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Reproduction numbers for epidemic models with households and other social structures II: comparisons and implications for vaccination

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Abstract

In this paper we consider epidemic models of directly transmissible SIR (susceptible $\rightarrow$ infective $\rightarrow$ recovered) and SEIR (with an additional latent class) infections in fully-susceptible populations with a social structure, consisting either of households or of households and workplaces. We review most reproduction numbers defined in the literature for these models, including the basic reproduction number R_0 introduced in the companion paper of this, for which we provide a simpler, more elegant derivation. Extending previous work, we provide a complete overview of the inequalities among these reproduction numbers and resolve some open questions. Special focus is put on the exponential-growth-associated reproduction number R_r, which is loosely defined as the estimate of R_0 based on the observed exponential growth of an emerging epidemic obtained when the social structure is ignored. We show that for the vast majority of the models considered in the literature $R_r \geq R_0$ when $R_0 \geq 1$ and $R_r \leq R_0$ when $R_0 \leq 1$. We show that, in contrast to models without social structure, vaccination of a fraction $1-1/R_0$ of the population, chosen uniformly at random, with a perfect vaccine is usually insufficient to prevent large epidemics. In addition, we provide significantly sharper bounds than the existing ones for bracketing the critical vaccination coverage between two analytically tractable quantities, which we illustrate by means of extensive numerical examples.

1 Introduction

The basic reproduction number R_0 is arguably the most important epidemiological parameter because of its clear biological interpretation and its properties: in the simplest epidemic

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models, where individuals are all identical, mix homogeneously, the population is large and the initial number of infectives is small, (i) a large epidemic is possible if and only if $R_0 > 1$ (threshold property), (ii) when $R_0 > 1$, vaccinating a fraction $1 - 1/R_0$ of individuals chosen uniformly at random – or, equivalently, isolating the same fraction of infected individuals before they have the chance to transmit further – is sufficient to prevent a large outbreak (critical vaccination coverage) and (iii) the fraction of the population infected by a large epidemic depends only on R_0. The definition of R_0 is straightforward in single-type homogeneously mixing models and has been successfully extended to multitype models (see Diekmann et al. [9], Chapter 7).

In our earlier paper, we showed how to extend the definition of R_0 to many models with a social structure, namely the households models and certain types of network-households and households-workplaces models (Pellis et al. [22]). The extension proposed there aims at preserving both the biological interpretation of R_0 as the average number of cases a typical individual generates early on in the epidemic and its threshold property. However, already in the case of multitype populations the simple relationship between R_0 and the epidemic final size no longer holds. In this paper we show that, for models involving mixing in small groups, also the simple relationship between R_0 and the critical vaccination coverage breaks down. In particular, we find that vaccinating a fraction $1-1/R_0$ of the population is generally insufficient to prevent a major outbreak. This result stems from a series of inequalities which extend the work done by Goldstein et al. [11], and leads to sharper bounds for the critical vaccination coverage than previously available.

The definition of R_0 given in [22] may be described briefly for an SIR (susceptible $\rightarrow$ infective $\rightarrow$ recovered) epidemic in a closed population as follows. Consider the epidemic graph (see [22], Section 1, and Section 2.1 of this paper), in which vertices correspond to individuals in the population and for any ordered pair of distinct individuals, (i, i') say, there is a directed edge from i to i' if and only if i, if infected, makes at least one infectious contact with i' (see Figure 1). Suppose that initially there is one infective and the remainder of the population is susceptible. The initial infective is said to belong to generation 0 (say, individual 0 in Figure 1). Any other individual, i say, becomes infected if and only if in the epidemic graph there is a chain of directed edges from the initial infective to individual i, and in that case the generation of i is defined to be the number of edges in the shortest such chain. Thus, generation 1 consists of those individuals with whom the initial infective has at least one infectious contact (individuals 1 and 2 in Figure 1), generation 2 consists of those individuals that are contacted by at least one generation-1 infective but not by the initial infective (individuals 4 and 5 in Figure 1) and so on. For $k = 0, 1, \cdots$, let $X_k^{(N)}$ denote the the number of generation-k infectives, where N denotes the population size. Thus, in Figure 1, $X_0^{(6)} = 1$, $X_1^{(6)} = 2$, $X_2^{(6)} = 2$, $X_3^{(6)} = 1$ and $X_k^{(6)} = 0$ for $k \geq 4$. Then R_0 is defined by

$$R_0 = \lim_{k\to\infty} \lim_{N\to\infty} \left(\mathbb{E}\left[X_k^{(N)} \right] \right)^{1/k}, \tag{1}$$

i.e. by the limit, as the population size tends to infinity, of the asymptotic geometric growth rate of the mean generation size [22].

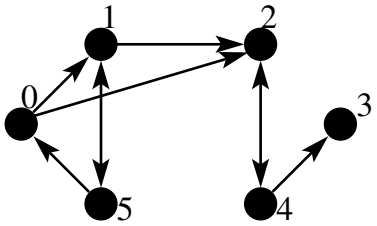

Figure 1: Example of epidemic graph in a population of size $N = 6$.

For single- and multi-type unstructured populations the value of R_0 obtained using (1) coincides with that obtained using the usual definition as "the expected number of secondary cases produced by a typical infected individual during its entire infectious period in a population consisting of susceptibles only" (see Heesterbeek and Dietz [14]). (Note that, for fixed k, as $N \to \infty$ the epidemic process converges to a Galton-Watson branching process, i.e. we consider a linear approximation of the early phase of the epidemic.) However, unlike the usual definition of R_0, definition (1) extends naturally to models with small mixing groups, such as the households and households-workplaces models. In Pellis et al. [22], R_0 for these two models was obtained by exploiting difference equations describing variables related to the mean generation sizes. In the present paper, we show that R_0 for these models may be obtained more easily from the discrete-time Lotka-Euler equation (cf. Equation (5)) that describes the asymptotic (Malthusian) geometric growth rate of the mean population size of an associated branching process, which approximates the early phase of the epidemic.

Note that the construction of the epidemic graph, and therefore most of the work of [22] and of this paper is based on the assumption that the behaviour of any infected individual can be decided before the epidemic starts. This is a common assumption in epidemic modelling, but it is quite a restrictive one. As noted by Pellis et al. [19], this condition is violated when the infectious behaviour of an individual depends on the time when he/she is infected (for example, if the number of other infectives at the time of infection matters or if a control policy is implemented at a certain time) and, in multi-type populations, on the type of the infector. Theoretically, (1) and all results in this paper require only that the epidemic admits a description in terms of generations of infection, which seems biologically plausible for most epidemic models. However, analytical progress is limited without invoking the assumption above.

In Section 2 we study reproduction numbers for the households model in great detail: in Sections 2.1 and 2.2, we introduce the households model and provide a simpler, more elegant derivation of the basic reproduction number R_0 than that presented in Pellis et al. [22]; we then review the vast majority of the reproduction numbers defined in the literature for the households model in the remainder of Section 2 and we formulate our main results in Theorems 1 and 2 in Section 3, where virtually all comparisons are carefully examined and new, sharper bounds on the critical vaccination coverage are obtained. For ease of reference, Table 1 collects all the households reproduction numbers with a reference to where they are discussed, and Table 2 summarises known and novel results, again with appropriate

references. In Sections 4 and 5 we define and compare reproduction numbers for models with households and workspaces. Here we again provide a new and simpler derivation of R_0 than in [22]. Reproduction numbers are collected in Table 3 and the inequalities among them are reported in Theorem 3 and in the extension of Theorem 2 to the households-workplaces model. Extensive numerical illustrations are presented in Section 6, while in Section 7 we provide the proofs of the comparisons presented in Sections 3 and 5. Section 8 is devoted to comments and conclusions. We summarise the main notation used in the paper in Table 4.

Table 1: Reproduction numbers for the **households** model (analogues of R_0, R_*, R_I, R_V, R_{HI}, R_2, $\hat{R}_{HI}$ and $\hat{R}_2$ are considered also for the network-households model).

Symbol	Meaning	Section
R_0	Basic reproduction number (by default, based on rank generation numbers)	2.2
R_*	Household reproduction number	2.3
R_I	Individual reproduction number	2.4
R_{HI}	Individual reproduction number	2.5
$\hat{R}_{HI}$, $\bar{R}_{HI}$	Variants of R_{HI} from [11] ($\bar{R}_{HI}$ is *not* a threshold parameter)	2.5
R_2	Individual reproduction number	2.6
$\hat{R}_2$	Variant of R_2 from [7]	2.6
R_V	Perfect vaccine-associated reproduction number	2.7
R_{VL}	Leaky vaccine-associated reproduction number	2.7
R_r	Exponential-growth-associated reproduction number	2.8
$\widetilde{R}_r$	Variant of R_r	2.8
R_0^{r}	Basic reproduction number based on rank generation numbers	2.1, 3.1.3
R_0^{g}	Basic reproduction number based on true generation numbers	2.1, 3.1.3
R_A, R_B	Generic reproduction numbers	3.1.3

Table 2: Existing, newly proved and conjectured inequalities.

Result for growing epidemics	Reference
$R_* > R_I \geq R_V \geq R_0$ ($\geq R_2$, conjecture) $> R_{HI} > 1$	Thm 1 & App A
$R_I \geq R_2 > R_{HI} > 1$	Thm 1
$\hat{R}_{HI} \geq \bar{R}_{HI}$ ($\bar{R}_{HI}$ *not* a threshold parameter)	Eq A4.1 of [11]
$R_{HI} \geq \bar{R}_{HI}$	App C
$\hat{R}_{HI} \geq R_{HI}$, but $\hat{R}_{HI}$ and R_0 cannot be ordered	App C
$R_0^{\mathrm{r}} \geq R_0^{\mathrm{g}}$	Sec 3.1.3
$R_* > R_{VL} \geq R_V \geq \bar{R}_{HI}$, but R_{VL} and R_I cannot be ordered	Thm 1 of [11] & App B
$R_* \geq R_r$	Thm 1 of [11]
$R_r \geq R_0$ in most commonly used models, but not in general	Thm 2
$R_r \geq \widetilde{R}_r \geq R_0$ in important special cases, but not in general	Thm 2
R_r and R_{VL} cannot be ordered	App E
R_r and R_V cannot be ordered	Sec 6.2
R_r (or $\widetilde{R}_r$) and R_I cannot be ordered	Sec 6.1
Result for declining epidemics	**Reference**
$R_* < R_I \leq R_0 \ \leq$ (conjecture) $R_2 < R_{HI} < 1$	Thm 1 & App A
$\hat{R}_{HI} \geq \bar{R}_{HI}$	Eq A4.1 of [11]
$R_{HI} \geq \bar{R}_{HI}$	App C
$\bar{R}_{HI} \leq \hat{R}_{HI} \leq R_{HI} < 1$, but $\bar{R}_{HI}$ and $\hat{R}_{HI}$ cannot be ordered with R_0	App C
$R_* \leq R_r$	Sec 3.2
$R_r \leq R_0$ in most commonly used models, but not in general	Thm 2
$R_r \leq \widetilde{R}_r \leq R_0$ in important special cases, but not in general	Thm 2

Table 3: Reproduction numbers for the **households-workplaces** model.

