Related Work

Vaccination is a critical way to control epidemic spreadings by adjusting the composite structure of susceptible, infected and vaccinated populations [16]. However, in real practice, the effective deployment of vaccines for a pandemic virus might be limited by several factors, they are (1) how many doses of vaccine are required; (2) when vaccines are available to start to be released; (3) what is the distribution priority for individuals with different demographical features. In addition, prior to and during the vaccine deployment process, the composite structure of infected population are dynamically evolved as a result of virus spreading. These vaccine deployment factors and infection dynamics will change the landscape of epidemic spreading and should be considered in order to schedule an effective vaccine deployment plan.

The same as the previous influenza pandemic experience, current H1N1 infection is characterized by age distributions that a higher attack rates and increased proportionate mortality are associated with younger population[13] [9]. This heterogeneity of infection vulnerability by age will have important implications for optimal vaccination distribution strategies.

To control the H1N1 infection spreadings in US, the Centers for Disease Control and Prevention (CDC) projected a vaccination plan that a total of 45 million doses would be available by mid-October, followed by 20 million doses every week thereafter [1]. Under this plan H1N1 vaccine was distributed mainly to health care personnel and young children [2] with the concern that it is more efficient to protect those who are more vulnerable to be infected.

Recently many discussion have been proposed to debate whether a higher priority for vaccination distribution method based on individuals' infection vulnerability is really effective[18][19]. It has been suggested that an vaccine distribution strategy based on individuals' transmissibility would have a greater impact on reducing overall infection than the current practice of focusing vaccination efforts on infection vulnerable populations [11] [14]. In particular, the potential benefit of preferentially vaccinating school-aged children has been discussed, since this age group is disproportionately responsible for influenza transmission [17][10][6].

However all of these discussions mentioned above ignore a critical aspect of vaccination deployment in real practice – the availability of vaccine, such as the total amount of vaccine doses and the available time for first batch of vaccine releasing. Given limitations of our knowledge of a newly emerged virus and constraints of production and logistical ability, the time of vaccine releasing is always delayed than infection dynamics and the amount of available vaccine are always a fractal of current needs. Based on these practical limitations, how to optimally distribute vaccine requires a deep understanding of relative impacts of vaccine deployment factors on disease infection dynamics.

3 Problem Statement

The compartmental model of virus infection is still been used to simulate epidemic dynamics. The host population in model are divided into different compartments depending on the stage of virus infection, for instance, susceptible (denoted by **S**), infected (**I**) and other kinds of compartment. The infection differential equations will represent the dynamics of virus spreading process.

Based on the previous infection model, it would be difficult to present heterogeneities of host population, especially (1) heterogeneity of populations' demographical features, such as, age, infection vulnerability and so on, (2) heterogeneity of contact relationship, such as, the contact frequency within and cross different demographical communities. In order to observe the influence of different factors in infection dynamics, in our study, we will first introduce a modified compartmental virus infection model together with the heterogeneities of population vulnerability and contact transmissibility.

Vaccination is an epidemic intervention strategy by immunizing amount of susceptible individuals, which can change the composite structure of each compartmental populations, to prevent the infection spreading. An effective deployment of vaccination plan includes two issues, (1) vaccine availability, which is related with the total amount of available vaccine and vaccine releasing time, (2) vaccine distribution, which is about the vaccine releasing priority. In order to estimate the relative impact of each deployment factors on infection dynamics, the following research question should be answered.

- **Stable state of epidemic dynamics**. Which deployment factors might influence final scenario of epidemic spreading, such as, the percentage of infections can be hold on a lower level or the infection cased will be self eliminated.
- **Dynamical process of epidemic dynamics**. In this section we want to observe the relative influence of each factors on dynamical process of infection spreading. The elements to evaluate the dynamical process include lasting time of an infection stage, tipping points of stage transition, rising time of infection curve and the speed of convergence to stable state.

In order to answer the above questions, we will, first of all, provide a detailed description of a modified compartmental infection model (SIV model) to simulate the virus

spreading dynamics which can provide a simulation foundation for our discussion in vaccination deployment.

4 SIV Infection Model

In this section, we will present the detailed formulations of SIV virus infection model, introducing the age structure of host population and the contact relationship among them.

4.1 Model Formulation

In our model, each individual's health status will be labeled as S (susceptible), I (infected) or V (vaccinated) during virus infection process, and the composite structure of these three compartmental population is a representation of infection dynamics. We represent the heterogeneity of virus infection by dividing population into different age groups, which have different infection parameters, and depict the heterogeneity of virus spreading based on population's contact structure both within and cross each age groups. Finally, We use a set of difference equations together with virus infection and spreading parameters of current H1N1 virus to model the dynamics of H1N1 epidemic spreading process. More details will be presented in the following subsections.

