Household Epidemics: Modelling Effects of Early Stage Vaccination

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A Markovian susceptible → infectious → removed (SIR) epidemic model is considered in a community partitioned into households. A vaccination strategy, which is implemented during the early stages of the disease following the detection of infected individuals is proposed. In this strategy, the detection occurs while an individual is infectious and other susceptible household members are vaccinated without further delay. Expressions are derived for the influence on the reproduction numbers of this vaccination strategy for equal and unequal household sizes. We fit previously estimated parameters from influenza and use household distributions for Sweden and Tanzania census data. The results show that the reproduction number is much higher in Tanzania (6 compared with 2) due to larger households, and that infected individuals have to be detected (and household members vaccinated) after on average 5 days in Sweden and after 3.3 days in Tanzania, a much smaller difference.

Key words: Delay time; Epidemic model; Household; Reproduction number; Vaccination strategy.

1 Introduction

When modelling infectious diseases, it is important to include structures which describe the way in which individuals interact in the community. To gain a deeper understanding of the real-world epidemic process, attempts have been made to partition the population (assumed to be large) into small groups, for example households, workplaces, schools, age groups and so on (*e.g.* see Longini and Koopman, 1982; Addy, Longini, and Haber, 1991; Ball, Mollison, and Scalia-Tomba, 1997; Andersson and Britton, 2000). The social structure we are considering is typically a small unit (a household), and our model has two levels of mixing: locally within the households and globally in the population at large according to two rates. That is, each person in the community has both probabilities of making contacts with other individuals in the population as a whole (global contacts) and within its own household (local contacts). Consequently, the spread of an infectious disease is greatly facilitated between such households, which have a high level of mixing among individuals belonging to same household. For example, the rate of transmission for influenza A is much higher within a household than between households (see *e.g.* Addy *et al.*, 1991). These results imply that control strategies such as vaccination can be directed toward reducing the spread of the disease within households.

Much work has been done on modelling epidemics and control in a community of households. For example, Becker and Dietz (1995) studied the critical immunity level for preventing epidemics in a community of households consisting of different individuals. Ball *et al.* (1997) studied the spread

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of infections in a single type household population, and discussed the effects of different vaccination strategies. For other important contributions to the theory and practical application of epidemics and control strategies in a community of households, see also Longini and Koopman (1982), Becker and Hall (1996), Islam, O'Shaughnessy, and Smith (1996), Becker and Starczak (1997), Andersson and Britton (1998), Ball and Lyne (2002), Ball and Neal (2002), Lipsitch *et al.* (2003), Ferguson *et al.* (2005), Wu *et al.* (2006), Fraser (2007).

In the present paper, we consider a Markovian epidemic model of susceptible → infectious → removed (SIR) in a closed population partitioned into households. Initially all individuals are assumed to be susceptible except one randomly selected individual who is infected from outside the community. During the infectious period, an infected individual may infect other susceptible individuals within the household and in the community as a whole. For this household epidemic, we investigate the effects of a vaccination strategy, which is implemented during the early stages of epidemic. The vaccination strategy assumes that infectious individuals are detected after some delay time, and once detected, other susceptible household members are vaccinated. The term "vaccination" could also mean isolation or some other type of immunization. We assume that whenever an infectious individual is detected, the spreading of the disease from that household is stopped (either by isolation, quarantine or vaccination). Ball, O'Neill, and Pike (2007) study a related vaccination strategy, but then assuming that the detection time is equal to removal time, with the motivation that removal corresponds to the appearance of symptoms which in turn implies detection. In the present work, a person may as well be detected before the end of the infectious period.

For this closed community of households and epidemic model, we derive the reproduction number of a household epidemic without vaccination by computing the probabilities of final size outbreak within a household. By the reproduction we will, in this paper, mean the number of households infected by a (typical) infected person in a totally susceptible population. We also derive the reproduction number for the case of equal and unequal household sizes when the vaccination strategy is in place by analyzing the expected force of infection of a household outbreak, and this is done by studying a weighted time to extinction of a two-dimensional Markov process.