Symbol	Meaning	Section
R_0	Basic reproduction number (by default, based on rank generation numbers)	4.2
R_*	Clump reproduction number	4.3
R_H	Household-household reproduction number	4.4
R_W	Workplace-workplace reproduction number	4.4
R_I	Individual reproduction number	4.5
R_V	Perfect vaccine-associated reproduction number	4.6
R_{VL}	Leaky vaccine-associated reproduction number	4.6
R_r	Exponential-growth-associated reproduction number	4.7
$\widetilde{R}_r$	Approximation of R_r	4.7

Table 4: Main symbols used in the paper, with reference to their first occurrence.

Symbol	Meaning	Section
$a^{(n)}$	$= \mu_H^{(n)} / \left(1 + \mu_H^{(n)}\right)$ (construction of R_{HI})	2.5
a	$= \max\left(a^{(n)} : n = 1, 2, \cdots, n_H\right)$ (construction of R_{HI})	2.5
b	Mean number of secondary cases attributed to other secondary cases (construction of R_2)	2.6
$\mathcal{D}^{\mathcal{C}}$	Complement of event $\mathcal{D}$	7.1
$\mathbb{E}_X$	Expectation with respect to random variable X	1
$\mathcal{E}$	Vaccine efficacy	2.7
$\mathcal{E}_C$	Critical vaccine efficacy	2.7
$g_A(\lambda)$	Characteristic equation (discrete Lotka-Euler equation) derived from M_A defining reproduction number R_A	Throughout
H, W	Subscripts/superscripts referring to household or workplace	Throughout
i, i'	Individuals' indices	1
$\{\mathcal{I}(t), t \geq 0\}$	Random infectivity profile	2.8
k	Generation index	1
$\mathcal{L}_f$	Laplace transform of non-negative function f, i.e. $\mathcal{L}_f(\theta) = \int_{-\infty}^{\infty} \mathrm{e}^{-\theta f(x)} \mathrm{d}x$	2.8
$\mathcal{M}_X$	Moment-generating function of random variable X, i.e. $\mathcal{M}_X(\theta) = \mathbb{E}\left[\mathrm{e}^{-\theta X}\right]$	2.8
M_A	Mean matrix associated with reproduction number R_A	Throughout
n	Household size index	2.1
n_H	Maximum household size	2.1
N	Total population size	1
$N_{ii'}$	Number of infectious contacts from i to i' between the infection and the recovery of i (Perhaps delete this one)	7.2
p_C	Critical vaccination coverage	2.7
r	Real-time growth rate, i.e. Malthusian parameter for the epidemic growth	2.8
R_A	Reproduction number associated with construction process A	Throughout
T_i	Time of infection of i	7.2
T_E	Duration of latency period in SEIR model	6.1
T_I	Duration of infectious period in SIR and SEIR models	2.8
W_G	Random variable describing the time of an infectious contact between two individuals (since infection of the infector)	2.8
w_G	Probability density function of W_G, also called generation-time distribution	2.8

$\widetilde{W}_G$	Random variable describing the time of the first infectious contact between two individuals (since infection of the infector), assuming at least one occurs	2.8
Y_k	Number of infected cases in generation k of a (randomised) Reed-Frost model	7.1
α	Shape parameter of the gamma distribution	6.2
$\beta_H(t)$	Mean rate at which global infections emanate from a household	2.8
δ	Rate of progressing from latent to infectious state in SEIR model	6.1
γ	Recovery rate for SIR and SEIR models when T_I is exponentially distributed; also, scale parameter of the gamma distribution	2.8
λ_G	Multiplicative coefficient affecting rate at which each infective makes infectious contacts in the population at large	2.8
λ_H	Multiplicative coefficient affecting the rate at which each infective makes infectious contacts to any specified susceptible within household	2.8
μ_G	Mean number of global contacts made by a typical infective	2.1
μ_H	Mean size of a within-household epidemic	2.1
μ_k	Mean number of cases in generation k of a within-household epidemic ($\mu_0 = 1$ always)	2.1
$\mu_H^{(n)}, \mu_k^{(n)}$	Mean size of a within-household epidemic, or of generation k in such epidemic, in a household of size n	2.1
π_n	Probability that the household of an individual selected uniformly at random has size n (size-biased distribution)	2.1
$\mathbb{1}_{\mathcal{D}}$	Indicator function, with value 1 if $\mathcal{D}$ occurs and 0 otherwise	3.2
$\overset{st}{\leq}$	Stochastically smaller	3.1.3
$\overset{n}{\leq}$	Inequality, which is strict only if at least one household or workplace has size larger than n and is an equality if all households and workplaces have size $\leq n$	7.1
$\overset{D}{=}$	Equal in distribution	App F

2 Households model and reproduction numbers

2.1 Model and generations of infections

In this section we outline the definition of the households model, giving sufficient detail so that R_0 can be calculated. The salient features for this purpose are that the population is partitioned into households and that infectives make two types of infectious contacts, *local* contacts with individuals in the same households and *global* contacts with individuals chosen uniformly at random from the entire population. The expected number of global contacts made by a typical infective during his/her infectious period is assumed to be μ_G and is the same for all infectives. The precise detail of local transmission is not required in order to define R_0, as long as we can compute the generations of infection in the *local* epidemic (i.e. in the within-household epidemic obtained if all *global* contacts are ignored). We show now how this may be done.

Consider a local epidemic in a household of size n, with 1 initial infective, labelled 0, and $n-1$ initial susceptibles, labelled $1, 2, \cdots, n-1$ (See Figure 1). For $i = 0, 1, \cdots, n-1$, construct a list of whom individual i would attempt to infect in the household if i were to become infected. Then construct a directed graph, $\mathcal{G}^{(n)}$ say, with vertices labelled $0, 1, \cdots, n-1$, in which for any ordered pair of distinct vertices (i, i'), there is a directed edge from i to i' if and only if individual i' is in individual i's list of attempted infections. The initial infective, i.e. individual 0, is said to have (household) generation 0. Those individuals who are in individual 0's list (i.e. individuals 1 and 2 in Figure 1) are said to have generation 1. Those individuals who are not in generations 0 or 1 but who are in a generation-1 infective's list (i.e. individuals 4 and 5 in Figure 1) have generation 2, and so on. The set of people ultimately infected by the epidemic comprises those individuals in $\mathcal{G}^{(n)}$ that have a chain of directed edges leading to them from individual 0, and the generation number of such an infected individual, i say, is the length of the shortest chain joining 0 to i, where the length of a chain is the number of edges in it. Following Ludwig [17], we call these generation numbers *rank* generation numbers.

The rank generations of infectives may not correspond to real-time generations of infectives. The latter may be obtained by augmenting the graph $\mathcal{G}^{(n)}$, so that for each directed edge, $i \to i'$ say, in $\mathcal{G}^{(n)}$ there is a number $t_{ii'}$ giving the time elapsing between i's infection and time at which i first attempts to infect i'. Then the generation number of an individual, i say, that is infected in the single-household epidemic is the number of directed edges in the shortest chain joining 0 to i, where now the length of a chain is the sum of the $t_{ii'}$ of its directed edges. We call these generation numbers *true* generation numbers. As an example, suppose for the epidemic graph of Figure 1 that $t_{01} + t_{12} < t_{02}$, then the true generation of individual 2 is 2, instead of 1, which is his/her rank generation. For ease of exposition, unless stated explicitly otherwise, we assume rank generation numbers throughout this paper. This is in line with the choice of the definition of R_0 made in [22]. For further clarification, when both generation constructions are considered, as in Section 3.1.3, we refer to the rank-generation basic reproduction number by using R_0^{r}, as opposed to the basic reproduction number R_0^{g} which is obtained using the true generations. As explained

in [22], the reasons for the above choice are both analytical tractability and the fact that R_0^{r} depends (in addition to the household structure) only on the distribution of the total infectivity of an individual, and not on the particular shape of his/her infectivity profile (i.e. the distribution of the random development of the infectivity of an individual after he/she gets infected).

Consider a household of size n. For $k = 0, 1, \cdots, n-1$, let $\mu_k^{(n)}$ be the mean size of generation k in the above single-household epidemic. Thus $\mu_0^{(n)} = 1$ and $\mu_H^{(n)} = \mu_1^{(n)} + \mu_2^{(n)} + \cdots + \mu_{n-1}^{(n)}$ is the mean size of the epidemic, not including the initial case. (Note that $\mu_H^{(1)} = 0$.) If the population contains households of different sizes then we need to take appropriate averages of these quantities. Let n_H denote the size of the largest household in the population and, for $n = 1, 2, \cdots, n_H$, let p_n denote the proportion of households in the population that have size n. Then the probability that an individual chosen uniformly at random from the population resides in a household of size n is given by

$$\pi_n = \frac{np_n}{\sum_{j=1}^{n_H} jp_j} \qquad (n = 1, 2, \cdots, n_H). \tag{2}$$

Global contacts are made with individuals chosen uniformly at random from the population, so the mean generation sizes of a typical single-household epidemic are given by

$$\mu_k = \sum_{n=k+1}^{n_H} \pi_n \mu_k^{(n)} \qquad (k = 0, 1, \cdots, n_H - 1). \tag{3}$$

The mean size of a typical single-household epidemic, not including the initial infective, is then given by

$$\mu_H = \sum_{n=1}^{n_H} \pi_n \mu_H^{(n)} = \sum_{k=1}^{n_H - 1} \mu_k. \tag{4}$$

In what follows we assume that $\mu_G > 0$, otherwise the infection does not spread between households, and that $\mu_H > 0$ and $n_H \geq 2$, otherwise the model is homogeneously mixing.