4.2 Population Age Structure

During virus infection process, the response to an infection exposure are quite different for people with different demographical features. For example, the probability of a successful infection might be totally different in terms of individuals' virus resistibility. These difference can be generalized as the heterogeneity of virus infection which is viewed as the result of diversities in individuals' demographical features, such as, age, gender, ethnicity and so on. With the aim of analyzing the impact of the heterogeneity of population's infection vulnerability, we introduce population's age structures that each individual will be divided into groups in terms of their age and each age groups will have a set of parameters of virus infection rate and recovery rate to represent the diversities in individuals' vulnerability.

In this model, the whole population are divided into 6 age groups, which contain A_1(0-4), A_2(5-14), A_3(15-24), A_4(25-44), A_5(45-64), A_6(64+). The number of population in each age groups are parameterized by the demographical statistics of United Kingdom in 2007 by Office for National Statistics of UK [20].

Based on the above mentioned population age structure, the epidemiological parameters of each age group are listed in Table 2. Infection rate β is the probability of an successful infection when an susceptible individual is exposed in an infectious contact. We propose that the heterogeneity of individuals' infection rate is the result of the natural immunization ability of each age groups. Based on Miller's cross-sectional serological survey on H1N1 immunization in different age groups [12], we can parameterize the diversity of individuals' infection vulnerability.

Table 1: Age Structure of Population in UK (2007)

Age Groups	Population (Million)	Percentage (%)
A_1 (0-4)	3.446	5.7
A_2 (5-14)	7.380	12.2
A_3 (15-24)	7.841	13.0
A_4 (25-44)	17.156	28.5
A_5 (45-64)	14.738	24.5
A_6 (65+)	9.699	16.1
All	60.26	100

Recovery rate σ describes the percentage of infected individuals that will be recovered in a computing time unit, which is the reverse of the infection periods. On the basis of data regarding viral shedding from studies of seasonal influenza, most patients with flu infection might shed virus from 1 day before the onset of symptoms through 5 to 7 days after the onset of symptoms or until symptoms resolve; in young children or severely ill patients, the infectious period might be longer. Because of the limited knowledge of infection period, in our model the recovery rate for each age groups are homogeneously model as 0.143, which means the infection period is 7 days.

4.3 Contact Matrix based on Age Groups

In our study, we assume that virus infection spreading is the result of contact activities between the susceptible individuals and the infectious ones. To study the virus spreading dynamics, first, we should provide a foundation of individual's contact relationship. In this paper, we use a contact matrix $C = \{c_{i,j}|i,j \in (1,2,...,N)\}$, N is the number of age groups, here $N = 6$, to characterize contact frequency within and between each age groups. $c_{i,j}$ means the average times of contact for an individual in age group i with individuals in age group j. We parameterize the matrix elements $c_{i,j}$ by using the results of a study in European countries which keep a record of participants' daily report about their contact activities [15].

Based on the basic contact frequency matrix in Mossong's results, which provide a contact matrix of all reported contacts consisting of the average number of contact persons recorded per day per participant in his survey, we can get an estimation of the number of total contacts, that is $M_{i,j}$, between age group A_i and group A_j.

Thus, the total number of contacts from group A_i to group A_j should be equal to that of contacts from group

Table 2: H1N1 Epidemiological Parameters based on Age Groups

	A_1(0-4)	A_2(5-14)	A_3(15-24)	A_4(25-44)	A_5(45-64)	A_6(64+)
Infection Rate β_i	0.213	0.420	0.206	0.206	0.15	0.313
Recovery Rate σ_i	0.143	0.143	0.143	0.143	0.143	0.143

A_j to group A_i. So we have

$$c_{ij} \cdot P_i = M_{ij} = c_{ji} \cdot P_j \tag{1}$$

P_i, P_j are the total number of population in age group A_i and A_j. So the element c_{ij} of contact matrix C denotes the average contacts between an individual in age group i with individuals in age group j.

The value of contact matrix $C = \{c_{i,j}|i,j \in (1,2,...,N)\}$ is presented in table 3.

Table 3: Contact Matrix of Age Groups

	A_1	A_2	A_3	A_4	A_5	A_6
A_1	1.49	1.165	0.658	2.396	0.938	0.303
A_2	0.613	4.130	0.734	2.276	0.805	0.403
A_3	0.300	0.634	2.794	1.218	0.927	0.488
A_4	0.528	0.953	0.590	1.634	0.842	0.408
A_5	0.218	0.356	0.474	0.888	1.049	0.589
A_6	0.109	0.276	0.387	0.669	0.914	1.484

4.4 SIV Model

In this section, we propose a modified population based virus infection model, SIV model, to simulate the dynamics of virus infection process. In this model, we introduce three status to label individuals' state transition, which include susceptible state **(S)**, infected state **(I)** and vaccinated state **(V)**. Individuals' status can transit from one to other based on the result of whether they are infected, recovered or vaccinated by exterior interventions in current computing unit. As mentioned in the previous sections, the population in our model are divided into 6 age groups, which is aimed at representing the heterogeneity of virus infection in terms of their age distribution. Based on this age structure, we assume that individuals within an age group are homogenous, which means they have the same parameters of infection rate and recovery rate and the identical probability to contact with individuals of outside age groups. We also propose that the heterogeneity of virus infection and virus spreading are presented by the value of virus infection parameter sets and the matrix of cross group contact frequency.