The rest of the paper is organized as follows: In Section 2, we define the household epidemic model, and then derive the reproduction number for equal and unequal household sizes. Section 3 describes the vaccination model during the early stages of epidemic and the reproduction number is derived. Numerical illustrations are given in Section 4, and some concluding remarks are presented in Section 5.

2 A Household Epidemic Model

The model we now describe is a stochastic SIR epidemic for a closed single type population partitioned into households. That is, at any time, individuals are in one of the three states: susceptible, infectious or removed. So, a susceptible individual can be infected (and become infectious) upon contact with an infectious person. An infected individual remains infectious for an exponentially distributed time, and is then removed meaning recovered and immune to the disease.

2.1 Definition of the model

Initially there is one newly infected individual who is chosen completely at random among all the individuals in the community. The remaining individuals are assumed to be susceptible to the disease. During the infectious period, the individual has global contacts with other individuals in the community according to a homogeneous Poisson process with rate λ_c, each contact being independent and chosen completely at random from the whole community. As a result, the global

contact rate with a given individual is λ_c/N, where N is the number of individuals in the community. Also an infectious individual makes "local" contacts independently with each household member at rate λ_h. If the (globally or locally) contacted person is still susceptible, she will get infected and immediately become infectious to other individuals, (so there is no latent period). When the infectious period ends, the individual recovers and becomes immune (a state called removed) and plays no further role in the epidemic process. Infectious periods of different individuals are assumed to be independent and identically distributed according to a finite random variable I, which is exponentially distributed with mean $1/\gamma$. The epidemic terminates as soon as there are no more infectious individuals in the community, because all individuals will then be either susceptible or removed and immune to the disease. We assume that all Poisson processes describing infectious contacts and random variables describing infectious periods are mutually independent.

2.2 The reproduction number for equal households sizes

Suppose that the number of households is large and for now that all households have the same size k. Then, during the early stages of an epidemic initiated by a single infectious individual, most households are still susceptible to the disease, implying that the probability of making a global contact with an individual living in a previously infected household is small. This implies that the initial growth of the epidemic can be approximated by a branching process. The approximation can be made mathematically fully rigorous by considering a sequence of epidemics and using coupling arguments as in Ball (1996), but we leave out the details. The initial infectious person contacts (globally) on average λ_c/γ individuals who belong to distinct households, (recall that $E(I) = 1/\gamma$ is the mean of infectious period). Furthermore, all these new infected individuals make global contacts spreading the disease to new households. Note that, each individual contacted in this way will cause an outbreak in her own household, so it is of interest to determine the expected size of such an outbreak. The expected number of individuals infected in that household, including the initial infectious person, denoted $\mu^{(k)}$, is given by

$$\mu^{(k)} = 1 + \sum_{j=0}^{k-1} j P_j^{(1,k-1)}$$

where $P_j^{(1,k-1)}$ is the probability that j out of $k-1$ susceptible get infected, starting with one infectious individual. That is, $\mu^{(k)}$ denotes the expected number of infected individuals in a household of size k, starting with one initially infected person and $k-1$ susceptible individuals, neglecting infections from outside.

The final size probabilities $P_j^{(1,k-1)}$ for $0 \le j \le k-1$ can be determined recursively by using the following formula (see Andersson and Britton, 2000, Section 2.4 for details):

$$P_j^{(1,k-1)} = \binom{k-1}{j} [\phi(\lambda_h(k-1-j))]^{j+1} - \sum_{i=0}^{j-1} \binom{k-1-i}{j-i} [\phi(\lambda_h(k-1-j))]^{j-i} P_i^{(1,k-1)} \quad (1)$$

where $\phi(\lambda_h) = E(e^{-\lambda_h I})$ is the Laplace transform of the infectious period I. Because $I \sim \text{Exp}(\gamma)$, *i.e.* I is exponentially distributed with mean $1/\gamma$, Eq. (1) becomes

$$P_j^{(1,k-1)} = \binom{k-1}{j} \left[\frac{\gamma}{(k-1-j)\lambda_h + \gamma}\right]^{j+1} - \sum_{i=0}^{j-1} \binom{k-1-i}{j-i} \left[\frac{\gamma}{(k-1-i)\lambda_h + \gamma}\right]^{j-i} P_i^{(1,k-1)}. \quad (2)$$