2.2 The basic reproduction number R_0

Consider the branching process that approximates the early spread of the epidemic, in which each individual in the branching process represents an infected household and the time of its birth is given by the global generation of the corresponding household primary case in the epidemic process. (The global generation of an infective is its generation in the epidemic in the population at large. A household primary case is the first infected individual in the household and all other cases are called secondary.) See Figure 2 for a graphical representation. A typical, non-initial individual in this branching process (i.e. a household) reproduces only at ages $1, 2, \cdots$ and its mean number of offspring at age $k+1$ is ν_k, where $\nu_k = \mu_G \mu_k$ $(k = 0, 1, \cdots, n_H - 1)$ and $\nu_k = 0$ otherwise. The asymptotic (Malthusian) geometric growth rate of this branching process is given by the unique positive solution

of the discrete-time Lotka-Euler equation $\sum_{k=0}^{\infty} \nu_k/\lambda^{k+1} = 1$; see, for example, Haccou et al. [12], Section 3.3.1, adapted to the discrete-time setting. The above branching process may be augmented to include the local spread within each household, i.e. considering all individuals in Figure 2. Assume, as in Figure 2, that all households live up to age n_H, even if local epidemics finish earlier. (Note that this assumption does not alter the asymptotic geometric growth rate of the branching process.) Then, for $k \geq n_H$, the expected number of households in global generation k of the branching process is

$$\mu_G \left(x_{k-1} + x_{k-2} + \cdots + x_{k-n_H} \right),$$

where x_k denotes the the expected number of individuals in global generation k of the augmented process. Therefore, the asymptotic geometric growth rate of the total number of infectives in the augmented process is the same as that of the branching process[1], so the basic reproduction number R_0 for the above households model is given by the unique positive root of the function

$$g_0(\lambda) = 1 - \sum_{k=0}^{n_H-1} \frac{\nu_k}{\lambda^{k+1}} = 1 - \mu_G \sum_{k=0}^{n_H-1} \frac{\mu_k}{\lambda^{k+1}}, \tag{5}$$

yielding a simpler proof of Corollary 1 in [22]. For future reference, we note that

$$g_0(\lambda) = \sum_{n=1}^{n_H} \pi_n g_0^{(n)}(\lambda),$$

where

$$g_0^{(n)}(\lambda) = 1 - \mu_G \sum_{k=0}^{n-1} \frac{\mu_k^{(n)}}{\lambda^{k+1}}. \tag{6}$$

In the above we assume that all infected individuals make the same expected number of global contacts μ_G. This is the case for most households models that have appeared in the literature. One exception is the network-households model of Ball et al. [6, 7], in which the mean number of global contacts made by primary and secondary household infectives are $\tilde{\mu}_G$ and μ_G, respectively, where $\tilde{\mu}_G$ and μ_G may be unequal. Pellis et al. [22] show that R_0 for the network-households model is given by the unique positive root of g_0 but with $\nu_0 = \tilde{\mu}_G \mu_0$ (all other ν_k remain unchanged).

2.3 The household reproduction number R_*

The most commonly used reproduction number for the households model is given by the mean number of households infected by a typical infected household in an otherwise susceptible population. It is usually denoted by R_* and in our notation is given by

$$R_* = \mu_G(1 + \mu_H) = \sum_{k=0}^{n_H-1} \nu_k. \tag{7}$$

[1] A formal proof of this can easily be obtained using arguments similar to those in the proof of Lemma 3 of [2] (though note that the left-hand side of the second display after (3.15) should read $A_{n_H}^n$).

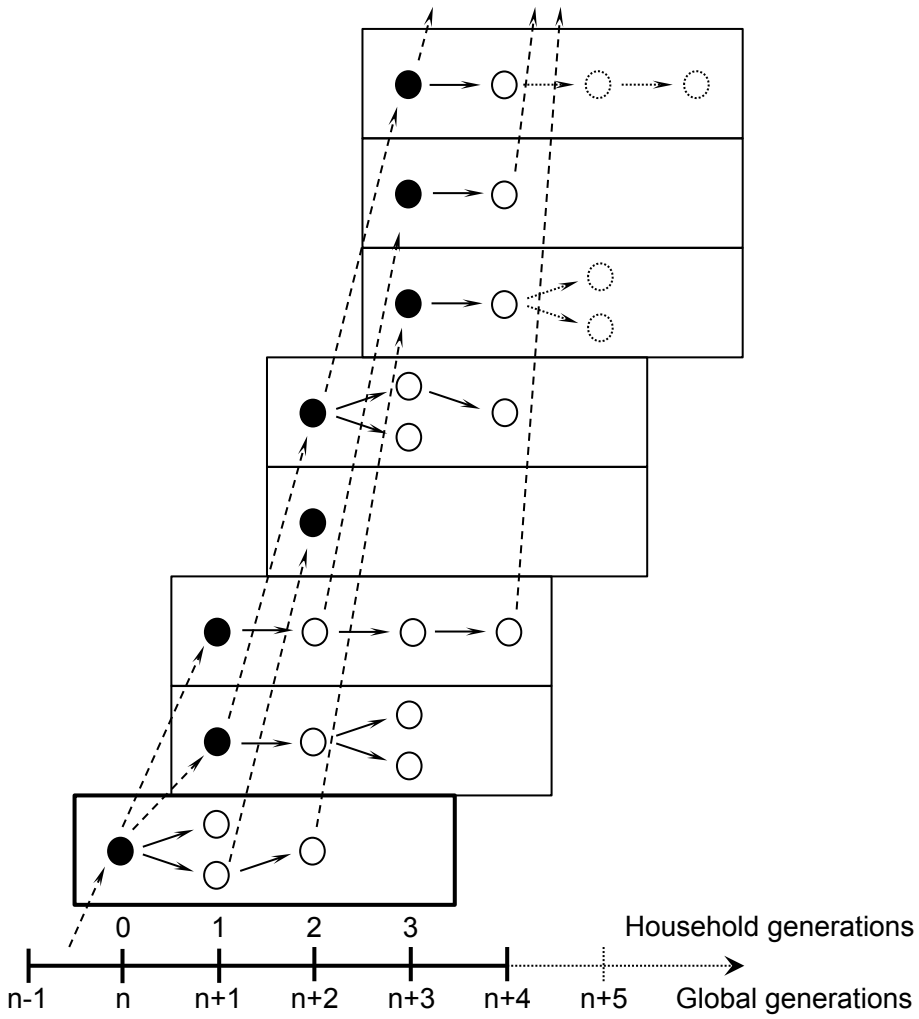

Figure 2: Graphical representation of the branching process construction used in the derivation of R_0, for a population of households of size 4. At global generation n, a specific household (thick borders) is infected, i.e. a global infection generates its primary case (black dot), who then starts a within-household epidemic driven by household infections (normal arrows). Household and global generations then proceed at the same pace, with both primary and secondary cases generating only new household primary cases through global contacts (dashed arrows). Note that all households have lifespans of 4 generations (the latest time, measured in generations, at which global contacts can be made given their size), even if the within-household epidemics are shorter.

The popularity of R_* stems largely from its ease of calculation and from the fact that, if $R_* > 1$, selecting a fraction $1 - 1/R_*$ of households uniformly at random and vaccinating all their members is enough to prevent an epidemic.

2.4 The individual reproduction number R_I

Several authors have proposed individual-based reproduction numbers for the households model. One approach (see, for example, Becker and Dietz [8] and Ball et al. [4]) is to attribute all secondary cases in a household to the primary case, leading to the reproduction number R_I given by the dominant eigenvalue of the next-generation matrix

$$M_I = \begin{bmatrix} \mu_G & \mu_H \\ \mu_G & 0 \end{bmatrix}.$$

It is easily verified that R_I is given by the unique solution in $(0, \infty)$ of $g_I(\lambda) = 0$, where

$$g_I(\lambda) = 1 - \frac{\mu_G}{\lambda} - \frac{\mu_H \mu_G}{\lambda^2}. \tag{8}$$

2.5 The individual reproduction number R_{HI}

Goldstein et al. [11] consider an individual reproduction number, which they denote by R_{HI}, and which represents "the expected number of secondary cases caused by an average individual from an average infected household, including those outside and inside the household" (see also Trapman [26]). Suppose first that all households have the same size. Then, in an "average" household epidemic, there are μ_H secondary cases caused by $\mu_H + 1$ infectives, leading to

$$R_{HI} = \mu_G + \frac{\mu_H}{1 + \mu_H}. \tag{9}$$

Goldstein et al. [11] also consider an extension of (9) to variable household sizes[2], defined by

$$\bar{R}_{HI} = \mu_G + \sum_{n=1}^{n_H} \pi_n \left(\frac{\mu_H^{(n)}}{1 + \mu_H^{(n)}} \right). \tag{10}$$

However, $\bar{R}_{HI}$ given by (10) is not necessarily a threshold parameter. For this reason, Goldstein et al. [11] proposed another extension of (9), defined by[3]

$$\hat{R}_{HI} = \mu_G + \frac{\mu_H}{1 + \mu_H}, \tag{11}$$

with μ_H as in (4), which is a threshold parameter. The advantages and disadvantages of $\bar{R}_{HI}$ and $\hat{R}_{HI}$ are discussed in [11]. The problem with $\bar{R}_{HI}$ is that it is not generally a threshold parameter. The problem with $\hat{R}_{HI}$ is that (unlike $\bar{R}_{HI}$) there exist household structures for which $\hat{R}_{HI}$ does not satisfy the general orderings of reproduction numbers proved in [11]. We renamed the original definitions because we now introduce a new definition of R_{HI} for populations of unequally sized households, which overcomes both these shortcomings and coincides with both $\bar{R}_{HI}$ and $\hat{R}_{HI}$ when all households have the same size.

[2] In [11], this extension is also denoted by R_{HI}.

[3] In [11], this is denoted by R'_{HI}.

Returning to the setting where all households have the same size, note that (9) assumes that each household member produces on average $a = \mu_H/(1+\mu_H)$ secondary cases within the household, so the mean generation sizes are given by $\eta_k = a^k$ $(k = 0, 1, \cdots)$ and, cf. (5), R_{HI} $(= \mu_G + a)$ is given by the unique root in (a, ∞) of the function

$$g_{HI}(\lambda) = 1 - \mu_G \sum_{k=0}^{\infty} \frac{\eta_k}{\lambda^{k+1}} = 1 - \frac{\mu_G}{\lambda - a}. \tag{12}$$

Using this approach, if the households are not all the same size, then the mean generation sizes are given by $\eta_k = \sum_{n=1}^{n_H} \pi_n \left(a^{(n)}\right)^k$ $(i = 0, 1, \cdots)$, where $a^{(n)} = \mu_H^{(n)}/(1+\mu_H^{(n)})$ for $(n = 1, 2, \cdots, n_H)$, which leads to the reproduction number R_{HI} given by the unique root in (a, ∞), where now $a = \max(a^{(n)} : n = 1, 2, \cdots, n_H)$, of the function

$$g_{HI}(\lambda) = 1 - \mu_G \sum_{k=0}^{\infty} \frac{\eta_k}{\lambda^{k+1}} = 1 - \mu_G \sum_{n=1}^{n_H} \frac{\pi_n}{\lambda - a^{(n)}} \qquad (\lambda > a). \tag{13}$$

2.6 The individual reproduction number R_2

A disadvantage of R_I is that every secondary case in a household is attributed to the primary case whereas in practice some should normally be attributed to other secondary cases. Suppose that all households have the same size, which is at least two. Ball et al. [7] consider a modification of R_I in which M_I is replaced by

$$M_2 = \begin{bmatrix} \mu_G & \mu_1 \\ \mu_G & b \end{bmatrix},$$

where $b = 1 - \mu_1/\mu_H$. Thus every secondary case produces on average b further secondary cases, with the value of b being chosen so that the within-household spread yields the correct expected final size, i.e. so that $\mu_H = \mu_1(1 + b + b^2 + \cdots) = \mu_1/(1-b)$. Note that R_2 satisfies $\hat{g}_2(R_2) = 0$, where

$$\hat{g}_2(\lambda) = 1 - \frac{\mu_G + b}{\lambda} + \frac{\mu_G(b - \mu_1)}{\lambda^2}. \tag{14}$$

At the end of the proof of Theorem 1 (see Section 7.3) we show that $b < \mu_1$. It then follows that R_2 is given by the unique root of $\hat{g}_2$ in $(0, \infty)$.