Within age group A_i, variable $S_i(t)$, $I_i(t)$ and $V_i(t)$ can represent the relative percentage of the susceptible, infected and vaccinated population. Thus the vector $\{(S_i, I_i, V_i)|i \in (1,...,6)\}$, can describe infection dynamics within each age groups. The virus infection dynamics among individuals in each age group can be described by the following difference equation:

For age group A_i, $i \in (1,...,6)$, k is the current computing moment,

$$\begin{aligned} S_i(k+1) =& S_i(k) + \tau_i \cdot I_i(k) + (-\lambda_i(k)) \cdot \beta_i \\ & \cdot [S_i(k) - \Delta v_i(k)] + (-\Delta v_i(k)) \end{aligned} \tag{2}$$

$$\begin{aligned} I_i(k+1) =& I_i(k) + (-\tau_i) \cdot I_i(k) + \lambda_i(k) \cdot \beta_i \\ & \cdot [S_i(k) - \Delta v_i(k)] \end{aligned} \tag{3}$$

$$V_i(k+1) = V_i(k) + (-\Delta v_i(k)) \tag{4}$$

In the moment of k, for the virus infection difference equations of age group A_i, $\tau_i \cdot I_i(k)$ represents the recovered case of infections. $\lambda_i \cdot \beta_i \cdot [S_i(k) - \Delta v_i(k)]$ is the newly increased infections which is the result of infectious contact activity within and cross each age groups. $\Delta v_i(k)$ is the number of vaccine that will be released with age group A_i in current moment. Thus based on the infection dynamics of current moment k, $\{S_i(k), I_i(k), V_i(k)\}$, and virus infection parameter set $\{\tau_i, \beta_i, \Delta v_i(k), \lambda_i(k)\}$, we can get the infection dynamics in next moment $\{S_i(k+1), I_i(k+1), V_i(k+1)\}$.

For the parameter set $\{\tau_i, \beta_i, \Delta v_i(k), \lambda_i(k)\}$,

- τ_i is the recovery rate for infected individuals in age group A_i.
- β_i represents the infection rate for susceptible individuals in age group A_i.
- $\Delta v_i(k)$ is the amount of vaccine that will be released within the population of age group A_i in current moment k.
- $\lambda_i(k)$ represents the risk of infectious contact both from its own located group A_i and from other age groups.

In our model, we assume that virus infection is a result of mixing contact between susceptible individuals and infectious ones. The infectious contact risk for each susceptible individuals is determined by two factors, (1) the frequency of individual contacts with other individuals within or cross age groups, (2) the probability of the contacted individual is a infected one. We use the infectious contact rate λ_i to

represent the average infection risk of susceptible individuals in age group A_i as a result of the contact relationships with infectious individuals both within its own age group and cross other groups.

By the definition of contact matrix C, $C = \{c_{i,j}|i,j \in (1,2,...,6)\}$, for each individuals in group A_i, the average times of contact with individuals in group A_j is $c_{i,j}$. Thus we can get the infectious contact rate λ_i by the following equation, in which $N \in (1,2,...,6)$.

$$(1-\lambda_i)^{\sum_{j=1}^{N} c_{i,j}} = \prod_{j=1}^{N} (1-\frac{I_j}{P_j})^{c_{ij}} \tag{5}$$

Where the left side of the equation is the probability of not being infected through $\sum_{j=1}^{6} c_{i,j}$ times of within or cross group contact with the average infectious contact rate λ_i. The right side of the equation is the probability of not being infected through the combination of $c_{i,j}$ times of contact with individuals in age group A_j, in which the infectious contact rate is $\frac{I_j}{P_j}$ for each age group A_j. We can get the average infectious contact rate $\lambda_i(k)$ as, where $N \in (1,2,...,6)$ is the number of age groups.

$$\lambda_i(k) = 1 - \left[\prod_{j=1}^{N} (1-\frac{I_j(k)}{P_j(k)})^{c_{ij}}\right]^{\left(\sum_{j=1}^{N} c_{i,j}\right)^{-1}} \tag{6}$$

Based on our SIV virus infection model, we can simulate the epidemic spreading dynamics of current H1N1 virus, in which two kinds of virus infection heterogeneities are been adopted in the model, one is the heterogeneity of population's vulnerability, the other is the heterogeneity of contact relationship within or between age groups. Thus together with this SIV model, we can evaluate the efficacy of vaccine deployment strategies which are designed with different releasing priorities, such as, vaccination based on host vulnerability and vaccination by individuals' transmissibility. In the following section, we will discuss several factors of vaccination deployment that might influence the epidemics spreading dynamics.