Note that we must first sequentially determine $P_0^{(1,k-1)}$ up to $P_{j-1}^{(1,k-1)}$ in order to compute $P_j^{(1,k-1)}$. This recursive process makes the formula in (2) practically useful for moderately small j. As an illustration, we solve Eq. (2) for a household of size $k = 3$ including one initially infected person and $k-1 = 2$ susceptible individuals. The final size probabilities are then given by

$$\{P_0^{(1,2)}, P_1^{(1,2)}, P_2^{(1,2)}\} = \left\{\frac{\gamma}{\gamma + 2\lambda_h}, \frac{2\lambda_h\gamma^2}{(\gamma+\lambda_h)^2(\gamma+2\lambda_h)}, \frac{2\lambda_h(\gamma+\lambda_h)^2 - 2\lambda_h\gamma^2}{(\gamma+\lambda_h)^2(\gamma+2\lambda_h)}\right\}.$$

During the early stages of the disease, all of these infected individuals in the household outbreak have global contacts with other individuals in the community, introducing the disease in other households and so on, which exhibits the property of a branching process. Hence, the basic reproduction number is given by

$$R_0 = \frac{\lambda_c}{\gamma}\mu^{(k)} = \frac{\lambda_c}{\gamma}\left[1 + \sum_{j=0}^{k-1} jP_j^{(1,k-1)}\right]. \tag{3}$$

The mean value $\mu^{(k)}$ (when only local infectious contacts count) has an amplification effect on R_0, which calls for control strategies to be directed toward reducing $\mu^{(k)}$ (see Ball *et al*., 1997). Of course, if we ignore household formations ($k = 1$) in the community, we arrive at the usual expression of the basic reproduction number $\lambda_c E(I)$ from the global contacts, because $\mu^{(1)} = 1$.

2.3 The reproduction number for different households sizes

In real-life, households sizes vary. Several studies have been done on modelling epidemics spreading in populations partitioned into households of varying sizes, the aim being to investigate possible control measures against epidemic outbreaks (see, *e.g*. Becker and Dietz, 1995; Becker and Starczak, 1997; Ball *et al*., 1997). In this section, we derive the reproduction number for the Markovian SIR epidemic in a closed, large community partitioned into households of different sizes. Consider a community of size N as before. Let $k_{\max}$ be the size of the largest household in the community. Suppose for $k = 1, 2, \ldots, k_{\max}$, that the community contains h_k households of size k, implying that the total number of households H say, is given by $H = \sum_{k=1}^{k_{max}} h_k$. Further, the number of individuals in the community can now be written as $N = \sum_{k=1}^{k_{max}} kh_k$.

Because the number of households H is assumed to be large, the probability of a global contact with an individual living in a previously infected household is small during the early stages of an epidemic. Thus, the initial behavior of the epidemic can be approximated by a branching process, where each global contact is with an individual in an otherwise susceptible household. In that respect, we consider a single household epidemic initiated by one externally infected household member. This individual will start a realization of a single household epidemic (without external infection), because we assume that all global contacts are with completely susceptible households. Recall that the mean number of infected individuals (including the initially infectious individual) in a household of size k is $\mu^{(k)}$, and that each infectious individual in this household makes global contacts at rate λ_c during the infectious period with mean $E(I) = 1/\gamma$. The basic reproduction number R_0 (derivation appears in Ball *et al*., 1997) for households of varying sizes can be calculated as follows. For $k = 1, 2, \ldots, k_{max}$, let $\pi_k = h_k/H$ be the proportion of households of size k and denote $\tilde{\pi}_k = kh_k/N = k\pi_k/\sum_{j=1}^{k_{max}} j\pi_j$, as the probability that a randomly selected individual resides

in a household of size k. If the globally infected person belongs to a household of size k, the mean outbreak equals $\lambda_c E(I)\mu^{(k)}$. Thus,

$$R_0 = \lambda_c E(I) \sum_{k=1}^{k_{\max}} \tilde{\pi}_k \mu^{(k)} = \frac{\lambda_c}{\gamma} \sum_{k=1}^{k_{\max}} \tilde{\pi}_k \left[1 + \sum_{j=0}^{k-1} j P_j^{(1,k-1)} \right].$$