Observe that the above assumes that the mean generation sizes are given by $\upsilon_0 = 1$ and $\upsilon_k = \mu_1 b^{k-1}$ $(k = 1, 2, \cdots)$. It follows that R_2 is given by the unique root in (b, ∞) of the function

$$g_2(\lambda) = 1 - \mu_G \sum_{k=0}^{\infty} \frac{\upsilon_k}{\lambda^{k+1}} = 1 - \frac{\mu_G}{\lambda}\left(1 + \frac{\mu_1}{\lambda - b}\right). \tag{15}$$

(It is easily verified that $\hat{g}_2(\lambda) = \left(1 - \frac{b}{\lambda}\right) g_2(\lambda)$.)

If the households are not all the same size, we can define the mean generation sizes as $\upsilon_0 = 1$ and $\upsilon_k = \sum_{n=2}^{n_H} \pi_n \mu_1^{(n)} \left(b^{(n)}\right)^{k-1}$ $(k = 1, 2, \cdots)$, where $b^{(n)} = 1 - \mu_1^{(n)}/\mu_H^{(n)}$ for

$(n = 2, 3, \cdots, n_H)$. The reproduction number R_2 is then given, to be the unique root in (b, ∞) of the function

$$g_2(\lambda) = 1 - \mu_G \sum_{k=0}^{\infty} \frac{\upsilon_k}{\lambda^{k+1}} = 1 - \frac{\mu_G}{\lambda}\left(1 + \sum_{n=2}^{n_H} \pi_n \frac{\mu_1^{(n)}}{\lambda - b^{(n)}}\right), \tag{16}$$

where b is now given by $b = \max(b^{(n)} : n = 2, 3, \cdots, n_H)$. Note that (16) reduces to (15) when all households have the same size.

This extension of R_2 to unequal household sizes differs from that in [7], where R_2 is defined to be the dominant eigenvalue of M_2 above, with μ_1 and μ_H as in (3) and (4). We denote the latter by $\hat{R}_2$, as it is similar in spirit to $\hat{R}_{HI}$. We do not consider it further.

2.7 The perfect and leaky vaccine-associated reproduction numbers R_V and R_{VL}

Goldstein et al. [11] consider two vaccine-associated reproduction numbers, R_V and R_{VL}, corresponding to perfect and leaky vaccines, respectively. Suppose that the epidemic is above threshold, i.e. $R_* > 1$, and individuals are selected uniformly at random and vaccinated with a perfect (i.e. 100% effective) vaccine. Let p_C be the proportion of the population that has to be vaccinated to reduce R_* to 1. Then

$$R_V = 1/(1 - p_C). \tag{17}$$

Thus R_V is defined in such a way that the critical vaccination coverage is given by $1 - 1/R_V$, paralleling the usual formula for a homogeneously mixing epidemic, where, if $R_0 > 1$, the critical vaccination coverage is $1 - 1/R_0$. Goldstein et al. [11] also introduce in Section 7.2 of their paper a reproduction number R_{VA}, which approximates R_V. In our notation, R_{VA} is obtained by multiplying both μ_H and μ_G by $(1 - p)$ in (7), finding the critical vaccination coverage p_C that reduces R_* to 1, and then using (17) to obtain an approximation R_{VA} to R_V. It is easily checked that $R_{VA} = R_I$ (see the proof in Section 7.1 of $R_I \geq R_V$ in Theorem 1*(b)*[4]).

A leaky vaccine with efficacy $\mathcal{E}$, is one which multiplies a vaccinee's susceptibility to a disease by a factor $1 - \mathcal{E}$ but has no effect on a vaccinee's infectivity if he/she becomes infected. More specifically, each time any infective attempts to infect a vaccinated susceptible individual that individual is infected independently with probability $1 - \mathcal{E}$. Suppose that $R_* > 1$ and the entire population is vaccinated with a leaky vaccine. Then

$$R_{VL} = 1/(1 - \mathcal{E}_C), \tag{18}$$

where $\mathcal{E}_C$ is the efficacy required to reduce R_* to 1.

The above definitions of R_V and R_{VL} assume that $R_* > 1$. Goldstein et al. [11] did not define R_V and R_{VL} when $R_* \leq 1$. In that case we define $R_V = R_{VL} = 1$, since a major outbreak cannot occur even if nobody is vaccinated.

[4]Note though that there is a small misprint in the formula for R_{VA} at the foot of page 19 of [11] ($\sqrt{4(f-1)/R_G}$ should be replaced by $\sqrt{1 + 4(f-1)/R_G}$).

2.8 The exponential-growth-associated reproduction number R_r

A final reproductive number considered in [11] is the exponential-growth-associated reproduction number R_r, whose definition requires a more detailed description of the transmission model. Goldstein et al. [11] consider a households models in which infectives have independent and identically distributed infectivity profiles. A typical infectivity profile, $\mathcal{I}(t)$ $(t \geq 0)$, is the realisation of a stochastic process; conditional upon its infectivity profile, an infectious individual, t time units after being infected, makes global contacts at overall rate $\mu_G \mathcal{I}(t)$ and contacts any given susceptible in his/her household at rate $\lambda_H^{(n)} \mathcal{I}(t)$, where n is the size of his/her household[5]. All infectious contacts, whether of the same or different type (i.e. local or global) are independent of each other. For $t \geq 0$, let $w_G(t) = \mathbb{E}[\mathcal{I}(t)]$ and note that, since μ_G is the mean number of global contacts made by a typical infective, $\int_0^\infty w_G(t)\mathrm{d}t = 1$. Thus w_G may be interpreted as the probability density function of a random variable, W_G say, describing an infectious contact interval (see e.g. [11] and [23]).

Suppose first that $\lambda_H^{(n)} = 0$ for all n, so the epidemic is homogeneously mixing, with basic reproduction number $R_0 = \mu_G$ and real-time growth rate r given by the implicit solution of the Lotka-Euler equation

$$\int_0^\infty \mu_G w_G(t) \mathrm{e}^{-rt} \mathrm{d}t = 1. \tag{19}$$

Thus, $R_0 = \left(\mathcal{M}_{W_G}(r)\right)^{-1}$, where $\mathcal{M}_{W_G}(\theta) = \int_0^\infty \mathrm{e}^{-\theta t} w_G(t)\mathrm{d}t$ is the moment-generating function of W_G. (Throughout the paper, for a random variable X we denote its moment-generating function by $\mathcal{M}_X(\theta) = \mathbb{E}\left[\mathrm{e}^{-\theta X}\right]$.) This provides a method of estimating R_0 from data on an emerging epidemic, when information on W_G and the exponential growth rate r are available, assuming a homogeneous mixing model (see Nowak et al. [18], Lloyd [16], Wallinga and Lipsitch [27] and Roberts and Heesterbeek [24]).

The exponential-growth-associated reproduction number R_r in [11] is given by

$$R_r = \frac{1}{\mathcal{M}_{W_G}(r)}, \tag{20}$$

where r is the real-time growth rate of the households model. Thus, in the above inferential setting, R_r is the estimate one obtains of R_0 if the household structure of the population is ignored.

To calculate R_r, it is necessary to calculate first the real-time growth rate r of the households model, which generally is far from straightforward. For $t > 0$, let $\beta_H(t)$ denote the mean rate at which global contacts emanate from a typical single-household epidemic t time units after the household was infected. Similarly to (19), the real-time growth rate r is now given by the unique real solution of the Lotka-Euler equation

$$\mathcal{L}_{\beta_H}(r) = 1, \tag{21}$$

where $\mathcal{L}_{\beta_H}(r) = \int_0^\infty \beta_H(t)\mathrm{e}^{-rt}\mathrm{d}t$. Note that $\mathcal{L}_{\beta_H}(r)$ is the Laplace transform of the household infectivity profile; hereafter, we denote by $\mathcal{L}_f(\theta)$ the Laplace transform of a function

[5]The notation has been changed to fit more closely that of our paper.

f calculated in $\theta \in (-\infty, \infty)$[6]. The difficulty in calculating r from (21) is that $\mathcal{L}_{\beta_H}(r)$ is generally not mathematically tractable unless the disease dynamics are Markovian. Consequently, Fraser [10] introduced an approximation, further explored in Pellis et al. [21], which essentially assumes that cases are attributed to generations according to the rank-based process and real infection intervals (not only infectious contact intervals) are independent realisations of the random variable W_G (see Pellis et al. [23] for an extensive discussion). With this approximation, the time elapsing from the initial infection of the household to the infection of a typical household generation-k infective is given by the sum of k independent copies of W_G, so $\mathcal{L}_{\beta_H}(r) \approx \mathcal{L}^{(0)}_{\beta_H}(r)$, where

$$\mathcal{L}^{(0)}_{\beta_H}(r) = \mu_G \mathcal{M}_{W_G}(r) \left\{ 1 + \sum_{k=1}^{n_H - 1} \mu_k \left(\mathcal{M}_{W_G}(r) \right)^k \right\}. \tag{22}$$

Substituting this approximation into (21), using (20) and recalling that $\mu_0 = 1$, yields

$$\mu_G \sum_{k=0}^{n_H - 1} \frac{\mu_k}{R_r^{k+1}} = 1,$$

so, recalling (5), $g_0(R_r) = 0$. Thus, using Fraser's approximation leads to R_r being given by R_0.

A second approximation to R_r is perhaps most easily introduced by considering the infectivity profile given by

$$\mathcal{I}(t) = \begin{cases} 1 & \text{if } 0 \leq t \leq T_I, \\ 0 & \text{if } t > T_I, \end{cases} \tag{23}$$

where $T_I \sim \text{Exp}(1)$. (For $\gamma > 0$, $\text{Exp}(\gamma)$ denotes an exponential distribution having rate γ, and hence mean γ^{-1}.) Thus, for $t \geq 0$, we have $w_G(t) = \mathbb{E}[\mathcal{I}(t)] = \mathbb{P}(T_I \geq t) = \mathrm{e}^{-t}$, so $W_G \sim \text{Exp}(1)$. Suppose that $\lambda_H^{(n)} = \lambda_H$ for all n. Let the random variable $\widetilde{W}_G$ describe the time of the first local infectious contact from a given infective to a given susceptible in the same household, conditional upon there being at least one such contact. The infective contacts the susceptible at rate λ_H and recovers independently at rate 1, so the time until the first event (contact of the susceptible or recovery of the infective) has an $\text{Exp}(1 + \lambda_H)$ distribution. Moreover, whether or not this event is a recovery is independent of its time. Thus $\widetilde{W}_G \sim \text{Exp}(1 + \lambda_H)$. Note that $\widetilde{W}_G$ has a different distribution from W_G, so another (and usually improved) approximation is $\mathcal{L}_{\beta_H}(r) \approx \widetilde{\mathcal{L}}_{\beta_H}(r)$, where

$$\widetilde{\mathcal{L}}_{\beta_H}(r) = \mu_G \mathcal{M}_{W_G}(r) \left\{ 1 + \sum_{k=1}^{n_H - 1} \mu_k \left(\mathcal{M}_{\widetilde{W}_G}(r) \right)^k \right\}. \tag{24}$$

[6]For ease of notation we give the domain as $(-\infty, \infty)$ but, as all the functions we consider are non-negative, we note that the domain usually takes the form (θ_f, ∞), where θ_f depends on the function f, as the integral is infinite for $\theta \leq \theta_f$.

