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Kress, Moshe

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The Effect of Social Mixing Controls on the Spread of Smallpox—A Two-Level Model

MOSHE KRESS
Operations Research Dept., Naval Postgraduate School, Monterey CA, 93943
E-mail: mkress@nps.edu

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Abstract. Responding to a possible bioterror attack of Smallpox has become a major concern to governments, local public officials and health authorities. This concern has been reflected in numerous studies that model and evaluate possible response strategies. Many of these studies consider only vaccination policies and assume homogeneous mixing, where all instances of contacts in the population are equally likely. Such a mixing pattern is rather unlikely to represent population interaction in a modern urban setting, which typically is separated into households on the one hand, and into daily meeting sites such as schools and offices, on the other hand. In this paper we develop a two-level social interaction model where an individual moves back and forth between home and a daily meeting site, possibly passing through a general meeting site such as mass transit system or other crowded areas. Based on the model, we evaluate the effect of social mixing controls, situational awareness of the public health system and mass vaccination on the spread of smallpox. It is shown that mixing controls and alertness of the response system may have a significant impact on the spread of the epidemic. Some policy recommendations are discussed.

Keywords: smallpox, response policies, social structure, SIR model, non-homogeneous mixing

1. Introduction

Responding to a bioterror attack of smallpox has become a major concern to governments, local public officials, and health authorities. This concern has been reflected in studies that model and evaluate possible response policies against smallpox [1–8]. A review of recent smallpox models, including a classification, is presented by Furgeson et al. [7]. Another review paper that compares analytic and simulative approaches for modeling smallpox response policies is by Koopman [8]. A common assumption in these models (e.g., [1–5]) is homogeneous mixing, where all instances of contacts between any two members of the population are equally likely. In other words, interactions in the population are uniformly random.

Such a mixing pattern is quite unlikely to represent actual interactions in an urban setting where the population is typically divided into interconnecting subsets. Halloran et al. [6] present a heterogeneous mixing simulation model for smallpox where social structure is considered. The model is applied to a small population of 2,000 people. A number of studies examine nonhomogeneous mixing in other epidemic settings. Some social mixing patterns are studied in [9] and [10]. Ball and Lyne [11] consider a population partitioned into households, with local mixing within households and global mixing throughout the population, and develop a vaccination optimization model. The effects of a similar social structure are studied by Koopman et al. [12]. Other heterogeneous mixing models have been studied by Kaplan [13,14] and Jacquez et al. [15] with respect to the AIDS epidemic.

The concept of small world networks [16,17] is utilized by several researchers to model nonhomogeneous transmission in a population [18–20]. Eubank et al. [19] develop a detailed large-scale urban traffic simulation, and find that interactions among people form a strongly connected small-world-like graph. They examine several response policies and conclude that outbreaks can be contained by a combination of targeted vaccination and early detection. Another recent model that takes into account detailed social interaction is reported in [21]. However, this microsimulation model does not represent response measures and the reported results of the "pure" epidemic model are based on only one replication of the simulation.

In this paper we develop a two-level social interaction model in which we represent households, daily meeting sites such as schools and offices, and highly crowded sites such as mass transit systems. The model comprises a set of SIR-based difference-equations, which represents dynamic features of daily contacts among individuals. We apply this model to a large urban area (9 million people) and evaluate the effect of situational awareness (early detection and response) and several response measures, such as mass vaccination, quarantine, closure, mass-transit shutdown, and voluntary self-quarantine on the spread of the epidemic and on the total number of casualties. The proposed model is deterministic and therefore is not intended to be predictive per se. The intention is to represent key social-structure and social-dynamics aspects in a conceptually simple model, and to use this model for comparing alternative response policies with respect to a large population.

Our difference-equation model is a special case of the model suggested by Jacquez et al. [15]. Similar to [15], we divide the population into *population subgroups* (households) and *activity subgroups* (daily meeting sites). Our model is positioned

between the purely homogenous mixing models (e.g., [1,4,5]) and the detailed individual-based heterogeneous simulations (e.g., [6,19]), but closer to the former than the latter. On the one hand, the embedded social structure enables evaluating a larger set of alternative response policies than purely homogeneous models, and on the other hand, it facilitates analysis of large size urban populations (millions) that cannot be handled by detailed individual simulations.

Applying the model to a set of commonly accepted epidemiological parameters, it is shown that social mixing controls may have significant effect on the spread of the epidemic. The effect is comparable to the effect of large-scale mass vaccination effort, an effort that may be difficult to execute in reality. We conclude that a combination of moderate mass vaccination effort with moderate implementation of mixing controls may be an effective response to an outbreak of smallpox.

The rest of the paper is organized as follows. Section 2 describes the social structure that forms the base for our model and analysis. Section 3 outlines the stages of the epidemic and discusses possible response actions. The two-level model and the basic data are described in Section 4. In Section 5, we report the results of the analysis that is based on our model. Summary and concluding remarks are presented in Section 6. A detailed description of the difference-equation model is given in the Appendix.

2. The two-level social structure

We assume that during each time period (i.e., a day) a person interacts with other persons mainly in two places: at home, which is referred from now on as *household* (HH), and in the *daily meeting site* (DMS), such as school or workplace. There may also be incidental contacts in public places such as mass transit systems, restaurants, shopping malls, cinema centers or theaters. We consider these contacts as occurring in a *general meeting site* (GMS). During the course of a day, a person is in (close) contact with a relatively small number of individuals in the HH, then she meets colleagues, fellow students, or co-workers in the DMS, and finally she may also contact (mostly strangers) in the GMS. Figure 1 presents this interaction pattern, We assume that the population is divided into m HHs of size h each. There are k DMSs, and one GMS. On each day, members of a HH visit certain DMSs. We make two assumptions regarding the mixing pattern. First, we assume that on each day each individual in a HH chooses the DMS randomly and independently. Second, we assume that, on any given day, no two individuals in a certain HH visit the same DMS. Since the number of DMSs (thousands) is much larger than the size of a HH (3–5), the two assumptions are consistent. Thus, members of the same HH do not interact in a DMS. They interact in the HH and possibly in the GMS (e.g., if both use the mass transit system on a certain day). Arguably, the two aforementioned assumptions may not be very realistic in real life where mixing may be even more segregated. Children go to the same schools every day, and adults usually work in the same offices every day. Also, two children from the same HH may be enrolled in the same school. The mixing within each subset of the population—HH, DMS, and GMS—is assumed to be homogeneous. However, the contact rates (and hence the transmission rates of the disease) are different in the three environments; the transmission rate is highest in a HH and lowest in the GMS.

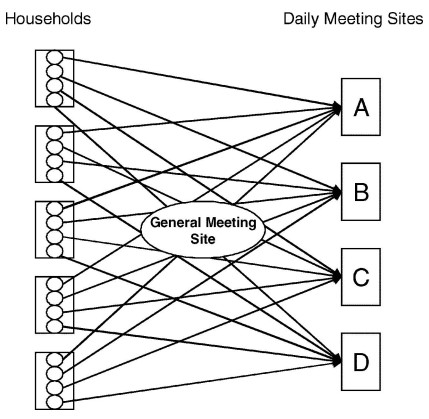

Figure 1. Interaction pattern in a two-level social structure.

Thus, our proposed two-level interaction model, which may be viewed as a "structured" homogeneous mixing model, is more of a small step away from the common "total" homogeneous mixing assumption towards the actual social mixing pattern, than an attempt to model this complex pattern accurately. The main objective is to use the model for evaluating response policies that involve mixing control measures. The model is robust in the sense that if for each subset of individuals (HH, DMS or GMS) we assume that the infection rate is inversely proportional to the size of the subset (see [22], p. 305) then the results of the model are invariant to changes in the number of HHs and DMSs. A similar invariance phenomenon is observed by Watts and Strogatz [16] in the context of small world networks. Sensitivity analysis to other mixing parameters is presented in Section 5.