3 Modelling Vaccination with Delay

In this section, we consider vaccination as a control strategy, the aim being to reduce further the spread of the disease. In any vaccination strategy, the main question is, who and how many individuals should be vaccinated to prevent epidemic outbreaks. Furthermore, given a particular vaccination scheme, one may wish to investigate the conditions in which large epidemic outbreaks can occur. In the household setting, we look into how detection of an infectious individual during the early stages of the epidemic and then vaccinating other household members, can reduce the spread of the disease. In practice, it is not easy to detect a person immediately when she/he gets infected. The time from the point at which a person is infected (and hence infectious) to the point at which she gets detected and other household members become vaccinated is here referred to as the delay time, and will be denoted S. We assume that a perfect vaccine is available and the strategy is that, each infected individual is detected while infectious at rate θ. As a consequence, the detection time S is exponentially distributed with mean $1/\theta$ ($S \sim \text{Exp}(\theta)$). Once this infectious person is detected, all other household members are vaccinated at the same time. We assume that susceptibles who are vaccinated have full protection from further infection and that vaccination has no effect on already infected (infectious or removed) individuals. We also assume that if the detection of an infectious individual occurs, then further spreading in the household is stopped (which can be achieved either by isolation of the household, vaccination, quarantine, restricted movement of the household members or some other method). From now on we use *vaccination* but the meaning could vary.

3.1 Force of infection and reproduction number for equal households sizes

Because the detected individual is unable to make global contacts, then its infectious period consists of two parts: the active infectious period, a length of time during which a person remains infectious before detection, and inactive infectious period, the length of time the person is still infectious after detection while other household members are vaccinated. We now consider a single household epidemic, and only the active infectious period is of interest. The sum of active infectious periods of all individuals who are infected in that household forms the active force of infection of the epidemic, (sometimes referred to as active severity as in Ball *et al.*, 2007, Section 2.2). Let T be the sum of active infectious periods of all individuals who get infected in that household (*i.e.* the active force of infection). Because infectious individuals make global contacts at rate λ_c during their active periods, the total number of global contacts emanating from that single household conditional on T is also a Poisson random variable with mean $\lambda_c T$. The mean number of individuals who get infected in the community by a single household epidemic (*i.e.* the reproduction number) is hence given by

$$R_\theta = \lambda_c E(T)$$

where $E(T)$ is the expected active force of infection (severity) from a household. Now, the task that remains is to compute $E(T)$, because the reproduction number R_θ depends on this mean.

By assumption, the infectious period I and delay time S are independent and exponentially distributed with means $1/\gamma$ and $1/\theta$, respectively, and the active infectious period is the smallest of the two. At any instant during an isolated household epidemic, three events compete: either an infectious individual infects another person in the household, or an infectious individual gets detected and all other household members are vaccinated, or an infectious person recovers from the disease and becomes removed. The competing events and their respective transition rates are given in Table 1. The transition from (s,i) to $(s,0)$ after detection implies that those who are still susceptible cannot get infected, thus sort of misusing the letter "s".

Consider a household of size k, which initially consists of i infectious individuals and $s = k-i$ susceptible individuals. Because the transitions between states (infection, detection or removal) follow a Markov process, we then look into different routes for which an outbreak can occur, and for each such route, we compute the expected active force of infection. Figure 1 shows such possible routes of the disease dynamics for the households of sizes $k = 2$ and $k = 3$, each time starting with one infectious individual (that is $(s,i) = (1,1)$ and $(2,1)$, respectively). Let $\mu_{s,i} = E(T|X(0) = s,\ Y(0) = i)$ be the expected active force of infection conditioned on the numbers of susceptible individuals $X(0) = s$ and the infectious individuals $Y(0) = i$ at the initial stage (time $t = 0$) of the epidemic. For $\mu_{s,i}$, $i = 1, 2, \ldots, s + i \leq k$, and using possible jumps of the states of the Markov process, we are now in a position to compute the expected active force of infection for a given household (see Fig. 1).