Note that the first $\mathcal{M}_{W_G}(r)$ in (22) is not replaced by $\mathcal{M}_{\widetilde{W}_G}(r)$ since it corresponds to a global contact (recall that, asymptotically, an infective makes at most one global contact to any given susceptible). The random variable $\widetilde{W}_G$ can be defined in a similar fashion for any arbitrary but specified infectivity profile (see [23] for numerous explicit examples). Using this approximation, the real-time growth rate r is approximated by $\tilde{r}$, where $\tilde{r}$ is the unique real solution of

$$\widetilde{\mathcal{L}}_{\beta_H}(r) = 1, \tag{25}$$

which leads to R_r being approximated by the reproduction number

$$\widetilde{R}_r = \frac{1}{\mathcal{M}_{W_G}(\tilde{r})}. \tag{26}$$

The above example shows that if λ_H varies with household size n then so does the distribution of $\widetilde{W}_G$. In that case, (24) becomes

$$\widetilde{\mathcal{L}}_{\beta_H}(r) = \mu_G \mathcal{M}_{W_G}(r) \left\{ 1 + \sum_{n=2}^{n_H} \pi_n \sum_{k=1}^{n-1} \mu_k^{(n)} \left(\mathcal{M}_{\widetilde{W}_G^{(n)}}(r) \right)^k \right\}, \tag{27}$$

where $\widetilde{W}_G^{(n)}$ is a random variable distributed as $\widetilde{W}_G$ when the household size is n, and $\widetilde{R}$ is then obtained as before.

Observe that the approximation $\mathcal{L}_{\beta_H}(r) \approx \widetilde{\mathcal{L}}_{\beta_H}(r)$ is exact if $n_H \leq 2$, so in that case $R_r = \widetilde{R}_r$.

3 Comparisons of households model reproduction numbers

We distinguish between an epidemic in which $R_* > 1$ and one in which $R_* < 1$; we call the former *growing* (following Goldstein et al. [11]) and the latter *declining*. As stated before, we assume implicitly that $n_H \geq 2$, $\mu_H > 0$ and $\mu_G > 0$. We also assume that if $n_H \geq 3$, then $\mu_1 \neq \mu_H$. Thus we exclude the highly locally infectious case studied by Becker and Dietz [8], in which the initial infective in a household necessarily infects all other susceptible household members. We comment on this case after Theorems 1 and 2.

3.1 Comparisons not involving R_r

3.1.1 Main theorem

The following theorem is proved in Section 7.1.

Theorem 1

(a) $R_* = 1 \iff R_I = 1 \iff R_0 = 1 \iff R_2 = 0 \iff R_{HI} = 1 \implies R_V = 1.$

(b) In a growing epidemic,

$$R_* > R_I \geq R_V \geq R_0 > R_{HI} > 1 \quad \textit{and} \quad R_I \geq R_2 > R_{HI} > 1,$$

and in a declining epidemic

$$R_* < R_I \leq R_0 < R_{HI} < 1 \quad \textit{and} \quad R_I \leq R_2 < R_{HI} < 1.$$

The inequalities $R_I \geq R_V$, $R_I \geq R_2$, $R_I \leq R_0$ and $R_I \leq R_2$ are strict if and only if $n_H > 2$. The inequality $R_V \geq R_0$ is strict if and only if $n_H > 3$.

Remark 1 *We conjecture that, in addition to Theorem 1(b), $R_0 \geq R_2$ in a growing epidemic and $R_0 \leq R_2$ in a declining epidemic, with strict inequalities if and only if $n_H > 2$, so that Theorem 1(b) should take the form $R_* > R_I \geq R_V \geq R_0 \geq R_2 > R_{HI} > 1$ and $R_* < R_I \leq R_0 \leq R_2 < R_{HI} < 1$ in the two cases, respectively. Although we have yet to find a complete proof, the conjecture is supported by extensive numerical results. We discuss it further in Appendix A, where it is proved for $n_H \leq 3$.*

Remark 2 *If the epidemic is highly locally infectious then $\mu_1 = \mu_H$ and it is readily seen that part (a) of Theorem 1 still holds, $R_* > R_I = R_V = R_0 = R_2 > R_{HI} > 1$ in a growing epidemic and $R_* < R_I = R_0 = R_2 < R_{HI} < 1$ in a declining epidemic.*

A key finding of Goldstein et al. [11] is that, for a growing epidemic, $R_* \geq R_V \geq \bar{R}_{HI}$, thus enabling upper and lower bounds to be obtained for the critical vaccination coverage when individuals are vaccinated uniformly at random with a perfect vaccine (note, though, that $\bar{R}_{HI}$ is not a threshold parameter and can be smaller than 1 even in a growing epidemic). Note that Theorem 1 implies that R_I is a sharper upper bound than R_* for R_V and R_0 is a sharper lower bound than R_{HI} (which coincides with $\bar{R}_{HI}$ when all households have the same size and, as shown below, is greater than or equal to $\bar{R}_{HI}$ in a growing epidemic). Goldstein et al. [11] show that $R_* \geq R_{VL} \geq R_V$ for a growing epidemic. We show in Appendix B that R_{VL} and R_I cannot in general be ordered.

In Appendix C we investigate the possible ordering of variants of R_{HI}. Concerning the reproduction numbers $\bar{R}_{HI}$ and $\hat{R}_{HI}$, Goldstein et al. [11] prove that[7] $\bar{R}_{HI} \leq \hat{R}_{HI}$ always holds (see their Proposition A4.1) and we show that $\bar{R}_{HI} \leq R_{HI}$. So we conclude that, by virtue of Theorem 1*(b)*, in a growing epidemic,

$$R_0 > R_{HI} \geq \bar{R}_{HI}.$$

(but note that even in a growing epidemic $\bar{R}_{HI}$ might or might not be greater than 1). However, in a declining epidemic, R_0 and $\bar{R}_{HI}$ cannot be ordered in general. Finally, we also construct an example to show that no general order exists between R_0 and $\hat{R}_{HI}$ (either in a growing or a declining epidemic).

[7] In our notation.

One may argue that our generalisation of R_{HI} to populations with unequal household sizes is more natural than $\bar{R}_{HI}$. Unlike $\bar{R}_{HI}$, it is a threshold parameter and, unlike $\hat{R}_{HI}$, it can always be ordered with R_0. Moreover, for a growing epidemic, R_{HI} is a sharper lower bound than $\bar{R}_{HI}$ for R_0, and hence also for R_V (see Theorem 1). In a similar vein, our generalisation of R_2 to populations with unequal household sizes seems more natural than that in [7].

3.1.2 Network-households model

We now consider briefly relations among reproduction numbers for the network-households model, for which the calculation of R_0 is outlined at the end of Section 2.2. Analogues of R_*, R_I, R_V, R_{HI} and R_2 are easily obtained. Omitting the details, $R_* = \tilde{\mu}_G + \mu_G\mu_H$, R_I is the unique root in $(0,\infty)$ of $g_I^{NH}(\lambda)$, where

$$g_I^{NH}(\lambda) = 1 - \frac{\tilde{\mu}_G}{\lambda} - \frac{\mu_H\mu_G}{\lambda^2},$$

R_V is defined in the usual way via the (perfect vaccine) critical vaccination coverage, R_{HI} is the unique root in (a,∞) of $g_{HI}^{NH}(\lambda)$, where (cf. (13))

$$g_{HI}^{NH}(\lambda) = 1 - \frac{\tilde{\mu}_G}{\lambda} - \frac{\mu_G}{\lambda}\sum_{n=2}^{n_H}\pi_n\frac{a^{(n)}}{\lambda - a^{(n)}} \qquad (\lambda > a),$$

and R_2 is the unique root in (b,∞) of $g_2^{NH}(\lambda)$, where (cf. (16))

$$g_2^{NH}(\lambda) = 1 - \frac{\tilde{\mu}_G}{\lambda} - \frac{\mu_G}{\lambda}\sum_{n=2}^{n_H}\pi_n\frac{\mu_1^{(n)}}{\lambda - b^{(n)}} \qquad (\lambda > b).$$

With the above definitions, Theorem 1 holds also for the network-households model; the proof is essentially the same as for the households model and hence omitted.

Analogues of $\hat{R}_{HI}$ and $\hat{R}_2$ can also be defined. On average, a fraction $1/(1+\mu_H)$ of infectives are household primary cases, who each make a mean of $\tilde{\mu}_G$ global contacts, and a fraction $\mu_H/(1+\mu_H)$ of infectives are household secondary cases, who each make a mean of μ_G global contacts. Arguing as in the derivation of (11) then leads to

$$\hat{R}_{HI} = \frac{\tilde{\mu}_G + \mu_H(1+\mu_G)}{1+\mu_H},$$

but note that $\hat{R}_{HI}$ does not necessarily equal R_{HI} when all households have the same size. Arguing as in the derivation of (14) yields that $\hat{R}_2$ is the largest positive root of $\hat{g}_2^{NH}(\lambda)$, where

$$\hat{g}_2^{NH}(\lambda) = 1 - \frac{b+\tilde{\mu}_G}{\lambda} + \frac{b\tilde{\mu}_G - \mu_1\mu_G}{\lambda^2}.$$

The reproductions numbers $\hat{R}_2$ and R_2 do coincide when all households have the same size. Comparisons involving $R_0, \hat{R}_2$ and $\hat{R}_{HI}$ are more involved and are not considered here.

3.1.3 Generational view of comparisons

For the households model, the reproduction numbers R_0, R_*, R_I, R_{HI} and R_2 can all be obtained by viewing local epidemics on an appropriate generation basis, with any such reproduction number, R_A say, being given by the unique positive root of the function g_A defined by

$$g_A(\lambda) = 1 - \mu_G \sum_{k=0}^{\infty} \frac{\mu_k^A}{\lambda^{k+1}}, \tag{28}$$

where $\mu_0^A, \mu_1^A, \cdots$ are the mean generation sizes associated with R_A, averaged with respect to the size-biased household size distribution $(\pi_n) = (\pi_n : n = 1, 2, \cdots, n_H)$. The mean generations sizes associated with R_0, R_{HI} and R_2 have been described previously and lead to (5), (13) and (16), respectively. For R_*, they are given by $\mu_0^* = 1 + \mu_H$ and $\mu_k^* = 0$ $(k = 1, 2, \cdots)$, so $g_*(\lambda) = 1 - \mu_G \frac{1+\mu_H}{\lambda}$, whence R_* is given by (7). For R_I they are given by $\mu_0^I = 1, \mu_1^I = \mu_H$ and $\mu_k^I = 0$ $(k = 2, 3, \cdots)$, leading to (8).