The spread of the epidemic is observed at discrete time periods (days). Each time period is divided into two parts: the *HH subperiod* and the *DMS subperiod*. During the HH subperiod individuals stay in their respective HHs (homes), while during the DMS subperiod they visit their respective DMSs (workplace, school, etc.). Some individuals may visit also the GMS in-between the two periods. The state of the epidemic in the HHs and DMSs is monitored at four points during a time period: at the beginning and end of the HH subperiod, and at the beginning and end of the DMS subperiod. At the beginning of the HH subperiod, we observe the state of the members of a HH after they return from the DMSs and possibly GMS. At the end of the HH subperiod, we observe the transitions that have occurred in the HH during that subperiod. Similar observations apply to the DMS subperiod.

3. The epidemic and possible response actions

The stages of the epidemic are:

(i) *Susceptible*; a person is not infected but can get infected.

(ii) *Infected and vaccine sensitive*; a person has been infected, the disease is at the incubation stage (the person is not infectious), vaccination is still effective.

(iii) *Infected and vaccine insensitive*; a person has been infected, the disease is at the incubation stage (the person is not infectious), vaccination is ineffective.

(iv) *Infectious*; a person is infectious (symptoms appear and the disease can be transmitted).

(v) *Quarantined*; a person is put in a quarantine.

We assume that following quarantine, a person is *removed*; he is either healthy and immune to the disease, or dead.

The *state* of a HH is defined as the most advanced stage of a member in the HH. That is, a HH is at state x, $x =$ i, ii, iii, iv, v, if at least one member of the HH is at stage x and no member is at stage y, $y > x$. Therefore, a HH is said to be *infected* if at least one member in the HH is infected, but no one is infectious. An infected HH may be *vaccine sensitive* (stage (ii)) if all of its infected members are vaccine sensitive. Otherwise, it is *vaccine insensitive* (stage (iii)). Clearly, some members in a vaccine insensitive infected HH may be susceptible (stage (i)) or infected and vaccine sensitive (stage (ii)). A HH is said to be *infectious* (stage (iv)) if at least one member in the HH is or has been infectious, and it is said to be *quarantined* (*stage*(v)) if it has been put in quarantine. Otherwise, a HH is said to be *susceptible* (stage (i)). The progression of the epidemic in a HH is similar to the progression of a given individual in the sense that there are no state bypasses. If a HH is at state x on day t, it can either remain in that state on day $t+1$, if no individual at stage x in that HH progressed to the next stage, or otherwise move to state $x+1$. We assume that vaccination and quarantine are applied to HHs and not to individuals. The vaccination efficacy is considered to be very high ($\sim$95% [1,6]). For the purpose of the comparative analysis, it would be sufficient to assume perfect and immediate vaccination efficacy. That is, a person at stages (i) or (ii), who is vaccinated, will never progress in the epidemic. Less than perfect efficacy would in fact strengthen the conclusions of our analysis. Therefore, susceptible or infected and vaccine sensitive HHs that are vaccinated, are removed from further consideration (see figure 2). We do not assume reduction in contagiousness due to the vaccination of a vaccine insensitive individual. We also ignore the potential mortality caused by the vaccine, which is negligible [3]. Once an infectious individual is detected, his entire HH is quarantined. If that HH has not been previously vaccinated, all asymptomatic members are vaccinated upon entering the quarantine. Only infectious HHs are quarantined. Since there are no indirect transmissions in smallpox, a DMS is said to be infectious on a certain day if at least one infectious individual (stage iv) visits it on that day.

HHs at states (iii) and (iv) may be vaccinated. Also, quarantined HH (stage (v)) could have been previously vaccinated. Figure 2 presents the transitions among stages for individuals and the transitions among states for HHs.

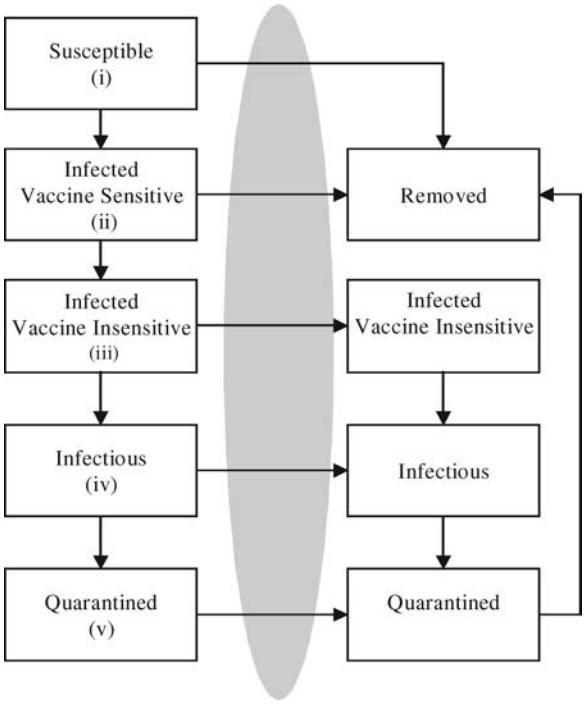

Figure 2. The stages of the epidemic.

Since we assume perfect vaccination efficacy, vaccinated HHs at stages (i) and (ii) are immune. Households at stages (iii) and (iv) may be vaccinated, but only the individuals at stages (i) and (ii) in those HHs become immune. The rest (those at stages (iii) and (iv)) are unaffected by the vaccination.

Without loss of generality we assume that transitions in the stage of a HH, including vaccination and quarantining, occur during the HH period. Infectious DMSs and infectious HHs (at stage (iv)) may generate new infected individuals.

We consider the following response actions:

- Mass vaccination;
- Quarantine;
- Shutdown of GMSs (e.g., shutdown of a mass transit system);
- Gradual closure of DMSs (e.g., closing up schools); and
- Encouraging people to stay home.

Note that while the first four actions are under the complete control of the authorities, the fifth action is not. The authorities may decide to what extent to utilize the media for encouraging people to stay home, but no one can really predict what would be the effect of such announcements. In this paper we explore however the effect of self quarantine to determine its relative impact compared to other response actions.

Mass vaccination and quarantine are applied to HHs. HHs are summoned to vaccination centers and get vaccinated. If an infectious case is detected, then his/her HH is immediately quarantined. If that HH has not been previously vaccinated

in the mass vaccination process, all of its non-symptomatic members get vaccinated.

The response actions are initiated after a certain number of individuals become infectious. We assume that the vaccination and the DMS closure processes start after there are $\Delta_{V/D}$ infectious individuals. This number is the *vaccination/DMS closure threshold*. The shutdown of the GMS is also triggered by the number of infectious cases. The GMS is shut down if this number exceeds Δ_G. The thresholds $\Delta_{V/D}$ and Δ_G indicate how fast can the authorities respond to the outbreak. Smaller thresholds imply better situational awareness, and therefore faster response. While the GMS is shut down completely following a decision to that effect, the process of closing up the DMSs is gradual and takes time. Once the DMS closure process is initiated, it proceeds with a rate δ. On each given day, a fraction δ of the still open DMSs is closed down and remain closed until the epidemic is over.

We assume that a fraction γ of the population passes through the GMS, and at any point in time a proportion β of the (not yet quarantined) population complies with requests of the authorities and voluntarily stay at home. Although in reality one would assume that this rate may change during the course of the epidemic, we assume it is constant throughout. This parameter simply indicates the general population compliance. Finally, infectious HHs are quarantined at a rate ρ and recover from the quarantine at a rate θ.

4. The model and its data

The proposed model is a special case of the structured mixing model presented in [20] in the context of the AIDS epidemic. A feature in our model is the clear distinction among three possible mixing sites: households, daily meeting sites and general meeting sites. Also, compared to past approaches that typically analyze alternative vaccination policies, this model can analyze also the effects of social mixing-control measures and the agility of the public health-care system.