Table 1 Transitions and rates of competing events in a household epidemic.

Event	Transition	Rates
Infection	$(s, i) \to (s-1, i+1)$	$\lambda_h is$
Detection	$(s, i) \to (s, 0)$	θi
Removal	$(s, i) \to (s, i-1)$	γi

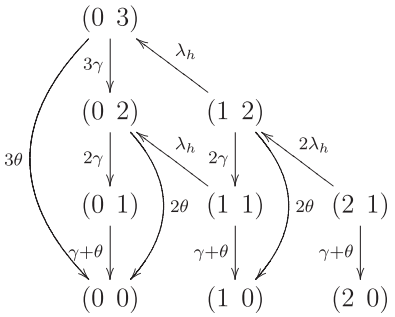

Figure 1 Schematic graph of the dynamics in our approximating SIR Markov jump process for households of size $k = 2$ and $k = 3$, where each vertex represents (number of susceptible individuals, number of infectious individuals).

For instance, consider $(s,i) = (0,1)$ (that is a household consisting of one single infected individual), then it follows immediately from Fig. 1 that $\mu_{0,1} = 1/\gamma + \theta$, because the person may only be removed or detected. Similarly, for $(s,i) = (1,1)$ (a household of size 2 including an initially infectious individual), the expected force of infection becomes

$$\mu_{1,1} = \frac{1}{\lambda_h + \gamma + \theta} + \frac{\lambda_h}{\lambda_h + \gamma + \theta}\mu_{0,2} \tag{4}$$

and

$$\mu_{0,2} = \frac{1}{\gamma + \theta} + \frac{\gamma}{\gamma + \theta}\mu_{0,1}$$

where $\mu_{0,1}$ is as given in Section 3.1. Thus, inserting $\mu_{0,2}$ in Eq. (4), $\mu_{1,1}$ then equals

$$\mu_{1,1} = \frac{1}{\lambda_h + \gamma + \theta} + \frac{\lambda_h}{\lambda_h + \gamma + \theta} \cdot \frac{2\gamma + \theta}{(\gamma + \theta)^2}.$$

In general, given that initially the household consists of s susceptible individuals and i infectious individuals, the expected active force of infection is given by

$$\mu_{s,i} = i \cdot \frac{1}{is\lambda_h + i\gamma + i\theta} + \frac{is\lambda_h}{is\lambda_h + i\gamma + i\theta}\mu_{s-1,i+1} + \frac{i\gamma}{is\lambda_h + i\gamma + i\theta}\mu_{s,i-1}. \tag{5}$$

(Note that i cancels out in all terms). We describe briefly the right hand terms of Eq. (5). The first ratio is the mean time to make a jump: the rate of any jump is equal to its denominator. During the time before the jump, i individuals contribute to the active force of infectious period T. The quantity which is multiplied by $\mu_{s-1,i+1}$ in the middle term is the probability to jump to state $(s-1, i+1)$, whereas the last term contains $\mu_{s,i-1}$ and the probability to jump to state $(s,i-1)$. The third type of jump (detection) gives no further contribution to T. We see that Eq. (5) is a recursive formula, implying that in order to compute $\mu_{s,i}$, one must first compute $\mu_{s-1,i+1}$ and $\mu_{s,i-1}$. Note that, for $s \geq 0$, $\mu_{s,0} = 0$ (*i.e.* absorbing states in Markov process) if the process jumps to $(s,0)$ because there is no more infectious force. Here, we consider a household of size k including one initially infectious person and $k-1$ susceptible individuals (*i.e.* $(s,i) = (k-1,1)$). Thus, Eq. (5) becomes

$$\mu_{k-1,1} = \frac{1}{(k-1)\lambda_h + \gamma + \theta} + \frac{(k-1)\lambda_h}{(k-1)\lambda_h + \gamma + \theta}\mu_{k-2,2} + \frac{\gamma}{(k-1)\lambda_h + \gamma + \theta}\mu_{k-1,0}. \tag{6}$$