5 Vaccination Deployment Strategies

Epidemic interventions can be used to control epidemics spreading dynamics, and suppress or prevent the intense infection outbreaks. Vaccination is one of the most important method to reduce virus infection risk. If an individual is vaccinated, it will immunize or have a lower probability of being infected when exposed to an infectious contact.

The impact of vaccination on epidemic infection dynamics can be evaluated in the two points, the individual's status and the global spreading dynamics.

- For the vaccinated individuals, they will have a lower infection rate when have a contact with their infectious counterparts.
- For the global infection dynamics, the vaccinated subpopulation can reshape the epidemic spreading landscape, which can be designed as the intervention strategies to control the infection dynamics.

A vaccine deployment schedule contains three components: (1) total amounts of vaccine available, (2) vaccine releasing time, (3) vaccine distribution methods. In epidemic infection environment, vaccinated population can be viewed as the part of function losing agglomerate, which means the new infection landscape is the confined within the unvaccinated part. Thus we can use different kind of vaccination deployment strategies to modify the epidemic infection landscape, aiming at suppressing the epidemic infection severity.

- **Amounts of Vaccine Available**
  In our study, the amount of vaccine available means the total number of vaccine that will be released in the whole process of vaccination deployment schedule. This factor is directly determine the percentage of total vaccinated population.
- **Releasing Time**
  The factor of releasing time means when the first batch of vaccine can be adopted and how long it will be lasting. The study of vaccination released in different time aims at observing the efficacy of vaccine deployment under different virus infection severity.
- **Distribution Methods**
  Vaccine distribution method means the vaccination priority of each population groups during vaccine deployment procedure. Such as, population with higher contact frequency should be first vaccinated with concern of suppressing the virus spreading speed.

Yet the impacts of these vaccine deployment factors still remain to be systematically understood. Because of the insufficient information about an unknown infectious disease, it becomes impossible to prepare a vaccine deployment in advance. In this regard, we believe it is important as well as practically desirable to find a reasonable vaccine deployment criteria before making a effective epidemic intervention schedule. This should draw on a deep understanding of relative impacts of vaccine deployment factors on disease infection dynamics.

In the following sector, we will observe the impact of the three deployment factors with different kinds of vaccination parameter settings.

6 Simulation and Results

In this section, we use SIV model with difference equations to simulate H1N1 swine flu infection dynamics. The age groups are parameterized with the demographical statistics of United Kingdom in 2007 [20]. The contact matrix between age groups are derived from Mossong's results of contact activities in European countries [15]. The value of virus infection parameters are adopted by current H1N1 virus infection study [12].

6.1 Epidemic Dynamics with Nonvaccination

Figure 1 shows epidemic curve for 2009 H1N1 influenza pandemic under SIV model with no vaccine released. It is clear that the development of the virus infection spreading can be separated into three stages in terms of the rate of newly-increased infections. They are: incipient infection stage, infection mass spreading stage, and infection stable stage.

- **Incipient infection stage.** In this stage, infection cases increase slightly and the total number of infection is less than 1% of the whole population (Figure 1(a)). In this stage the probability of infectious contacts with infected individuals both within and cross age groups is near zero (Figure 1(c)), which means the infected cases are mainly confined in their initial groups (Figure 1(b)), and the cross group infection is scare.
- **Infection mass spreading stage.** In mass infection stage, the most obvious feature is the total number of newly infected population increase sharply (Figure 1(a)). Meanwhile the probability of infectious contacts also begin shooting up (Figure 1(c)), which is a sign that infection will spread out among each groups through their contacts activities. The cross group infectious contacts work as the positive feedback mechanism to create mass infections in all of the age groups.
- **Infection stable stage.** In this stage, the increase of total infections will be stagnant; however the total number of infections is very high. This stage is an equilibrium state for epidemic spreading, which is balanced by the recovery from infection and newly infections of contact activities.

6.2 Epidemic Dynamics with Vaccination

As discussed above, three factors will impact the efficacy of vaccination deployment, including (1) the amount of total vaccine available, (2) vaccine releasing time, (3) vaccine distribution methods. In this section, we will observe the relative influence of these three deployment factors by simulating epidemics spreading dynamics adopted with different settings of vaccination deployment.

6.2.1 Vaccination Settings

In our simulations, total vaccine availability is divided into three levels, (1)low quantity (5million, 8% of total population), (2) middle quantity (10million, 16% of total population), (3) ample quantity (20million, 32% of total population). Vaccine releasing time has four choices, (1) pre-epidemic spreading ($T_1 = 0$ day), (2) incipient infection stage ($T_2 = 50$ day), (3) infection mass spreading stage ($T_3 = 100$ day), (4) infection stable stage ($T_4 = 150$ day). The vaccine will be distributed following three methods, (1) vaccination by random, in which the number of vaccine released to each age group is totally random; (2) vaccination by transmissibility, which means that two of the age groups with the highest contact frequency will be vaccinated with prime priority; (3) vaccination by vulnerability, which assign the high vaccination priority to two groups of population with higher infection rate.