The model is a set of deterministic difference-equations shown in the Appendix. It is a deterministic with embedded transition rates among stages. The spread of the disease is observed at two levels: *high level*, at which we observe the transitions *among* sets of HHs and DMSs, and *low level*, at which we observe the transitions *within* sets. At any time period t, we record the number of sets of a certain type (e.g., HHs at stage (i), Infectious DMSs) at the high level, and the average *profile* (composition) of disease stages within a set, at the low level. We denote numbers associated with stages (i), (ii), (iii), (iv) and (v) with the letters S, A, B, I and Q, respectively. Capital letters denote the cardinality of sets, and lower case letters indicate average numbers of individuals within a HH, GMS or DMS. For example, $B(t)$ is the number of HHs at stage (iii) at time t, and $s_B(t)$, $a_B(t)$, $b_B(t)$ are the average numbers of individuals in such HHs that are at stages (i), (ii), and (iii), respectively. These average numbers, which are computed by simply dividing the total number of individuals in that status by the number of corresponding sets (see equation (2) and the Appendix), form a *profile* of a set. The difference equations, shown in the Appendix, describe transitions among sets at the high level, and among profiles at the low level.

Recall that at each time period (day) the epidemic is observed four times: at the beginning and end of the HH sub-period, and the beginning and end of the DMS sub-period.

The symbol $X^j(t)$ denotes the number of sets (HHs or DMSs) of type X at time t. The index j is 0,1 where $j = 0$ (1) indicates a beginning (end) of a sub-period (HH or DMS).

Let,

- S Number of susceptible HHs.
- A Number of infective and vaccine sensitive HHs.
- B Number of infective vaccine insensitive HHs.
- BV Number of infective vaccine insensitive HHs that have been vaccinated (Only individuals at stage B remain infective, the rest—S and A individuals—are vaccinated and removed).
- I Number of infectious HHs that have not been vaccinated yet. I_0 are newly infected HHs.
- IV Number of infectious HHs that have been vaccinated. VI_0 are newly infected HHs.
- Q Number of isolated HHs.
- QV Number of isolated, previously vaccinated, HHs.
- D Number of open DMSs.
- ID Number of open infectious DMSs.

In the model the values of these parameters are real numbers.

The notation at the low level is of the form $y_X^j(t)$, where y indicates the stage of the epidemic, X is the type of HH or DMS, and j is a 0,1 parameter as before. Thus, for example:

- $s_A^0(t)$ Average number of susceptible individuals, at the beginning of the t-th HH period, in an infective and vaccine sensitive HH that has not been vaccinated yet.
- $s_{IV}^1(t)$ Average number of susceptible individuals, at the end of the t-th HH period, in an infectious HH that has been vaccinated.
- $a_A^0(t)$ Average number of vaccine sensitive infective individuals, at the beginning of the t-th HH period, in an infective HH that has not been vaccinated yet.
- $b_{BV}^1(t)$ Average number of vaccine insensitive infective individuals, at the end of the t-th HH period, in an infective vaccine insensitive HH that has been vaccinated.
- $i_I^1(t)$ Average number of infectious individuals, at the end of the t-th HH period, in an infectious HH that has not been vaccinated yet.
- $s_{ID}^0(t)$ Average number of susceptible individuals in an infectious DMS at the beginning of the DMS period.

Table 1
General model parameters and their default values.

Parameter	Description	Default values	Reference
M	Number of HHs (integer)	3,000,000	Assumed
h	Average size of a HH (integer)	3	Assumed
K	Number of DMSs (integer)	10000	Assumed
α_H	Infection rate in a HH ($R_0 = 6$)	0.67	Based on [23]
α_D	Infection rate in a DMS ($R_0 = 4$)	0.0015	Based on [23]
α_G	Infection rate in the GMS ($R_0 = 3$)	0.0000002	Based on [23]
p	Disease stage (ii) exit rate	0.3	[1]
q	Disease stage (iii) exit rate	0.12	[1]
ρ	Disease stage (iv) exit rate	0.3	[1]
θ	Disease stage (v) exit rate	0.083	[1]
γ	Visit rate at the GMS	0.5	Assumed
δ	Closure rate of DMSs	0	Assumed
β	Fraction of infectious individuals that stay home	0	Assumed
$\Delta_{V/D}$	Vaccination/DMS closure Threshold (integer)	20	Assumed
Δ_G	GMS shutdown threshold (integer)	No Closure	Assumed
V	Vaccination capacity (HHs/Day) (integer)	100,000	Assumed

In the model the values of these parameters are real numbers.

In addition, we denote

$a_X^{\text{New}}(t)$ Average number of newly infected individuals in an infectious DMS, who belong to a HH of type X, $X = S, A, B, BV, I, IV$. $a_{ID}^{\text{New}}(t)$ is the average total number of newly infected individuals in an infectious DMS.

Note that while the number of individuals in a HH remains constant throughout the epidemic, the average number of individuals in a DMS changes over time as HHs are isolated and infectious persons stay home.

The general parameters of the model and their default (Base Case 1) values are shown in table 1.

We consider a large urban area; 9 million people and 10000 DMSs. A HH comprises 3 individuals. The infection rates in the three possible mixing sites correspond to basic reproductive rate values of 6, 4 and 3, for HH, DMS and GMS, respectively. The basic reproductive rate R_0 is the number of secondary infections generated by an infectious individual if all the rest of the population is susceptible ([22], p. 17). The range of R_0 values is consistent with the estimates in [23] (see also sensitivity analysis with respect to these parameters in Section 5). The infection rate α in a susceptible population of size X is given by $\alpha = \frac{R_0}{X\tau}$, where R_0 is the basic reproductive rate and τ is the average duration of the infectious period. The values of the transition rates p, q, ρ and θ are based on [1]. The parameters δ and V are decision variables, $\Delta_{V/D}$ and Δ_G indicate situational awareness and responsiveness capabilities, and β reflects the possible effect of a self-quarantine campaign. There are no known references for the possible values of these parameters. The values chosen in table 1 below and table 2 in Section 5 seem reasonable and are subject to sensitivity analysis later on.

Table 2
Values of policy parameters in base Cases 1 and 2.

Parameter	Description	Base case 1	Base case 2
δ	Closure rate of DMSs	0	.03
β	Fraction of infectious individuals that stay home	0	.25
$\Delta_{V/D}$	Vaccination/DMS Closure Threshold	20	20
Δ_G	GMS Shutdown Threshold	No Closure	70
V	Vaccination Capacity (HHs/Day)	100,000	0

To demonstrate the basic idea of the model we present a sample of three typical equations. In the Appendix we present the full model with some additional detailed explanations.

1. High level transition during the HH subperiod:

$$B^1(t) = \left[\underbrace{B^0(t)(1-q)^{b_B^0(t)}}_{\substack{\text{Expected number of HHs at state iii that remain in that state.}}} + \underbrace{A^0(t)\left(1-(1-p)^{a_A^0(t)}\right)}_{\substack{\text{Expected number of HHs at state ii that progressed to state iii.}}} \right] \times (1 - v(t)). \tag{1}$$

Equation (1) gives the number of HHs of type B (not yet vaccinated) at the end of the HH subperiod.

2. Low level transition:

$$s_B^1(t) = \frac{1}{B^1(t)} \times \left[\underbrace{s_B^0(t)B^0(t)\left(1-q\right)^{b_B^0(t)}}_{\substack{\text{Total expected number of susceptibles (stage i) in HHs at state iii that have not changed their state}}} + \underbrace{s_A^0(t)A^0(t)(1-(1-p)^{a_A^0(t)})}_{\substack{\text{Total expected number of susceptibles (stage i) in HHs that progressed from state ii to iii.}}} \right] \times (1 - v(t)). \tag{2}$$

Equation (2) gives the average number of susceptible individuals in HHs of type B.