But $\mu_{k-1,0} = 0$, implying that (6) reduces to

$$\mu_{k-1,1} = \frac{1}{(k-1)\lambda_h + \gamma + \theta} + \frac{(k-1)\lambda_h}{(k-1)\lambda_h + \gamma + \theta}\mu_{k-2,2}.$$

showing that we need to compute $\mu_{k-2,2}$ and $\mu_{k-1,0}$ in order to calculate $\mu_{k-1,1}$ (and this also done using Eq. (5)). Now that we have derived the expected force of infection $\mu_{k-1,1} = E(T|k-1,1)$, the reproduction number R_θ is hence given by

$$R_\theta = \lambda_c E(T) = \lambda_c \mu_{k-1,1} \tag{7}$$

which can be solved numerically in order to determine the effect of the detection parameter θ, on the dynamics of the disease.

3.2 Reproduction number for households of different sizes

In this section, we investigate the performance of the vaccination strategy in a large community of households of varying sizes, with the motivation that we now know the form of the reproduction number (see Eq. (7)) for equal size households. Recall that $\tilde{\pi}_k$ is the probability that a randomly chosen individual resides in a household of size k (Section 2.3), and $\mu_{k-1,1}$ is the expected infection force from a household epidemic initiated by one infectious individual in such a household. If the globally contacted individual belongs to a household of size k, then the mean outbreak is equal to $\lambda_c\mu_{k-1,1}$. Hence, the reproduction number is given by

$$R_\theta = \sum_{k=1}^{k_{\max}} \lambda_c \tilde{\pi}_k \mu_{k-1,1} \tag{8}$$

which is used in Section 4 to give a numerical example to assess the effectiveness of the vaccination strategy.

4 Application to Potential Influenza Outbreaks in Sweden and Tanzania

We now illustrate numerically the performance of the vaccination strategy for pandemic influenza using Eq. (8). That is, given disease and community parameter values, we illustrate how the reproduction number R_θ is affected by the detection rate θ. As model parameters, we use estimates from previous investigations for disease transmission within and between households in a population infected by influenza. Several studies have estimated from data the parameters required to compute the household reproduction number for influenza (*e.g.* Longini *et al.*, 1982; Cauchemez *et al.*, 2004; Ferguson *et al.*, 2006).

We use parameter estimates which are derived from Fraser (2007) for the French influenza. Because our model is somewhat different from the model of Fraser, the results should be interpreted with caution. The model assumes that all individuals are equally susceptible, and infectious in case of getting infected. This is a simplification but still reasonable for modelling pandemic influenza, because there is then no or little pre-immunity. In Fraser's study, the mean infectious period of an individual is 2.85 days, implying that the removal rate is $\gamma = 1/2.85 = 0.351$. The mean household size in the community of interest is 2.38. The estimate of the within household transmission parameter from Fraser's study is $1.35/k$, where k is the household size. This parameter is an accumulated infection force over the whole infectious period, and it is similar to our $\lambda_h E(I)$ (though not exactly). This means that $\lambda_h = 1.35/kE(I)$. Then we replace k by the mean household size (2.38), yielding $\lambda_h = 0.199$, because our model assumes that all individuals have the same local contact rate irrespective of household size. Fraser's estimate of the mean number of people an individual infects outside the household (*i.e.* the out of household reproduction number) is $R_c = 1.21$. This is equivalent to $R_c = \lambda_c E(I)$, implying that $\lambda_c = R_c/E(I) = 0.425$. These parameter values, $1/\gamma = 2.85$, $\lambda_h = 0.199$ and $\lambda_c = 0.425$, will be used in Figure 2, Section 4 when estimating R_θ as a function of θ for two different communities. We also make a sensitivity analysis to see how sensitive R_θ is to uncertainty in model parameters. Unfortunately, the parameter estimates in Fraser (2007) are not equipped with standard errors, and to derive such standard errors is a research topic in its own right. Instead our sensitivity analysis is performed by modifying each parameter (λ_h, λ_c and $1/\gamma$) by 10% up and down from the estimates mentioned in Section 4, and for each combination we compute R_0 for the community of interest.