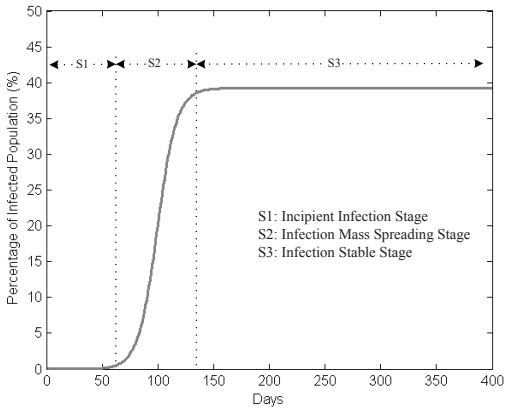
Given the practical limitation of vaccine deployment, the vaccine releasing sequence is designed as followings: (1) in each time unit (day), 1 million vaccine will be released to susceptible individuals; (2) the amount of vaccine adopted to each age groups is determined by their vaccination priorities, which is defined in vaccination distribution methods.

6.2.2 Impact of Vaccination Deployment Factors

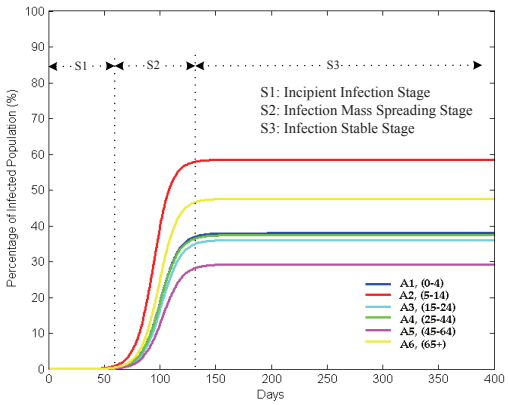
For epidemic intervention by releasing vaccine to susceptible population, the following three concerns determine the efficacy of infection dynamics control: (1) how many vaccine are available; (2) when the vaccine can be started to release; (3) how to distribute vaccine to individuals with different priority. To schedule an effective vaccination deployment plan, first, we should analysis the relative impact of three factors on each stage of epidemics spreading dynamics.

As we has discussed in the previous section, the epidemic spreading dynamics can be separated into three stage concerned with the newly increased infections.

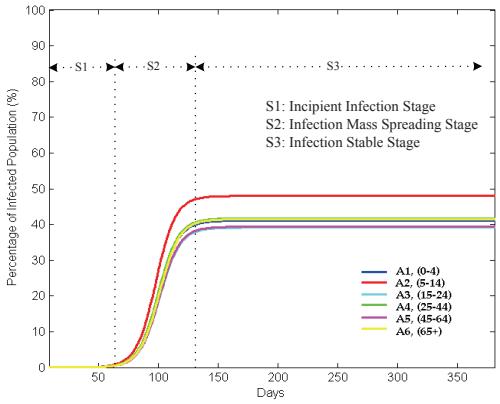
- **Infection Stage 1: Incipient Infection Stage**
  In the first stage, incipient infection stage, the absolute number of infection are relatively low and the infection spreading are mainly confined within the initial infected population groups. Thus the infection risk imposed by cross group contact is less than 1%,



(a) Infection Dynamics of the Whole Population with Nonvaccination



(b) Infection Dynamics of Age Groups with Nonvaccination



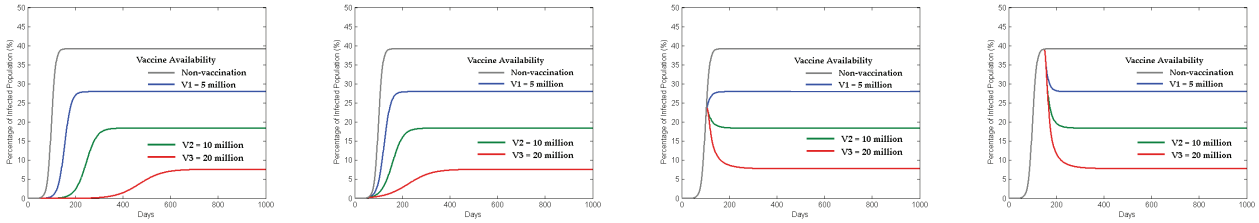
(c) Probability of Infectious Contact within and cross Age Groups