3. Low level in a DMS.

$$a_{ID}^{New}(t) = \alpha_D s_{ID}^0 i_{ID}^0. \tag{3}$$

Equation (3) gives the average number of newly infected in an infectious DMS.

5. Analysis

Two base cases are considered. In Base Case 1, shown in table 1, we assume that the response policy is based only on mass vaccination and quarantine of infectious HHs. Other response measures such as DMSs closure, GMS shutdown, and compliance with self-imposed quarantine are not implemented. In base case 2 there is no mass vaccination, only quarantine (and vaccination) of infectious HHs that are detected. However, DMSs are gradually closed up, the GMS is shut down after a while, and a certain proportion of the population (not yet quarantined) stays home. We assume that the initial bio-attack

results in ten infected people in each one of five DMSs, plus ten infected in the GMS.

Table 2 presents the values of policy parameters that change in Base Case 2.

Based on these parameters, Base Case 1 (vaccination, no mixing control, no self quarantine) results in 2,138 infectious individuals, in addition to the casualties of the initial attack. Base Case 2 (no vaccination, mixing control, self quarantine) results in 2,144 additional casualties. The total numbers of casualties in both cases are essentially equal. That is, preventive measures that include closure of DMSs at a rate of 3% per day, shutting down the GMS when there are 70 infectious cases, and 25% "stay-home" compliance is equivalent to the mass vaccination of 100,000 HHs (300,000 individuals) per day with no other mixing controls. However, the epidemic evolves over time in these two cases differently, as shown in figure 3.

Figure 4 presents the daily number of people in quarantine in both base cases.

As shown in figure 3, the epidemic in Base Case 1 is shorter, but with a higher daily peak than Base Case 2. Figure 4 shows the ramification of this effect; higher demand in Base Case 1 for peak quarantine capacity than in Base Case 2. The results of the two base cases indicate that under reasonable assumptions mixing controls may be as effective as mass vaccination. Clearly, this comparison is largely theoretical. It is highly unlikely that in reality the response to the epidemic will rely entirely on mass vaccination or entirely on mixing controls and voluntary behavior of the public. The results of the comparison

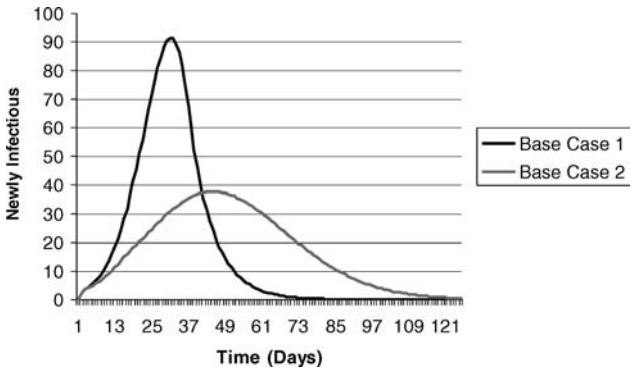

Figure 3. Daily numbers of newly infectious.

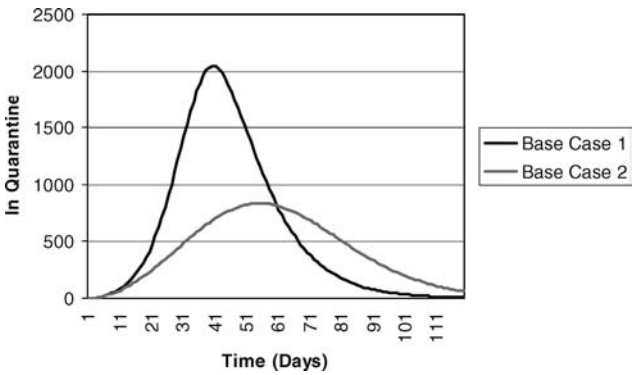

Figure 4. Daily numbers of people in quarantine.

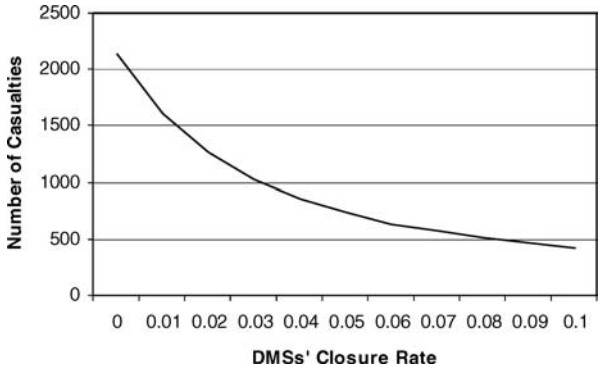

Figure 5. The effect of DMSs' closure rate δ.

underscore however the potential benefits from combining the two types of epidemic control measures.

Next we explore the effect of each one of the control measures δ, β, $\Delta_{V/D}$ and Δ_G on the mass vaccination policy in Base Case 1. Figure 5 shows the effect of DMSs' closure rate δ, ($\Delta_{V/D} = 20$). A closure rate of 0.03 (as in Base Case 2) results in a decrease of more than 50% in the number of casualties compared to Base Case 1. Figure 6 depicts the effect of voluntary self quarantine. While the value of β is not fully controllable, the authorities can affect it by encouraging people to minimize their stay outside their home—a situation similar to cases of severe weather. If the effect of this campaign is that at any time during the epidemic 10% of the population stays voluntarily at home, then the number of casualties decreases by more than 40%. Figures 7 and 8 present the effect of situational awareness and responsiveness of the public health system. Absent DMS closure in Base Case 1, the parameter $\Delta_{V/D}$ applies only to the vaccination process. Notice that the effect of this parameter is linear. A "slower" system that needs 100 cases to get started may result in number of casualties that is more than 3.5 times the number in Base Case 1. Figure 8 shows the effect of the GMS shutdown threshold Δ_G, which is more moderate than the other parameters. Shutting down, say, the mass transit system when there are 200 infectious individuals in the population results in 20% reduction in the number of casualties compared to Base Case 1.

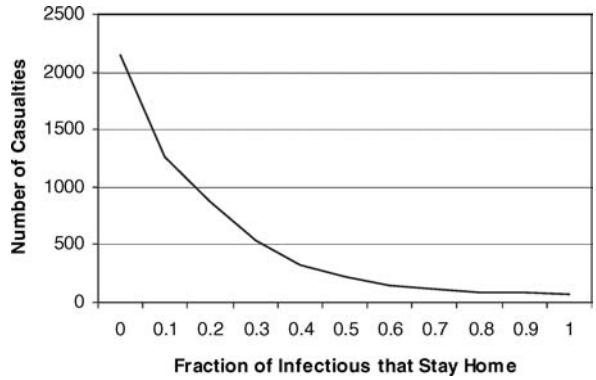

Figure 6. The effect of self quarantine β.

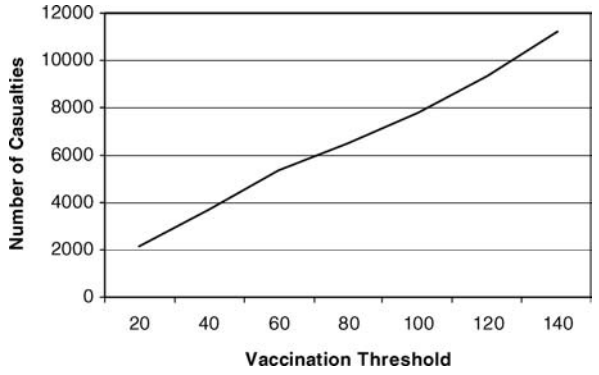

Figure 7. The effect of vaccination threshold $\Delta_{V/D}$.