We compare the effectiveness of the vaccination strategy by using household size distributions from Sweden (taken from Statistical Yearbook of Sweden 2007, Table 78, page 99), and Tanzania (taken from the Analytical Report of the National Bureau of Statistics 2000/2001, Chapter 10, page 123). The data of household size distributions for Sweden and Tanzania are shown in Table 2.

Table 2 Household size distributions for Tanzania and Sweden.

No. of persons in household	Tanzania	Sweden
1	0.064	0.5830
2	0.079	0.2703
3	0.103	0.0592
4	0.129	0.0611
5	0.148	0.0264
6	0.130	
7	0.109	
8	0.089	
9	0.060	
10	0.089	

Table 3 R_0 values for different parameter combinations.

λ_h	λ_c	$1/\gamma$	R_0 (Sweden)	R_0 (Tanzania)
0.179	0.383	2.565	1.85	5.82
0.179	0.383	3.135	1.45	4.32
0.179	0.467	2.565	2.31	7.12
0.179	0.467	3.135	1.89	5.43
0.219	0.383	2.565	2.15	6.21
0.219	0.383	3.135	1.53	4.84
0.219	0.467	2.565	2.42	7.50
0.219	0.467	3.135	1.95	5.91

The Swedish household size is truncated at size 5 and that from Tanzania is truncated at size 10, and we simplify by assuming that all households of sizes 5 or greater and 10 or greater have sizes exactly 5 and 10, respectively. This implies that 2.64% of Swedish households have size 5, and 8.9% of Tanzania households have size 10. The average household sizes for Sweden and Tanzania are 3.2 and 5.7, respectively.

Now inserting the previously obtained values of λ_h, λ_c and γ, together with the two countries' household distributions, and using Eq. (3), gives the R_0 estimates 1.95 for Sweden and 5.92 for Tanzania. In Table 3, we have plotted the corresponding R_0 estimates when varying the three model parameters by a factor 10% as described in Section 4.

From the table, we clearly see that uncertainty in the three parameters clearly induce uncertainty in R_0. The smallest R_0 value is for the case where the two infectious forces λ_h and λ_c, and the mean infectious period $1/\gamma$, all are 10% smaller than the estimates based on Fraser (2007). For this scenario, the R_0 values are 1.45 and 4.32 for Sweden and Tanzania, respectively. The largest R_0 values are for the case where the three parameters all are 10% *larger* than the points estimates based on Fraser (2007). For this case, the corresponding R_0 values are 2.42 and 7.50, respectively. To conclude, varying all parameter estimates $\pm 10\%$ make the R_0 values lie in the intervals (1.45,2.42) and (4.32,7.50) for Sweden and Tanzania, respectively. We have not taken uncertainty in the household size distribution into account. The reason why not is that we believe this uncertainty is of smaller magnitude than uncertainty in model parameters for the disease dynamics.

We now study effects of vaccination with delay, and in particular, study how the reproduction number R_θ depends on the detection intensity θ (recall that higher θ means that infectious people are detected quicker with the effect that friends are vaccinated). In Fig. 2 we have plotted R_θ as a function of θ, where we use the same parameter estimates as before, for Sweden and Tanzania. The solid lines correspond to the point estimates of the parameters (and R_0) and the dashed upper and lower curves are computed for the upper and lower bounds discussed in the previous paragraph (note for instance that the lower and upper curves for Sweden start in $R_0 = 1.45$ and $R_0 = 2.42$, respectively).

The point estimate of the critical detection rate θ_c say (for which $R_\theta = 1$), for Sweden is approximately 0.20 and for Tanzania is about 0.30 (see Fig. 2). This means that it is necessary to detect individuals after $1/0.20 = 5$ days (on average) to surely prevent a major outbreak in Sweden.