Figure 1: Three Stages in Disease Infection Dynamics with Nonvaccination. *S1: incipient infectious stage, S2: mass infection stage, S3: stable infected stage. In incipient infectious stage, infections increase slightly and the total number of infection is relatively low compared with the whole population. In this stage infected cases are confined in initial groups. In mass infection stage, the most obvious feature is the rate of newly infected cases increase sharply. The infection will spread out among each group through their social contacts. In stable infected stage, the increase of total infections will be stagnant; however the total number of infections is very high. This stage is an equilibrium state for epidemic spreading.*

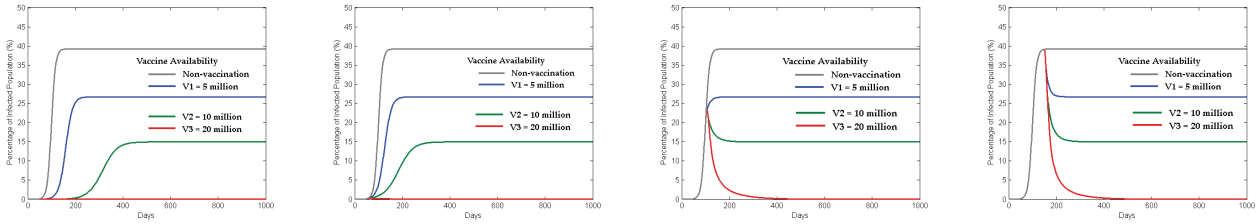
shown in Figure 1(c). However the individuals with a higher infection rate are more likely been infected. Our simulation results show that if the vaccine are released in this stage and distributed by individuals' vulnerability, the lasting time of the incipient infection stage can be prolonged, as shown in Figure 4(a),4(e), 4(i).

- **Infection Stage 2: Infection Mass Spreading Stage**
  In the second infection stage, infection mass spreading stage, the number of infection cases in each subpopulation groups increase sharply, which is the result of positive feedback effect between rate of infectious contact and infected population. As the accumulation of infected population in each age groups, the susceptible individuals will face with an increased probability of cross group infection risk if the contact frequency with outside is higher. Our simulation results show that the vaccination strategy based on individuals' vulnerability can suppress the speed of infection spreadings, as shown in Figure 4(b),4(f), 4(j).

- **Infection Stage 3: Infection Stable Stage**
  In the last stage, infection stable stage, this stage is an equilibrium state for epidemic spreading, which is balanced by the recovery from the infected population and newly infections through infectious contacts. There



(a) $T_{start} = 0$ day, Distribution by Transmissibility (b) $T_{start} = 50$ day, Distribution by Transmissibility (c) $T_{start} = 100$ day, Distribution by Transmissibility (d) $T_{start} = 150$ day, Distribution by Transmissibility



(e) $T_{start} = 0$ day, Distribution by Vulnerability (f) $T_{start} = 50$ day, Distribution by Vulnerability (g) $T_{start} = 100$ day, Distribution by Vulnerability (h) $T_{start} = 150$ day, Distribution by Vulnerability

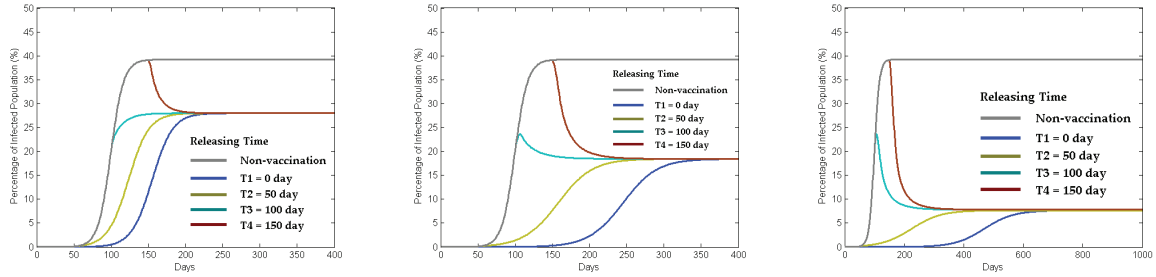
Figure 2: Impact of Vaccine Availability on Infection Dynamics. *Grey: contrast curve of non-vaccination; Blue: 5 million vaccine availability (8% of total population); Green: 10 million vaccine availability (16%); Red: 20 million vaccine availability (32%). The impact of vaccine availability is reflected at the percentage of infected population in infection stable stage. The simulation results show that as the total amount of available vaccine increased from 5 million (8% of total population) to 10 million (16%) and finally to 20 million (32%), the percentage of stable infected population would decrease from 28% to 18.4% and finally to 7.6% (vaccine distributed by transmissibility as shown in Figure a - d and from 26.7% to 15% and finally to infection decayed (vaccine distributed by vulnerability as shown in Figure e - f. The more vaccine released to population, the less infected population in the stable stage of epidemic spreading process.*