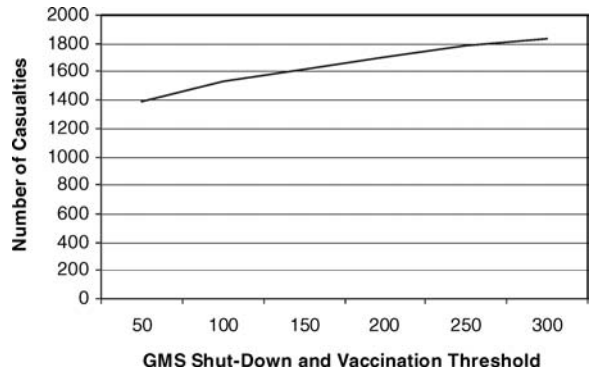

Figure 8. The effect of GMS shutdown threshold Δ_G.

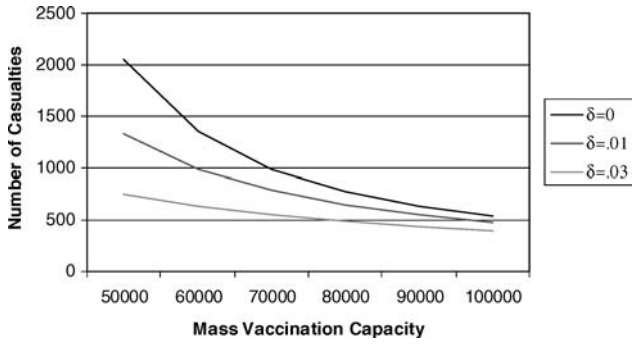

Figure 9. The effect of mass vaccination V—base Case 2.

Next we consider Base Case 2 and examine the effect of adding mass vaccination. Figure 9 presents this effect for three values of δ : 0 (no closure), .01 and .03.

Consider Base Case 3 shown in table 3, which is a mixture of Base Cases 1 and 2.

Table 3
Base case 3.

Parameter	Description	Base case 3
δ	Closure rate of DMSs	.02
β	Fraction of the population that stays home	.1
$\Delta_{V/D}$	Vaccination/DMS closure threshold	20
Δ_G	GMS shutdown threshold	100
V	Vaccination capacity (HHs/Day)	70,000

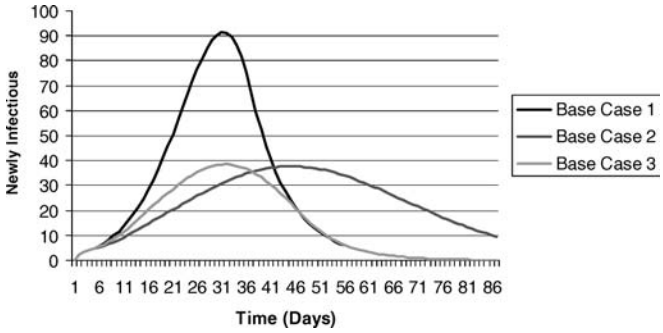

Figure 10. Daily number of newly infectious—base Cases 1, 2, 3.

Base Case 3 represents a reasonable and cautious scenario in terms of vaccination capacity, system responsiveness and possible effects of mixing controls. The estimated number of casualties in this case is 1264—more than 40% decrease compared to Base Cases 1 and 2. Similarly to figure 3, figure 10 compares the three base cases over the period of the epidemic.

While the peak of the epidemic in Base Case 3 is about the same as in Base Case 2, the epidemic is eradicated much faster—as fast as in Base Case 1. Base Case 3 has a clear advantage over Base Cases 1 and 2; under these mixture of responses the epidemic is shorter and less harmful.

Finally, we analyze the sensitivity of Base Case 3 to some of the general model parameters given in table 1. First recall that the independent mixing assumptions imply that our model is essentially a "structured" homogeneous mixing model and therefore the results are not affected by the actual numbers of HHs or DMSs. Since R_0 is fixed for any population size, the infection rate is inversely proportional to the size of the relevant population and therefore the actual segmentation of the population into HHs and DMSs does not affect the results. This segmentation however facilitates the analysis of social control measures. Arguably, in more realistic (and complex) mixing patterns this property would not hold. Figure 11 depicts the effect of varying the basic reproductive rates in three scenarios. In all three scenarios we assume that R_0 remains the same at 6. In Scenario 1 we assume lower infectiveness in the DMSs and GMSs—$R_0(\text{DMS}) = 3$, $R_0(\text{GMS}) = 2$, while in Scenario 3 we assume higher infectiveness—$R_0(\text{DMS}) = 5$, $R_0(\text{GMS}) = 4$. Scenario 2 is the default case—$R_0(\text{DMS}) = 4$, $R_0(\text{GMS}) = 3$. When the infectiveness outside the household is relatively small (scenario 1) Base Case 2

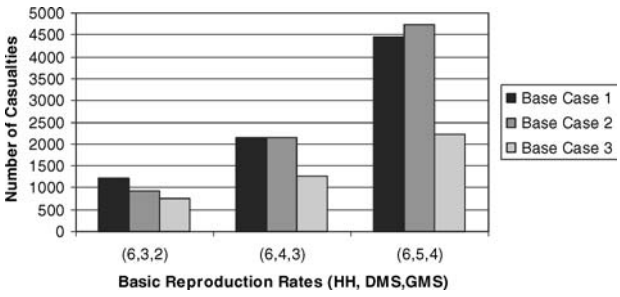

Figure 11. The effect of varying R_0.

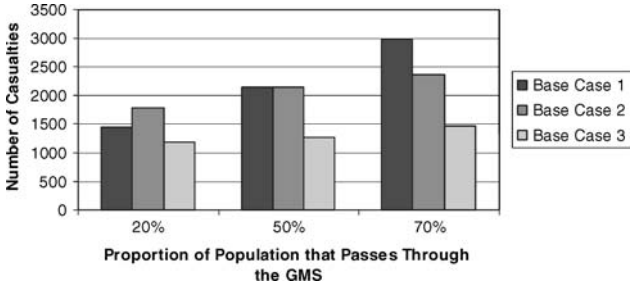

Figure 12. The effect of varying the GMS visit intensity γ.

performs better than Base Case 1. This relation is reversed for relatively high values of R_0. In the absence of mass vaccination, the high infectiveness cannot be effectively handled by mixing controls only. For all three scenarios Base Case 3 results in the least number of casualties.

Figure 12 presents the sensitivity of the results to the assumption regarding the proportion of the population that passes through the GMS.

Low rate of visits to the GMS (20%) imply that shutting it down would not affect significantly the number of casualties. Therefore Base Case 1 is more effective than Base case 2. This relation is reversed for a high visit rate (70%). Once again, for all three visit rates, Base Case 3 results in the least number of casualties.

6. Summary and conclusions

In this paper a deterministic difference-equation model is presented that is one step closer to the reality of social interaction from homogeneous mixing. The objective is to gain insight about the possible effects of epidemic response measures on real-size population (millions). The model is applied to three base cases that reflect three response approaches to an outbreak of the disease: mass vaccination, population mixing control, and combination of the two. It is shown that mixing controls—imposed or voluntary—are effective. Specifically, moderate and gradual closure of schools, offices, etc., and some success in persuading the population to stay home as much as possible, can decrease the number of casualties by considerable numbers—especially when combined with mass vaccination (see figures 5 and 6). We conclude that a response policy that combines moderate (and realistic) effort of mass vaccination and moderate application of mixing controls, may be preferred to a policy that relies entirely on more extensive implementation of one approach or the other. The effectiveness of the proposed "hybrid" policy, represented by Base Case 3, is manifested in the total number of casualties and in the length of the epidemic (see figure 10). This policy seems to be consistently superior to the two others when some input assumptions vary (see figures 11 and 12). The closest reference to this paper is [19] where the authors report results from implementing a highly resolved agent-based simulation for simulating the progression of smallpox in Portland, Oregon, USA (1.5 million people). The focus there is on evaluating alternative vaccination policies, and measuring the effect of delays in implementing the vaccination process. Although evaluated on different scales, the results shown in figure 4 in [19] are consistent with our findings as shown in figure 7. Another recent work that relates to our paper is reported in [21]. The spread of smallpox in the vicinity of Stockholm, Sweden, is modeled by a high-resolution simulation—similar to the Portland simulation in [19]. The model, called *MicroPox*, captures detailed social interactions based on real Swedish demographic statistics. However, the model does not represent response measures and the reported results of the "pure" epidemic model are based on only one replication of the simulation.