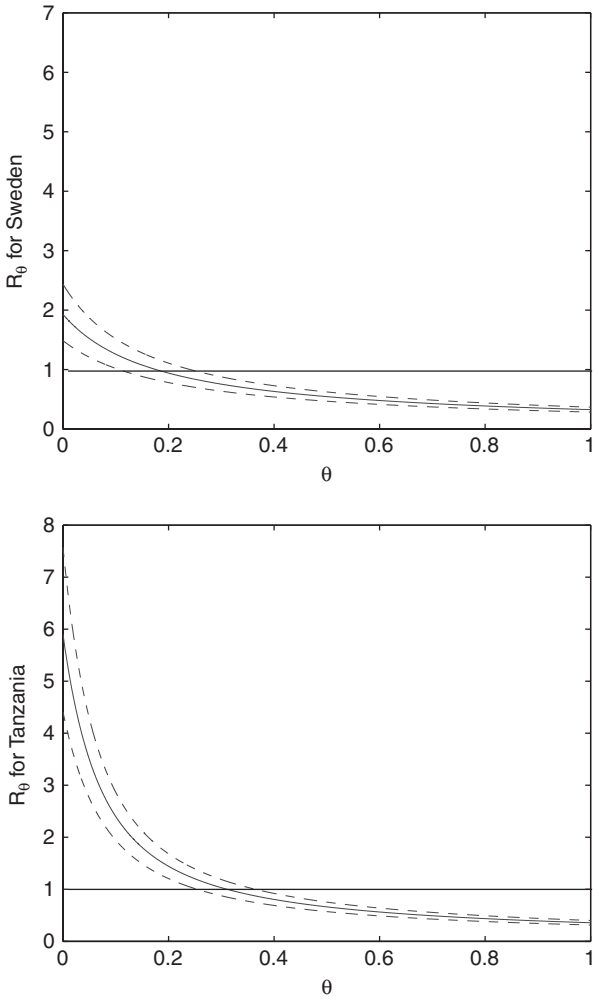

Figure 2 The reproduction number R_θ as a function of the detection rate θ for household distributions from Sweden (above) and Tanzania (below). Solid lines give point estimates and dashed lines sensitivity bounds (see text for further comments).

The corresponding number for Tanzania having larger households (assuming the same transmission parameters) is $1/0.30 \approx 3.3$ days. We note that the difference in R_0 between Tanzania and Sweden is quite large but the difference in the critical detection rates between the two countries is moderate (approximately 1.7 days). Using the sensitivity bounds for the curve R_θ also gives bounds on θ_c: where the lower and upper curves intersect $y = 1$. The result is that a sensitivity interval for θ_c equals (0.16,0.28) for Sweden and (0.26,0.38) for Tanzania, corresponding to (3.6,6.2) days for Sweden and (2.6,3.8) days for Tanzania.

5 Discussion

We have studied the effects of early stage vaccination for an SIR epidemic among a community of households. Vaccination of household members takes place after the detection of an infectious individual in the household. The reproduction numbers for this vaccination strategy were derived for the case of equal and unequal household sizes. The usefulness of the strategy was assessed numerically by using some estimated transmission parameters (local and global contact rates) from the study of influenza data (Fraser, 2007).

The models we developed here are not fully realistic, but we believe that they can capture some relevant properties also valid in more complex household models. For instance, to make the model more realistic, the household can be extended to incorporate individuals of different types (Becker and Dietz, 1995; Becker and Hall, 1996), assuming that disease transmission depends on the type of individuals. For example, it would be interesting to investigate the performance of the vaccination strategy in the community of households made up of individuals of varying infectivity and susceptibility to the disease. Other interesting extensions would be to consider a general distribution for the infectious period and delay time, and to derive the probability of a major outbreak and the outbreak size in case of such an outbreak.

The most obvious continuation of the present paper is however to include a latent period on top of allowing different distributions for infectious periods and delay times. Our model assumes that the "*per* individual" transmission rate within households is independent of household sizes. It would also be important to consider the effects of the dependence of "*per* person" transmission rate on the household size (see *e.g.* Fraser, 2007).

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Conflict of Interests Statement
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