two factors influence the results of this stage: (1) the total amount of vaccine availability, (2) how vaccine distributed among each population groups. The simulation results show that as the total amount of available vaccine increased from 5 million (8% of total population) to 10 million (16%) and finally to 20 million (32%), the percentage of stable infected population would decrease from 28% to 18.4% and finally to 7.6% (vaccine distributed by transmissibility as shown in Figure 2(a) - 2(d) and from 26.7% to 15% and finally to infection decayed (vaccine distributed by vulnerability as shown in Figure 2(e) - 2(h). The more vaccine released to population, the less infected population in the stable stage of epidemic spreading process. The distribution of vaccine reshape the epidemics spreading landscape. The vaccination method based on individuals' vulnerability can decrease the population with high infection rate and vaccination method based on individuals' transmissibility can decrease the number of individuals with a higher infectious contact activities. Thus both of these two vaccine distribution method can significantly lower the percentage of infection in the final stable infection stage, as shown in Figure 4.

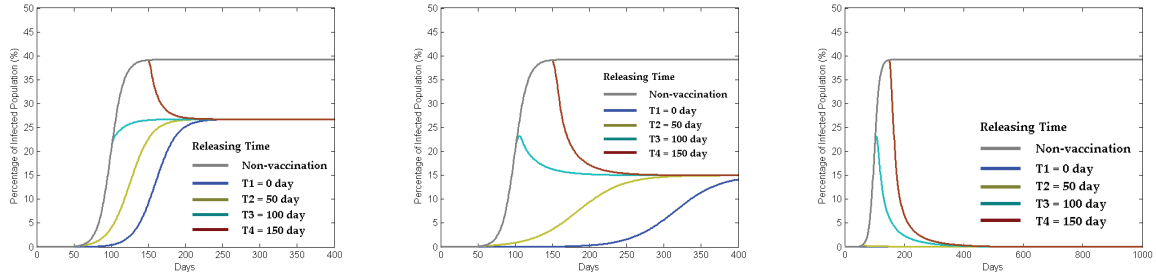
7 Conclusions

We develop a mathematical model to simulate H1N1 epidemic dynamics, which is adopted with heterogeneities individuals' vulnerability and transmissibility based on populations' age structure. In our study, we propose that the infection risk is the combination of two driven forces, one is the probability of being engaged in an infectious contact, the other one is the probability of being successful infected when exposed in a infectious contact. In our study we found that the leading force of the two are shifted from one to another during the development of epidemic spreading process.

We also focus on our analysis on the impact of deployment factors on the efficacy of vaccination distribution, the factors we concerned include total amount of vaccine, vaccine releasing time and distribution methods. By adopting different vaccination deployment settings, we found that increasing vaccine available doses can lower the percentage of final infected cases in the stable infected stage. The releasing of vaccines earlier in each infection stages can im-



(a) V_{amount} = 5 million, Distribution by Transmissibility (b) V_{amount} = 10 million, Distribution by Transmissibility (c) V_{amount} = 20 million, Distribution by Transmissibility



(d) V_{amount} = 5 million, Distribution by Vulnerability (e) V_{amount} = 10 million, Distribution by Vulnerability (f) V_{amount} = 20 million, Distribution by Vulnerability

Figure 3: Impact of Vaccine Releasing Time on Infection Dynamics. *Grey:contrast curve of non-vaccination; Blue: vaccination at pre-spreading of epidemics (0 day); Yellow: vaccination at incipient infection stage (50 day); Cyan: vaccination at infection mass spreading stage (100 day); Magenta Red:vaccinaiton at infection stable stage (150 day). The impact of vaccine releasing time mainly appears at infection mass spreading stage. In the simulation results, topping time of phase transition from stage 1 to stage 2 have been delayed and the rising time of infection curve have been prolonged, as shown in blue curve (pre-spreading vaccination) and yellow curve (incipient infection vaccination). The cyan curve (vaccination at mass spreading stage) and magenta red curve show that the peak value of infection will be reduced and the convergence of infection stable stage will be accelerated.*

prove the dynamical process of infection dynamics by both suppressing the overshoot and accelerating the convergence of infection dynamics. Our results have also shown that, if the grouped population with a higher infection force, which characterizes the dynamical infectious contribution based on their current infection dynamics and social contact patterns, is vaccinated with a priority, both the dynamical infection process and the final stable infection state can be improved.

Our study does not consider the variability of contact pattern, such as, individuals will reduce their contact frequency with outsider as the response of epidemic outbreak. We also ignore other aspects of demographical features that might influence the infection dynamics, such as, gender, occupation and ethics. These factors will be discuss in the future works. Our current work highlights the impact of three vaccine deployment factors on each stage of epidemic infection process and based on these observations efficient vaccination deployment plan can be made to control epidemic spreading.