As mentioned before, the model presented in this paper is neither predictive nor prescriptive. Its purpose is to facilitate in-context evaluation of alternative response policies. Since it is deterministic, it may give different outcomes compared to models that consider stochastic mixing (see Koopman et al. [12]). The modeling approach presented in this paper may be further explored to represent better social interactions and to account for stochasticity. These extensions may be important areas for future research.

Acknowledgment

I would like to thank the three anonymous reviewers for their valuable comments and suggestions which have improved considerably the content and exposition of the paper. This research was supported by the Naval Postgraduate School via the RIP program.

Appendix: Difference-equations model

Selected equations—(7), (16), (22), (53) and (76)—are annotated for clarification.

Appendix A. HH subperiod

Let

$$v(t) = \mathrm{Min}\left\{1,\ \frac{V}{S^0(t) + A^0(t) + I^0(t)}\right\} \tag{4}$$

$v(t)$ is the vaccination rate.

High Level

$$S^1(t) = S^0(t)(1 - v(t)) \tag{5}$$

$$A^1(t) = A^0(t)(1 - p)^{a_A^0(t)}(1 - v(t)) \tag{6}$$

$$\underbrace{B^1(t)}_{\substack{\#\text{ of HHs at stage (iii) at the end of the HH period}}} = \Big[\ \underbrace{B^0(t)}_{\substack{\#\text{ of HHs at stage (iii) at the beginning of the HH period}}}\ \underbrace{(1-q)^{b_B^0(t)}}_{\substack{\text{Proportion of HHs at stage (iii) that stay at that stage}}} + \underbrace{A^0(t)}_{\substack{\#\text{ of HHs at stage (ii) at the beginning of the HH period}}}$$

$$\times \underbrace{\left(1-(1-p)^{a_A^0(t)}\right)}_{\substack{\text{Proportion of HHs at stage (ii) that moved up to the next stage}}}\Big] \underbrace{(1-v(t))}_{\substack{\text{Fraction of HHs not yet vaccinated}}} \tag{7}$$

$$BV^1(t) = BV^0(t)(1-q)^{b_{BV}^0(t)} + \big[B^0(t)(1-q)^{b_B^0(t)} + A^0(t)(1-(1-p)^{a_A^0(t)})\big]v(t) \tag{8}$$

$$I_0^1(t) = B^0(t)\big[1-(1-q)^{b_B^0(t)}\big](1-v(t)) \tag{9}$$

$$IV_0^1(t) = BV^0\big[1-(1-q)^{b_{BV}^0(t)}\big] + B^0(t)\big[1-(1-q)^{b_B^0(t)}\big]v(t) \tag{10}$$

$$I^1(t) = I^0(t)(1-v(t))(1-\rho) \tag{11}$$

$$IV^1(t) = (IV^0(t) + I^0(t)v(t))(1-\rho) \tag{12}$$

$$Q(t) = I^0(t)\rho + Q(t-1)(1-\theta) \tag{13}$$

$$QV(t) = IV^0(t)\rho + QV(t-1)(1-\theta). \tag{14}$$

Low Level

Susceptible HH

$$s_S^1(t) = s_S^0(t) = h \tag{15}$$

$$\underbrace{a_S^1(t) = b_S^1(t) = i_S^1(t) = a_S^0(t) = b_S^0(t) = i_S^0(t) = 0}_{\substack{\text{HH at stage (i) comprises susceptible members only}}}. \tag{16}$$

Infective vaccine sensitive HH

$$s_A^1(t) = s_A^0(t) \tag{17}$$

$$a_A^1(t) = a_A^0(t) \tag{18}$$

$$b_A^1(t) = b_A^0(t) = 0 \tag{19}$$

$$i_A^1(t) = i_A^0(t) = 0. \tag{20}$$

Infective vaccine insensitive HH

$$s_B^1(t) = \frac{1}{B^1(t)}\big[s_B^0(t)B^0(t)(1-q)^{b_B^0(t)} + s_A^0(t)A^0(t)(1-(1-p)^{a_A^0(t)}\big](1-v(t)) \tag{21}$$

$$\underbrace{a_B^1(t)}_{\substack{\text{Average number of individuals at stage (ii) in a HH at stage (iii) at the end of the HH period}}} = \frac{1}{\underbrace{B^1(t)}_{\substack{\text{Number of HHs at stage (iii) at the of the HH period}}}}$$

$$\times \Bigg[\underbrace{a_B^0(t)(1-p)B^0(t)(1-q)^{b_B^0(t)}}_{\substack{\text{Number of individuals that remain at state (ii) in HHs that remain at state (iii)}}} + \underbrace{a_A^0(t)\left(1-\frac{p}{1-(1-p)^{a_A^0(t)}}\right)A^0(t)\big(1-(1-p)^{a_A^0(t)}\big)}_{\substack{\text{Number of individuals that remain at state (ii) in HHs that moved up from state (ii) to state (iii)}}}\Bigg]$$

$$\times \underbrace{(1-v(t))}_{\substack{\text{Fraction of the population not yet vaccinated}}} \tag{22}$$

$$b_B^1(t) = \frac{1}{B^1(t)}\Bigg[\big(b_B^0(t)+a_B^0p\big)B^0(t)(1-q)^{b_B^0(t)} + a_A^0(t)\frac{p}{1-(1-p)^{a_A^0(t)}}A^0(t)(1-(1-p)^{a_A^0(t)})\Bigg] \times (1-v(t)) \tag{23}$$

$$i_B^1(t) = i_B^0(t) = 0. \tag{24}$$

Vaccinated Infective vaccine insensitive HH

$$s_{BV}^1(t) = s_{BV}^0(t) = a_{BV}^1(t) = a_{BV}^0(t) = i_{BV}^0(t) = i_{BV}^1(t) = 0 \tag{25}$$

$$b_{BV}^1(t) = \frac{1}{BV^1(t)}\Bigg[b_{BV}^0(t)BV^0(t)(1-q)^{b_{BV}^0(t)} + \Bigg[(b_B^0(t)+a_B^0p)B^0(t)(1-q)^{b_B^0(t)} + a_A^0(t)\frac{p}{1-(1-p)^{a_A^0(t)}}A^0(t)(1-(1-p)^{a_A^0(t)})\Bigg]v(t)\Bigg] \tag{26}$$

Newly Infectious HH (I_0)

$$s_{I_0}^1(t) = s_B^0(t) \tag{27}$$

$$a_{I_0}^1(t) = a_B^0(t)(1-p) \tag{28}$$

$$b_{I_0}^1(t) = b_B^0(t)\left(1-\frac{q}{1-(1-q)^{b_B^0(t)}}\right) + a_B^0(t)p \tag{29}$$

$$i_{I_0}^1(t) = b_B^0(t)\frac{q}{1-(1-q)^{b_B^0(t)}}. \tag{30}$$

Vaccinated Newly Infectious HH

$$s_{IV_0}^1(t) = s_{IV_0}^0(t) = a_{IV_0}^1(t) = a_{IV_0}^0(t) = 0 \tag{31}$$

$$b_{IV_0}^1(t) = \frac{1}{IV_0^1(t)}\Bigg\{b_{BV}^0(t)\left(1-\frac{q}{1-(1-q)^{b_{BV}^0(t)}}\right) \times BV^0(t)\big(1-(1-q)^{b_{BV}^0(t)}\big) + b_B^0(t)\left(1-\frac{q}{1-(1-q)^{b_B^0(t)}}\right) \times B^0(t)\big(1-(1-q)^{b_B^0(t)}\big)v(t)\Bigg\} \tag{32}$$

$$i^1_{IV_0}(t) = \frac{1}{IV^1_0(t)}\left\{qb^0_{BV}(t)BV^0(t) + qb^0_B(t)B^0(t)v(t)\right\} \tag{33}$$