Observe that, for each A, $\sum_{k=0}^{\infty} \mu_k^A = 1 + \mu_H$, so we can define a random variable X^A having probability mass function $\mathbb{P}(X^A = k) = \mu_k^A/(1 + \mu_H)$ $(k = 0, 1, \cdots)$, whose interpretation is the household-generation (associated with R_A) of an an infective chosen uniformly at random from all infectives in a household with size chosen according to the size-biased distribution (π_n). Moreover, R_A is then given by the unique solution in $(0, \infty)$ of the equation

$$\mathbb{E}\left[\lambda^{-(X^A+1)}\right] = \frac{1}{\mu_G(1 + \mu_H)}. \tag{29}$$

Now, for $x \geq 0$, λ^{-x} is increasing in x if $\lambda < 1$ and decreasing if $\lambda > 1$. Thus, if for two reproduction numbers, R_A and R_B say, $X^A \overset{st}{\leq} X^B$ (X^A stochastically smaller than X^B, i.e. $\mathbb{P}(X^A \leq x) \geq \mathbb{P}(X^B \leq x)$ for all $x \in \mathbb{R}$) then it follows that $R_A \geq R_B$ in a growing epidemic and $R_A \leq R_B$ in a declining epidemic.

The above observation provides an intuitive explanation for all of the comparisons in Theorem 1 (except those involving R_V) and also for the conjecture concerning R_0 and R_2. Indeed, the comparisons in Theorem 1 can be proved by showing stochastic ordering of the associated X^As, though this approach is generally no easier and sometimes harder than the proofs in Section 7.1.

The above approach provides a simple proof of comparisons of R_0^{r} and R_0^{g}, where R_0^{r} and R_0^{g} denote the values of R_0 obtained using rank and true generations, respectively (see Section 2.1). Suppose first that all households have size n. Let $\mu_0^{\mathrm{r}}, \mu_1^{\mathrm{r}}, \cdots, \mu_{n-1}^{\mathrm{r}}$ and $\mu_0^{\mathrm{g}}, \mu_1^{\mathrm{g}}, \cdots, \mu_{n-1}^{\mathrm{g}}$ denote the mean rank and mean true generation sizes, respectively, and let X^{r} and X^{g} denote the corresponding induced generation random variables. Consider a realisation of the augmented version of the random graph $\mathcal{G}^{(n)}$ defined in Section 2.1. If $n \leq 2$ then the rank and true generation numbers coincide for all infectives. Suppose that $n \geq 3$ and for any infective, i say, let r_i and g_i denote its rank and true generation numbers, respectively. Then $r_i \leq g_i$, since r_i is the number of edges in the *shortest* chain joining the initial infective 0 to i. However, if there is a chain joining 0 to i having strictly more edges than r_i but strictly less total time than any such chain of length r_i then $g_i > r_i$. It follows

that, for $n \geq 3$, $\sum_{j=0}^{k} \mu_j^{\mathrm{r}} \geq \sum_{j=0}^{k} \mu_j^{\mathrm{g}}$ $(k = 0, 1, \cdots, n-1)$, which implies that $X^{\mathrm{r}} \overset{st}{\leq} X^{\mathrm{g}}$. Taking expectations with respect to the size-biased household size distribution (π_n) shows that the same result holds for populations with unequal household sizes, provided $n_H \geq 3$. Hence in a growing epidemic $R_0^{\mathrm{r}} \geq R_0^{\mathrm{g}}$, whilst in a declining epidemic $R_0^{\mathrm{r}} \leq R_0^{\mathrm{g}}$.

3.2 Comparisons involving R_r

Although R_r and R_0 cannot in general be ordered (see Appendix D), Theorem 2 below (proved in Section 7.2) shows that, for the most commonly-studied models in the literature, in a growing epidemic $R_r \geq R_0$ and in a declining epidemic $R_r \leq R_0$. For this purpose, it is convenient to consider two broad classes of models. The first class contains those models for which $\mathcal{I}(t) = Jw_G(t)$ for all $t \geq 0$, for which the shape of the infectivity profile is not random, but the magnitude J is. (Recalling that $\int_0^\infty w_G(t)\mathrm{d}t = 1$, we have that $J = \int_0^\infty \mathcal{I}(t)\mathrm{d}t$ and $\mathbb{E}[J] = 1$.) Another class assumes that the duration of the infectious period is random but, conditioned on an individual being still infectious t time units after being infected, the infectivity is non-random, i.e., $\mathcal{I}(t) = f(t)\mathbb{1}(T_I > t)$ for $t \geq 0$, where $f(t)$ is a deterministic function and T_I is a random variable denoting the infectious period, which satisfy $\int_0^\infty f(t)\mathbb{P}(T_I > t)\mathrm{d}t = 1$. (Throughout the paper, for an event, $\mathcal{D}$ say, $\mathbb{1}(\mathcal{D})$ denotes its indicator function; i.e. $\mathbb{1}(\mathcal{D}) = 1$ if the event $\mathcal{D}$ occurs and $\mathbb{1}(\mathcal{D}) = 0$ if $\mathcal{D}$ does not occur. Thus, in the present setting, $\mathcal{I}(t) = f(t)$ if $t < T_I$ and $\mathcal{I}(t) = 0$ if $t \geq T_I$.) Note that the standard stochastic SIR model (Andersson and Britton [1], Chapter 2) is in this class ($f(t)$ is constant). A non-random time-varying infectivity profile, i.e. $\mathcal{I}(t) = w_G(t)$ for all $t \geq 0$ is a special case of both classes.

Theorem 2 *(a) For all choices of infectivity profile $\mathcal{I}(t)$ $(t \geq 0)$,*

$$R_r = 1 \iff \widetilde{R}_r = 1 \iff R_0 = 1.$$

(b) If $\mathcal{I}(t) = Jw(t)$ $(t \geq 0)$, where J is a non-negative random variable, then in a growing epidemic,

$$R_r \geq R_0 > 1,$$

and in a declining epidemic,

$$R_r \leq R_0 < 1.$$

(c) If $\mathcal{I}(t) = f(t)\mathbb{1}(T_I > t)$ $(t \geq 0)$, where $f(t)$ is a deterministic function and T_I a non-negative random variable, then in a growing epidemic,

$$R_r \geq \widetilde{R}_r \geq R_0 > 1,$$

and in a declining epidemic,

$$R_r \leq \widetilde{R}_r \leq R_0 < 1.$$

The above results still hold if a latent period independent of the remainder of the infectivity profile is added.

Remark 3 *Note that for Reed-Frost type models (i.e. models in which the latent period is constant and the infectious period is reduced to a single point in time, cf. Bailey [2], Section 14.2, and Diekmann et al. [9], Section 3.2.1), the approximation* $\mathcal{L}_{\beta_H}(r) \approx \mathcal{L}^{(0)}_{\beta_H}(r)$ *(see* (22)*) is exact, as all infectious intervals equal the constant latent period, so* $R_0 = R_r$*. Thus, it is not generally possible to obtain strict inequalities in Theorem 2(b). However, if* $w_G(t)$ *is a proper density function, i.e.* $w_G(t) < \infty$ *for all* $t \geq 0$*, then the inequalities are strict (recall that we have assumed that not all households have size 1). As noted in Section 2.8,* $R_r = \widetilde{R}_r$ *if* $n_H \leq 2$*. See Remark 6 after the proof of Theorem 2 in Section 7.2 for further details.*

Remark 4 *The proof of Theorem 2 also suggests how to construct the counterexample presented in Appendix D, which gives a model (not belonging to either of the classes considered in Theorem 2) for which* $R_r < R_0$ *in a growing epidemic.*

Remark 5 *Suppose that all secondary infections take place as soon as the primary individual in a household is infected. Then* $\beta_H(t) = (1 + \mu_H)\mu_G w_G(t) = R_* w_G(t)$ $(t \geq 0)$*. Hence,* $\mathcal{L}_{\beta_H}(r) = R_* \mathcal{M}_{W_G}(r)$ *and it follows from* (20) *and* (21) *that* $R_r = R_*$*. This happens in the highly locally infectious limit* $\lambda_H^{(n)} \to \infty$ $(n = 2, 3, \cdots)$*, provided* W_G *has mass arbitrarily close to zero, i.e. provided* $\inf\{t > 0 : w_G(t) > 0\} = 0$*.*

For a growing epidemic, Goldstein et al. [11] prove that $R_* \geq R_r$. They also note that in most numerical simulations $R_{VL} \geq R_r \geq R_V$, though they show that the second inequality can be violated if the latent period is very large and they do not have a proof for the first inequality. The first inequality held in all of their numerical simulations but the question whether or not the result holds in general was left open. In Appendix E we show that R_r and R_{VL} cannot in general be ordered. In their numerical simulations for a households SEIR model with exponentially distributed infectious and latent periods, Goldstein et al. [11] noted that R_r can be less than R_V when the mean latent period is very long and, in Appendix B of their paper, they give a mathematical explanation of that observation. However, their proof assumes a constant latent period and does not hold for the model with exponentially distributed latent periods. This is discussed further in Appendix F; see also the numerical example in Section 6.1.

Finally, although Goldstein et al. [11] consider only the growing epidemic case, it is easy to see (from (6.2.2) and Lemma 6.2.1 of their paper) that the same argument they use to prove $R_* \geq R_r$ leads, in a declining epidemic, to $R_* \leq R_r$.

4 Households-workplaces model and reproduction numbers

4.1 Model and generations of infections

In this model each individual belongs to a household and to a workplace, and infectives make three types of contacts: global contacts, with individuals chosen uniformly at random from

the entire population; household contacts, with individuals in the infective's own household; and workplace contacts, with individuals in the infective's own workplace. In order to make branching process approximations for the early stages of the epidemic, and thus define threshold parameters, it is necessary to assume that, as the population size tends to infinity, the only short cycles of local contacts (see below) that can occur with non-zero probability are either within the same household or within the same workplace, which implies that a household and a workplace cannot share more than one person; see Ball and Neal [5] and Pellis et al. [20, 22] for further detail.

The mean number of global contacts made by a typical infective is μ_G. Household and workplace contacts are called local contacts. As with the households model, we do not specify the full detail of local infection transmission, but we do assume that the spread within a household and the spread within a workplace can each be described in terms of generations of infection. Let n_H and n_W denote respectively the sizes of the largest household and the largest workplace in the population. Then, for $\ell = 0, 1, \cdots, n_H - 1$, let μ_ℓ^H be the mean size of the ℓth generation in a typical single-household epidemic with 1 primary case and, for $\ell' = 0, 1, \cdots, n_W - 1$, define $\mu_{\ell'}^W$ similarly for a typical single-workplace epidemic. By a typical single-household (workplace) epidemic we mean one in which the primary case is obtained by choosing an individual uniformly at random from the entire population, so μ_ℓ^H is household size-biased, as at (3), and $\mu_{\ell'}^W$ is size-biased using the workplace size-biased distribution corresponding to (2). We also assume that the sizes of any given individual's household and workplace are asymptotically independent as the population size tends to infinity.

Let $\mu_H = \mu_1^H + \mu_2^H + \cdots + \mu_{n_H-1}^H$ be the mean size of a typical single-household epidemic, not including the primary case, and define μ_W similarly for a typical single-workplace epidemic. We assume that $\mu_H > 0$ and $\mu_W > 0$, and that the population contains households and workplaces of size at least two. If any of these conditions fails to hold then the model effectively reduces to the households model. For simplicity we assume that $\mu_G > 0$. We comment on the case $\mu_G = 0$ at the end of Section 5.