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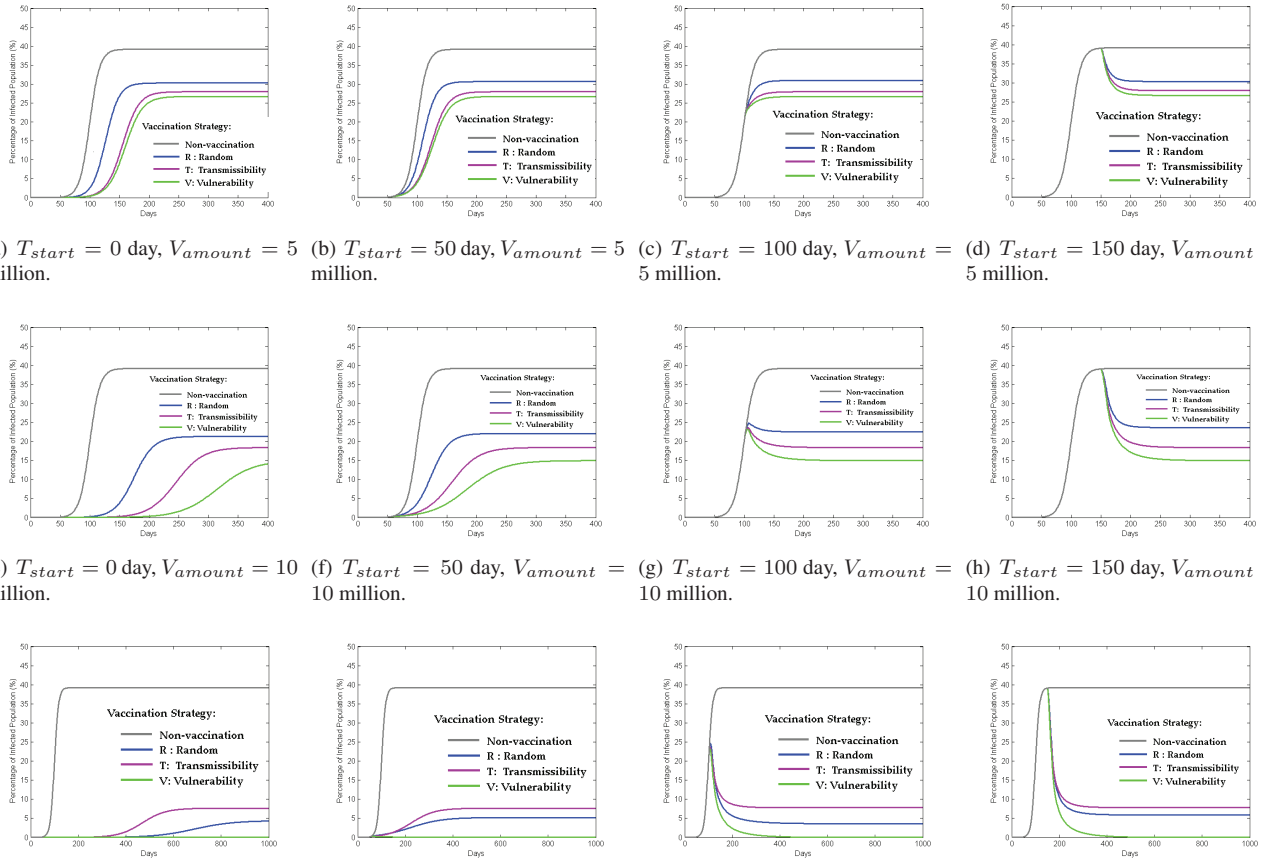

(a) $T_{start} = 0$ day, $V_{amount} = 5$ million. (b) $T_{start} = 50$ day, $V_{amount} = 5$ million. (c) $T_{start} = 100$ day, $V_{amount} = 5$ million. (d) $T_{start} = 150$ day, $V_{amount} = 5$ million.

(e) $T_{start} = 0$ day, $V_{amount} = 10$ million. (f) $T_{start} = 50$ day, $V_{amount} = 10$ million. (g) $T_{start} = 100$ day, $V_{amount} = 10$ million. (h) $T_{start} = 150$ day, $V_{amount} = 10$ million.

(i) $T_{start} = 0$ day, $V_{amount} = 20$ million. (j) $T_{start} = 50$ day, $V_{amount} = 20$ million. (k) $T_{start} = 100$ day, $V_{amount} = 20$ million. (l) $T_{start} = 150$ day, $V_{amount} = 20$ million.

Figure 4: Impact of Vaccine Distribution Methods on Infection Dynamics. *Grey: contrast curve of non-vaccination; Blue: vaccination by random distribution; Purple: vaccination by transmissibility; Green: vaccination by vulnerability. The impact of vaccine distribution methods can be observed at infection mass spreading stage and at final infection stable stage. The results of vaccination simulations with three distribution methods, vaccination by random (blue curve), vaccination by transmissibility (purple curve) and vaccination by vulnerability (green curve), show that the percentage of final infected population in stable stage is lower, topping time of stage transition to mass infection spreading have been delayed and the rising time of stable infection stage have been prolonged respectively.*

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