Infectious HH

$$s^1_I = s^0_I\left(1 - \alpha_H i^0_I\right) \tag{34}$$

$$a^1_I(t) = a^0_I(t)(1-p) + \alpha_H s^0_I i^0_I \tag{35}$$

$$b^1_I(t) = b^0_I(t)(1-q) + a^0_I(t)p \tag{36}$$

$$i^1_I(t) = i^0_I(t) + b^0_I(t)q. \tag{37}$$

Vaccinated Infectious HH

$$s^1_{IV}(t) = s^0_{IV}(t) = a^1_{IV}(t) = a^0_{IV}(t) = 0 \tag{38}$$

$$b^1_{IV}(t) = b^0_{IV}(t)(1-q) \tag{39}$$

$$i^1_{IV}(t) = i^0_{IV}(t) + b^0_{IV}(t)q \tag{40}$$

Isolated Not Previously Vaccinated HH

(Assumption: Individuals not previously vaccinated are vaccinated immediately upon arrival at the quarantine).

$$s^1_Q(t) = s^0_Q(t) = a^1_Q(t) = a^0_Q(t) = 0 \tag{41}$$

$$b_Q(t) = \frac{1}{Q(t)}\left\{(1-q)b_Q(t-1)Q(t-1) + (1-q)b^0_I(t)I^0(t)\rho\right\} \tag{42}$$

$$i_Q(t) = i_Q(t-1) + \frac{1}{Q(t)}\left\{qb_Q(t-1)Q(t-1) + (qb^0_I(t) + i^0_I(t))I^0(t)\rho\right\} \tag{43}$$

Isolated Previously Vaccinated HH

$$s^1_{QV}(t) = s^0_{QV}(t) = a^1_{QV}(t) = a^0_{QV}(t) = 0 \tag{44}$$

$$b_{QV}(t) = \frac{1}{QV(t)}\left\{b_{QV}(t-1)(1-q)QV(t-1) + b^0_{IV}(t)\,(1-q)\,IV^0(t)\rho\right\} \tag{45}$$

$$i_{QV}(t) = i_{QV}(t-1) + \frac{1}{QV(t)}\left\{qb_{QV}(t-1)QV(t-1) + (qb^0_{IV}(t) + i^0_{IV}(t))IV^0(t)\rho\right\} \tag{46}$$

At the end of the HH-cycle, the total number of susceptibles and vaccine sensitive infected are:

$$s^1_{\text{Total}}(t) = S^1(t)h + A^1(t)s^1_A(t) + B^1(t)s^1_B(t) + I^1_0(t)s^1_{I_0}(t) + I^1(t)s^1_I(t) \tag{47}$$

$$a^1_{\text{Total}}(t) = A^1(t)a^1_A(t) + B^1(t)a^1_B(t) + I^1_0(t)a^1_{I_0}(t) + I^1(t)a^1_I(t). \tag{48}$$

And the total number of infectious individuals is:

$$i^1_{\text{Total}}(t) = I^1_0(t)i^1_{I_0}(t)) + I^1(t)i^1_I(t)) + IV^1_0(t)i^1_{IV_0}(t)) + IV^1(t)i^1_{IV}(t)) \tag{49}$$

The number of commuting infectious individuals from an infectious HH is

$$ic^1_I(t) = (1-\beta)i^1_I(t) \tag{50}$$

$ic^1_{I_0}(t)$, $ic^1_{IV}(t)$ and $ic^1_{IV_0}(t)$ are defined similarly.

The total commuting infectious individuals is:

$$ic^1_{\text{Total}}(t) = I^1_0(t)ic^1_{I_0}(t)) + I^1(t)ic^1_I(t)) + IV^1_0(t)ic^1_{IV_0}(t)) + IV^1(t)ic^1_{IV}(t). \tag{51}$$

Appendix B. Transition HH → GMS → DMS

DMS

Comments:: (1) Equation (53) is a simple extension of the well-known Urn Model [24]. (2) Suppose $D(t) = uK$, $u < 1$.

$$D(t) = (1-\delta)D(t-1) \tag{52}$$

$$\underbrace{ID(t)}_{\substack{\text{Number of}\\ \text{open infected}\\ \text{DMSs}}} = \underbrace{D(t)}_{\substack{\text{Number of}\\ \text{open DMSs}}} \left(\underbrace{1 - \left(1 - \frac{ic^1_I(t)}{K}\right)^{I^1(t)} \overbrace{\left(1 - \frac{ic^1_{I_0}(t)}{K}\right)^{I^1_0(t)}}^{\substack{\text{Probability that}\\ \text{no newly infectious}\\ \text{visits a certain DMS}}} \left(1 - \frac{ic^1_{IV}(t)}{K}\right)^{IV^1(t)} \left(1 - \frac{ic^1_{IV_0}(t)}{K}\right)^{IV^1_0(t)}}_{\text{Probability that at least one infectious individual visits a ceratain DMS}} \right) \tag{53}$$

Only a proportion u of the DMSs are open and therefore only a proportion u of the population that would otherwise leave home actually does it. Since each member of a HH goes to a different DMS, this means that only ui_c infectious individuals leave home. $ui_c/uK = i_c/K$.

Individuals

We assume that the contacts in the GMS occur between the HH cycle and the DMS cycle.

$$i_{\text{GMS}}(t) = \gamma\frac{D(t)}{K}ic^1_{\text{Total}}(t) \tag{54}$$

$$s_{\mathrm{GMS}}(t) = \gamma s^1_{\mathrm{Total}}(t) \tag{55}$$

The number of newly infected individuals at the GMS is:

$$a^{\mathrm{New}}_{\mathrm{GMS}}(t) = \alpha_G s_{\mathrm{GMS}} i_{\mathrm{GMS}} \tag{56}$$

Let $a^{\mathrm{New}}_{\mathrm{GS}}(t)$, $a^{\mathrm{New}}_{\mathrm{GA}}(t)$, $a^{\mathrm{New}}_{\mathrm{GB}}(t)$ and $a^{\mathrm{New}}_{\mathrm{GI}}(t)$ denote the number of newly infected at the GMS that belong to belong to HHs at stages, (i), (ii), (iii) and (iv), respectively. Clearly, $(a^{\mathrm{New}}_{\mathrm{GS}}(t) + a^{\mathrm{New}}_{\mathrm{GA}}(t) + a^{\mathrm{New}}_{\mathrm{GB}}(t) + a^{\mathrm{New}}_{\mathrm{GI}}(t)) = a^{\mathrm{New}}_{\mathrm{GMS}}(t)$. Since the probability that a newly infective belongs to a certain type of a HH is proportional to the number of susceptibles in such a HH, we have:

$$a^{\mathrm{New}}_{\mathrm{GS}}(t) = a^{\mathrm{New}}_{\mathrm{GMS}}(t)\frac{S^1(t)h}{s^1_{\mathrm{Total}}(t)} \tag{57}$$

$$a^{\mathrm{New}}_{\mathrm{GA}}(t) = a^{\mathrm{New}}_{\mathrm{GMS}}(t)\frac{A^1(t)s^1_A(t)}{s^1_{\mathrm{Total}}(t)} \tag{58}$$

$$a^{\mathrm{New}}_{\mathrm{GB}}(t) = a^{\mathrm{New}}_{\mathrm{GMS}}(t)\frac{B^1(t)s^1_B(t)}{s^1_{\mathrm{Total}}(t)} \tag{59}$$

$$a^{\mathrm{New}}_{\mathrm{GI}}(t) = a^{\mathrm{New}}_{\mathrm{GMS}}(t)\frac{I^1_0(t)s^1_{I_0}(t) + I^1(t)s^1_I(t)}{s^1_{\mathrm{Total}}(t)}. \tag{60}$$

Infectious DMS

$$i^0_{ID}(t) = \frac{D(t)}{K}\frac{ic^1_{\mathrm{Total}}(t)}{ID(t)} \tag{61}$$

$$s^0_{ID}(t) = \frac{s^1_{\mathrm{Total}}(t) - a^{\mathrm{New}}_{\mathrm{GMS}}(t)}{K}. \tag{62}$$

Since response actions and transitions among disease stages are assumed to take place during the HHs cycle, we do not need to track either the noninfectious open DMSs or the individuals who are at the latent stages (vaccine sensitive and vaccine insensitive) of the disease.