4.2 The basic reproduction number R_0

The basic reproduction number R_0 for the households-workplaces model may be obtained by considering the following 3-type branching process, which approximates the process of infectives in the epidemic model. The three types of individual in the branching process are double-primary cases (type 1), household-primary cases (type 2) and workplace-primary cases (type 3), which correspond to cases who are infected by a global contact, a workplace contact and a household contact, respectively. In the branching process, the mother of a double-primary case is the person who infected it in the epidemic process, the mother of a household-primary case is the primary case in the corresponding single-workplace epidemic and the mother of a workplace-primary case is the primary case in the corresponding single-household epidemic. Time in the branching process corresponds to generation number in the epidemic at large. Thus, in the branching process, a typical double-primary case spawns on average μ_G double-primary cases at age 1, $\mu_{\ell'}^W$ household-primary cases at age ℓ'

($\ell' = 1, 2, \cdots, n_W - 1$) and μ_ℓ^H workplace-primary cases at age ℓ ($\ell = 1, 2, \cdots, n_H - 1$); a typical household-primary case spawns on average μ_G double-primary cases at age 1 and μ_ℓ^H workplace-primary cases at age ℓ ($\ell = 1, 2, \cdots, n_H - 1$); and a typical workplace-primary case spawns on average μ_G double-primary cases at age 1 and $\mu_{\ell'}^W$ household-primary cases at age ℓ' ($\ell' = 1, 2, \cdots, n_W - 1$). The total number of individuals at time k in this branching process corresponds to the total number of infectives in global generation k in the epidemic process, so R_0 is given by the asymptotic geometric growth rate of this branching process.

It is convenient to introduce the following notation for future reference. For $d, d' = 1, 2, 3$ and $k = 0, 1, \cdots$, let $\nu_k^{(dd')}$ be the mean number of type-d' individuals spawned by a typical type-d individual at age $k + 1$ and, for $\lambda \in (0, \infty)$, let $\nu_{dd'}(\lambda) = \sum_{k=0}^{\infty} \nu_k^{(dd')}/\lambda^{k+1}$. By the theory of multi-type general branching processes (see, for example, Haccou et al. [12], Section 3.3.2, and Jagers [15]), the asymptotic geometric growth rate of the branching process, and hence also R_0, is given by the value of λ such that the dominant eigenvalue of the matrix

$$A^{(HW)}(\lambda) = [\nu_{dd'}(\lambda)] = \begin{bmatrix} \dfrac{\mu_G}{\lambda} & \displaystyle\sum_{\ell'=1}^{n_W-1} \dfrac{\mu_{\ell'}^W}{\lambda^{\ell'}} & \displaystyle\sum_{\ell=1}^{n_H-1} \dfrac{\mu_\ell^H}{\lambda^\ell} \\ \dfrac{\mu_G}{\lambda} & 0 & \displaystyle\sum_{\ell=1}^{n_H-1} \dfrac{\mu_\ell^H}{\lambda^\ell} \\ \dfrac{\mu_G}{\lambda} & \displaystyle\sum_{\ell'=1}^{n_W-1} \dfrac{\mu_{\ell'}^W}{\lambda^{\ell'}} & 0 \end{bmatrix} \tag{30}$$

is 1. Letting $A = \mu_G/\lambda$, $B = \sum_{\ell'=1}^{n_W-1} \mu_{\ell'}^W/\lambda^{\ell'}$ and $C = \sum_{\ell=1}^{n_H-1} \mu_\ell^H/\lambda^\ell$, the characteristic polynomial of $A^{(HW)}(\lambda)$ is

$$f(x) = x^3 - Ax^2 - (AB + AC + BC)x - ABC, \tag{31}$$

which has a unique positive root. Thus, since the matrix $A^{(HW)}(\lambda)$ is non-negative, its dominant eigenvalue is 1 if and only if $f(1) = 0$.

Now

$$\begin{aligned} f(1) = 0 &\iff ABC + AB + AC + BC + A - 1 = 0 \\ &\iff A(B + 1)(C + 1) + BC - 1 = 0. \end{aligned}$$

Further,

$$BC = \left(\sum_{\ell=1}^{n_H-1} \frac{\mu_\ell^H}{\lambda^\ell} \right) \left(\sum_{\ell'=1}^{n_W-1} \frac{\mu_{\ell'}^W}{\lambda^{\ell'}} \right) = \sum_{k=1}^{n_H+n_W-3} \left(\sum_{\ell=\max(1,k-n_W+2)}^{\min(k,n_H-1)} \frac{\mu_\ell^H \mu_{k+1-\ell}^W}{\lambda^{k+1}} \right)$$

and, recalling that $\mu_0^H = \mu_0^W = 1$,

$$A(B+1)(C+1) = \frac{\mu_G}{\lambda}\left(\sum_{\ell=0}^{n_H-1}\frac{\mu_\ell^H}{\lambda^\ell}\right)\left(\sum_{\ell'=0}^{n_W-1}\frac{\mu_{\ell'}^W}{\lambda^{\ell'}}\right)$$
$$= \mu_G \sum_{k=0}^{n_H+n_W-2}\left(\sum_{\ell=\max(0,k-n_W+1)}^{\min(k,n_H-1)}\frac{\mu_\ell^H\mu_{k-\ell}^W}{\lambda^{k+1}}\right).$$

Thus, the dominant eigenvalue of $A^{(HW)}(\lambda)$ is 1 if and only if $g_0^{(HW)}(\lambda) = 0$, where

$$g_0^{(HW)}(\lambda) = 1 - \sum_{k=0}^{n_H+n_W-2}\frac{c_k}{\lambda^{k+1}}, \tag{32}$$

with $c_0 = \mu_G$ and, for $k = 1, 2, \cdots, n_H + n_W - 2$,

$$c_k = \mu_G \sum_{\ell=\max(0,k-n_W+1)}^{\min(k,n_H-1)}\mu_\ell^H\mu_{k-\ell}^W + \sum_{\ell=\max(1,k-n_W+2)}^{\min(k,n_H-1)}\mu_\ell^H\mu_{k+1-\ell}^W, \tag{33}$$

where the second sum in (33) is zero when $k = n_H + n_W - 2$.

It follows that R_0 is given by the unique positive root of $g_0^{(HW)}$, giving a new (and simpler) proof of Pellis et al. [22], Corollary 2.

4.3 The clump reproduction number R_*

The first reproduction number proposed for the households-workplaces model was the reproduction number for the proliferation of local infectious clumps, denoted by R_*; see Ball and Neal [5]. A local infectious clump is the set of individuals infected by chains of local infections (i.e. through households and workplaces) from a typical single initial infective in an otherwise fully susceptible population. In the early stages of an epidemic, initiated by few infectives in a large population, such clumps (which are initiated by global contacts) intersect with small probability, unless the local epidemic is itself supercritical. The clump reproduction number R_* is the expected number of clumps generated by a typical clump and is given by

$$R_* = \begin{cases} \frac{\mu_G(1+\mu_H)(1+\mu_W)}{1-\mu_H\mu_W} & \text{if } \mu_H\mu_W < 1, \\ \infty & \text{otherwise.} \end{cases} \tag{34}$$

Note that setting $\mu_W = 0$ in (34) yields (7); when $\mu_W = 0$, the model reduces to the households model and a typical local infectious clump becomes the set of people infected in a typical single-household epidemic.

4.4 The household-household and workplace-workplace reproduction numbers R_H and R_W

The clump reproduction number R_* has a number of disadvantages, as pointed out by Pellis et al. [20]. In particular, it can be infinite and the time for a clump to form increases as $\mu_H\mu_W$ tends to 1 and becomes comparable with the time of the entire epidemic. Thus a household-to-household reproduction number R_H, defined as the expected number of households infected by a typical infected household in an otherwise totally susceptible population, was introduced in [20]. A household may be infected either globally (i.e. via a global contact) or locally (i.e. via a contact within a workplace). It follows (see [20] for details) that R_H is the largest eigenvalue of the household next-generation matrix

$$M_H = \begin{bmatrix} \mu_G(1+\mu_H) & \mu_W(1+\mu_H) \\ \mu_G(1+\mu_H) & \mu_H\mu_W \end{bmatrix}, \tag{35}$$

whence R_H is given by the unique solution in $(0,\infty)$ of $g_H(\lambda)=0$, where

$$g_H(\lambda) = 1 - \frac{\mu_G + \mu_G\mu_H + \mu_H\mu_W}{\lambda} - \frac{\mu_G\mu_W(1+\mu_H)}{\lambda^2}. \tag{36}$$

A workplace-to-workplace reproduction number R_W can be defined in a similar fashion.

4.5 The individual reproduction number R_I

An individual-based reproduction number R_I can also be defined (see Pellis et al. [20], supplementary material), as for the households model, by attributing all secondary cases in a household or workplace to the corresponding primary case, leading to the next-generation matrix

$$M_I^{(HW)} = \begin{bmatrix} \mu_G & \mu_H & \mu_W \\ \mu_G & 0 & \mu_W \\ \mu_G & \mu_H & 0 \end{bmatrix}.$$

Calculating the characteristic polynomial of $M_I^{(HW)}$ shows that R_I is given by the unique solution in $(0,\infty)$ of $g_I^{(HW)}(\lambda)=0$, where

$$g_I^{(HW)}(\lambda) = 1 - \frac{\mu_G}{\lambda} - \frac{\mu_G\mu_H + \mu_G\mu_W + \mu_H\mu_W}{\lambda^2} - \frac{\mu_G\mu_H\mu_W}{\lambda^3}. \tag{37}$$

4.6 The perfect and leaky vaccine-associated reproduction numbers R_V and R_{VL}

The perfect and leaky vaccine-associated reproduction numbers, R_V and R_{VL}, can be defined in an analogous fashion as for the households model at (17) and (18), respectively, though we consider only the former in the comparisons in Section 3.1.

4.7 The exponential-growth-associated reproduction number R_r

An exponential-growth-associated reproduction number R_r can be defined in a similar vein as for the households model as follows. Consider the 3-type branching process used in Section 4.2 to derive R_0, but run in real time rather than in generations. Let r be the Malthusian parameter (real-time growth rate) of this branching process. Then R_r is defined as at (20) for the households model.

To determine R_r, a more-detailed description of the households-workplaces model is required, which we now give. As in the households model, suppose that infectives have independent infectivity profiles, each distributed as $\mathcal{I}(t)$ $(t \geq 0)$. Again $\mathcal{I}(t)$ is normalised so that $\mathbb{E}\left[\int_0^\infty \mathcal{I}(t)\mathrm{d}t\right] = 1$. If an infective has infectivity profile $\mathcal{I}(t)$ $(t \geq 0)$, then t time units after infection he/she makes global infectious contacts at overall rate $\mu_G \mathcal{I}(t)$, infectious contacts to any given member of his/her household at rate $\lambda_H^{(n)} I(t)$ and to any given member of his/her workplace at rate $\lambda_W^{(n')} I(t)$, where n and n' are the sizes of the infective's household and workplace, respectively. As previously, let $w_G(t) = \mathbb{E}[\mathcal{I}(t)]$ $(t \geq 0)$ and recall that w_G is the probability density function of a random variable W_G having moment-generating function $\mathcal{M}_{W_G}(\theta)$.