Appendix C. DMS cycle

Since transitions among disease stages are assumed to take place only in the HHs, the DMSs do not change their status during this cycle. The only parameter of interest during the DMS cycle is the number of newly infected.

Individuals

Infectious open DMS

The number of newly infected individuals in an open DMS is:

$$a^{\mathrm{New}}_{ID}(t) = \alpha_D s^0_{ID} i^0_{ID} \tag{63}$$

A newly infected individual may belong to a susceptible HH, an infective HH, or an infectious HH.

Let $a^{\mathrm{New}}_{\mathrm{DS}}(t)$, $a^{\mathrm{New}}_{\mathrm{DA}}(t)$, $a^{\mathrm{New}}_{\mathrm{DB}}(t)$ and $a^{\mathrm{New}}_{\mathrm{DI}}(t)$ denote the number of newly infectives that belong to HHs at stages, (i), (ii), (iii) and (iv), respectively. Clearly, $(a^{\mathrm{New}}_{\mathrm{DS}}(t) + a^{\mathrm{New}}_{\mathrm{DA}}(t) + a^{\mathrm{New}}_{\mathrm{DB}}(t) + a^{\mathrm{New}}_{\mathrm{DS}}(t)) = a^{\mathrm{New}}_{ID}(t)$, Since the probability that a newly infective belongs to a certain type of HH is proportional to the number of susceptibles in such a HH, we have:

$$a^{\mathrm{New}}_{\mathrm{DS}}(t) = a^{\mathrm{New}}_{ID}(t)\frac{S^1(t)h}{s^1_{\mathrm{Total}}(t)} \tag{64}$$

$$a^{\mathrm{New}}_{\mathrm{DA}}(t) = a^{\mathrm{New}}_{ID}(t)\frac{A^1(t)s^1_A(t)}{s^1_{\mathrm{Total}}(t)} \tag{65}$$

$$a^{\mathrm{New}}_{\mathrm{DB}}(t) = a^{\mathrm{New}}_{ID}(t)\frac{B^1(t)s^1_B(t)}{s^1_{\mathrm{Total}}(t)} \tag{66}$$

$$a^{\mathrm{New}}_{\mathrm{DI}}(t) = a^{\mathrm{New}}_{ID}(t)\frac{I^1_0(t)s^1_{I_0}(t) + I^1(t)s^1_I(t)}{s^1_{\mathrm{Total}}(t)} \tag{67}$$

Appendix D. DMS—HH transition

HH

Let

$$S^0(t) = S^1(t-1)\left(1 - \frac{a^{\mathrm{New}}_{\mathrm{DS}}(t-1)}{S^1(t-1)}\right)^{ID(t-1)} \times \left(1 - \frac{a^{\mathrm{New}}_{\mathrm{GS}}(t-1)}{S^1(t-1)}\right) \tag{68}$$

$$A^0(t) = A^1(t-1) + S^1(t-1) - S^0(t) \tag{69}$$

$$B^0(t) = B^1(t-1) \tag{70}$$

$$BV^0(t) = BV^1(t-1) \tag{71}$$

$$I^0(t) = I^1(t-1) + I^1_0(t-1) \tag{72}$$

$$IV^0(t) = IV^1(t-1) + IV^1_0(t-1). \tag{73}$$

Individuals

Susceptible HH

$$s^0_S(t) = h \tag{74}$$

$$a^0_S(t) = b^0_S(t) = i^0_S(t) = 0. \tag{75}$$

Infective vaccine sensitive HH

$$\underbrace{s_A^0(t)}_{\substack{\text{Average number of susceptible individuals in a HH at stage (ii) at the beginning of a HH period}}} = \frac{1}{\underbrace{A^0(t)}_{\substack{\text{Number of HHs at stage (ii) at the beginning of a HH period}}}} \Bigg[\underbrace{A^1(t-1)s_A^1(t-1)}_{\substack{\text{Number of susceptible Individuals in a HH at stage (ii) at the end of the HH period in the previous time step.}}} - \underbrace{ID(t-1)\big(a_{\mathrm{DA}}^{\mathrm{New}}(t-1)+a_{\mathrm{DS}}^{\mathrm{New}}(t-1)\big)}_{\substack{\text{New infected individuals at stage (ii) who got infected in the DMS}}}$$

$$- \underbrace{\big(a_{\mathrm{GA}}^{\mathrm{New}}(t-1)+a_{\mathrm{GS}}^{\mathrm{New}}(t-1)\big)}_{\substack{\text{New infected individuals at stage (ii) who got infected in the GMS}}} + \underbrace{\big(S^1(t-1)-S^0(t)\big)}_{\substack{\text{Number of susceptible HHs for which at least one member has been infected in the GMS/DMS.}}} h \Bigg] \tag{76}$$

$$a_A^0(t) = \frac{1}{A^0(t)}\big[A^1(t-1)a_A^1(t-1) + ID(t-1)\big(a_{\mathrm{DA}}^{\mathrm{New}}(t-1)+a_{\mathrm{DS}}^{\mathrm{New}}(t-1)\big) + a_{\mathrm{GA}}^{\mathrm{New}}(t-1)+a_{\mathrm{GS}}^{\mathrm{New}}(t-1)\big] \tag{77}$$

$$b_A^0(t) = 0 \tag{78}$$

$$i_A^0(t) = 0. \tag{79}$$

Infective vaccine insensitive HH

$$s_B^0(t) = \frac{1}{B^0(t)}\big[B^1(t-1)s_B^1(t-1) - ID(t-1)a_{\mathrm{DB}}^{\mathrm{New}}(t-1) - a_{\mathrm{GB}}^{\mathrm{New}}(t-1)\big] \tag{80}$$

$$a_B^0(t) = \frac{1}{B^0(t)}\big[B^1(t-1)a_B^1(t-1) + ID(t-1)a_{\mathrm{DB}}^{\mathrm{New}}(t-1) + a_{\mathrm{GB}}^{\mathrm{New}}(t-1)\big] \tag{81}$$

$$b_B^0(t) = b_B^1(t-1) \tag{82}$$

$$i_B^0(t) = 0. \tag{83}$$

Infectious HH

$$s_I^0(t) = \frac{1}{I^0(t)}\big[I^1(t-1)s_I^1(t-1) + I_0^1(t-1)s_{I_0}^1(t-1) - ID(t-1)a_{\mathrm{DI}}^{\mathrm{New}}(t-1) - a_{\mathrm{GI}}^{\mathrm{New}}(t-1)\big] \tag{84}$$

$$a_I^0(t) = \frac{1}{I^0(t)}\big[I^1(t-1)a_I^1(t-1) + I_0^1(t-1)a_{I_0}^1(t-1) + ID(t-1)a_{\mathrm{DI}}^{\mathrm{New}}(t-1) + a_{\mathrm{GI}}^{\mathrm{New}}(t-1)\big] \tag{85}$$

$$b_I^0(t) = \frac{I^1(t-1)b_I^1(t-1) + I_0^1(t-1)b_{I_0}^1(t-1)}{I^0(t)} \tag{86}$$

$$i_I^0(t) = \frac{I^1(t-1)i_I^1(t-1) + I_0^1(t-1)i_{I_0}^1(t-1)}{I^0(t)}. \tag{87}$$

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