Consider a typical single-household epidemic with one initial infective, who becomes infected at time $t = 0$. For $t \geq 0$, let $\xi_H(t)$ be the rate at which new infections occur in that single-household epidemic at time t. Define $\xi_W(t)$ $(t \geq 0)$ similarly for a typical single-workplace epidemic.

Recall the 3-type real-time branching process introduced in Section 4.2. For $t \geq 0$, let $M(t) = [m_{dd'}(t)]$, where $m_{dd'}(t)$ is the mean rate at which a type-d individual having age t spawns type-d' individuals $(d, d' = 1, 2, 3)$. Then

$$M(t) = \begin{bmatrix} \mu_G w_G(t) & \xi_W(t) & \xi_H(t) \\ \mu_G w_G(t) & 0 & \xi_H(t) \\ \mu_G w_G(t) & \xi_W(t) & 0 \end{bmatrix}.$$

For $r \in (-\infty, \infty)$, let $\mathcal{L}_M(r) = \int_0^\infty M(t)\mathrm{e}^{-\theta t}\mathrm{d}t$, where the integration is elementwise. Then the real-time growth rate r is given by the unique real value of r such that the dominant eigenvalue of $\mathcal{L}_M(r)$ is one.

Observe that the matrix $\mathcal{L}_M(r)$ has the same structure of non-zero elements as the matrix $A^{(HW)}(\lambda)$ defined at (30). The same argument as used in Section 4.2 shows that r is the unique real solution of the equation

$$\mu_G \mathcal{M}_{W_G}(r)(\mathcal{L}_{\xi_H}(r) + 1)(\mathcal{L}_{\xi_W}(r) + 1) + \mathcal{L}_{\xi_H}(r)\mathcal{L}_{\xi_W}(r) = 1. \tag{38}$$

Pellis et al. [21] determine the real-time growth rate of the households-workplaces model by using a two-type branching process having mean offspring matrix M_H (used at (35) to define R_H) but again run in real time, which of course gives the same result. We use the above 3-type branching process to facilitate comparison of R_r with R_0.

Similar to the households model, the difficulty in using (38) to calculate r is that generally there is no tractable expression for $\mathcal{L}_{\xi_H}(r)$ or $\mathcal{L}_{\xi_W}(r)$. However, we can use similar

approximations to those used in Section 2.8 for the households model. First, it is easily verified that using the approximations (cf. (22)) $\mathcal{L}_{\xi_H}(r) \approx \mathcal{L}^{(0)}_{\xi_H}(r)$ and $\mathcal{L}_{\xi_W}(r) \approx \mathcal{L}^{(0)}_{\xi_W}(r)$, where

$$\mathcal{L}^{(0)}_{\xi_H}(r) = \sum_{\ell=1}^{n_H-1} \mu^H_\ell \left(\mathcal{M}_{W_G}(r)\right)^\ell \tag{39}$$

and

$$\mathcal{L}^{(0)}_{\xi_W}(r) = \sum_{\ell'=1}^{n_W-1} \mu^W_{\ell'} \left(\mathcal{M}_{W_G}(r)\right)^{\ell'}, \tag{40}$$

leads to R_r being given by R_0.

Second, for $n = 2, 3, \cdots, n_H$, let $\widetilde{W}^{(n,H)}_G$ be a random variable describing the time of the first within-household contact from one specified individual to another specified individual in a household of size n and, for $n' = 2, 3, \cdots, n_W$, define $\widetilde{W}^{(n',W)}_G$ analogously for a workplace contact. Also, for $n = 1, 2, \cdots, n_H$, let π^H_n be the (size-biased) probability an individual chosen uniformly at random from the population resides in a household of size n and, for $n' = 1, 2, \cdots, n_W$, let π^W_n be the corresponding workplace size-biased probability. Then (cf. (24) and (27)), we have $\mathcal{L}_{\xi_H}(r) \approx \widetilde{\mathcal{L}}_{\xi_H}(r)$ and $\mathcal{L}_{\xi_W}(r) \approx \widetilde{\mathcal{L}}_{\xi_W}(r)$, where

$$\widetilde{\mathcal{L}}_{\xi_H}(r) = \sum_{n=2}^{n_H} \pi^H_n \sum_{\ell=1}^{n-1} \mu^{(n,H)}_\ell \left(\mathcal{M}_{\widetilde{W}^{(n,H)}_G}(r)\right)^\ell \tag{41}$$

and

$$\widetilde{\mathcal{L}}_{\xi_W}(r) = \sum_{n'=2}^{n_W} \pi^W_{n'} \sum_{\ell'=1}^{n-1} \mu^{(n',W)}_{\ell'} \left(\mathcal{M}_{\widetilde{W}^{(n',W)}_G}(r)\right)^{\ell'}, \tag{42}$$

and $\mu^{(n,H)}_\ell$ and $\mu^{(n',W)}_{\ell'}$ denote the mean size of generation ℓ in a single size-n household epidemic and generation ℓ' in a single size-n' workplace epidemic, respectively. Substituting the approximations (41) and (42) into (38) and solving for r yields an approximation, $\tilde{r}$ say, to the growth rate of the households-workplaces model. The reproduction number $\widetilde{R}_r$ is then defined as at (26) for the households model.

Note that if $\lambda^{(n)}_H$ and $\lambda^{(n')}_W$ are independent of household size n and workplace size n', respectively, then, in an obvious notation, (41) and (42) simplify to

$$\widetilde{\mathcal{L}}_{\xi_H}(r) = \sum_{\ell=1}^{n_H-1} \mu^H_\ell \left(\mathcal{M}_{\widetilde{W}^H_G}(r)\right)^\ell \text{ and } \widetilde{\mathcal{L}}_{\xi_W}(r) = \sum_{\ell'=1}^{n_W-1} \mu^W_{\ell'} \left(\mathcal{M}_{\widetilde{W}^W_G}(r)\right)^{\ell'}. \tag{43}$$

The approximations $\mathcal{L}_{\beta_H}(r) \approx \widetilde{\mathcal{L}}_{\beta_H}(r)$ and $\mathcal{L}_{\beta_W}(r) \approx \widetilde{\mathcal{L}}_{\beta_W}(r)$ are exact if $\max(n_H, n_W) \leq 2$, so in that case $R_r = \widetilde{R}_r$.

5 Comparisons of household-workplaces model reproduction numbers

As stated at the end of Section 4.1, we assume that μ_G, μ_H and μ_W are all strictly positive, and that $\min(n_H, n_W) \geq 2$. By interchanging households and workplaces, R_W and R_H relate in a similar fashion to the other reproduction numbers, so we do not consider R_W in the comparisons. As with the households model, an epidemic is called growing if $R_* > 1$ and declining if $R_* < 1$.

The following theorem is proved in Section 7.3.

Theorem 3 *(a)* $R_* = 1 \iff R_H = 1 \iff R_I = 1 \iff R_0 = 1 \Longrightarrow R_V = 1$.

(b) In a growing epidemic,

$$R_* > R_H > R_I \geq R_V \geq R_0 > 1,$$

and in a declining epidemic

$$R_* < R_H < R_I \leq R_0 < 1.$$

The inequalities $R_I \geq R_V$ and $R_I \leq R_0$ are strict if and only if $\max(n_H, n_W) > 2$. The inequality $R_V \geq R_0$ is strict if and only if $\max(n_H, n_W) > 3$.

(c) Theorem 2 holds also for the households-workplaces model.

The main practical use of Theorem 3 is that, as for the households model, $R_I \geq R_V \geq R_0$ for a growing epidemic. Thus, with a perfect vaccine, if individuals are selected for vaccination uniformly at random then the critical vaccination coverage p_C, assuming a growing epidemic, satisfies

$$1 - 1/R_0 \leq p_C \leq 1 - R_I.$$

Finally, consider the case $\mu_G = 0$. The reproduction numbers R_0, R_H, R_W, R_I, R_r and $\widetilde{R}_r$ can all be defined essentially as before but note, for example, that the branching process underlying R_0 is now 2-type, rather than 3-type, since double-primary cases no longer occur (apart from in global generation 0, i.e. the initial infectives in the epidemic at large). The reproduction number $R_* = 0$, since clumps no longer reproduce, though (cf. Section 4.4) a clump may be infinite in size. It is easily seen that Theorem 3, with R_* removed, continues to hold when $\mu_G = 0$, as does the generalisation of Theorem 2 to the households-workplaces model.

6 Numerical illustrations

In this section we present some numerical examples which illustrate the inequalities between reproduction numbers considered in the paper. Most of these reproduction numbers are fairly straightforward to compute for a wide range of modelling assumptions. This is not the case

for the exponential-growth-associated reproduction number R_r, which generally cannot be computed explicitly. A notable exception is if the underlying epidemic model is Markovian and therefore most of our numerical examples are for such models. The main practical interest in these illustrations is how well the various reproduction numbers approximate the perfect-vaccine-associated reproduction number R_V.

6.1 Markov SIR and SEIR households models

We consider the model introduced by Ball et al. [4], Section 3.1, specialised to exponential infectious periods. Thus we assume that all households have common size n, that the total population size is N and that the infectious period of an infective has an exponential distribution having mean one. (The unit of time may be chosen to be the mean of the infectious period.) During his/her infectious period, a given infective makes global contact with any given susceptible in the population at the points of a homogeneous Poisson process having rate μ_G/N and, additionally, local contacts with any given susceptible in his/her household at the points of a homogeneous Poisson process having rate λ_H. All the Poisson processes describing infectious contacts (whether or not either or both of the individuals involved are the same) and all the infectious periods are assumed to be independent. There is no latent period, so a susceptible becomes an infective as soon as he/she is contacted by an infective. Denote this epidemic model by $\mathscr{E}^H(n, \mu_G, \lambda_H)$.

We now describe briefly the calculation of the various reproduction numbers for this model. The mean generation sizes $\mu_1^{(n)}, \mu_2^{(n)}, \cdots, \mu_{n-1}^{(n)}$ for a single size-n household epidemic may be computed using the method described by Pellis et al. [22], Appendix A, thus enabling R_0 to be calculated. The reproduction numbers R_*, R_I, R_2 and R_{HI} are then easily calculated, since $\mu_H^{(n)} = \mu_1^{(n)} + \mu_2^{(n)} + \cdots + \mu_{n-1}^{(n)}$. Alternatively, $\mu_H^{(n)}$ may be computed more directly using Ball [3], equations (2.25) and (2.26).

The perfect-vaccine-associated reproduction number R_V is computed as follows. Suppose that a fraction p of the population is vaccinated, with individuals selected for vaccination uniformly at random from the population. After vaccination, the probability that a global contact is successful (i.e. is with an unvaccinated individual) is $1-p$, so the mean number of global contacts made by an infective is $(1-p)\mu_G$. If a global contact is successful then the number of other unvaccinated individuals in the globally contacted individual's household follows a binomial distribution, whence the expected number of households infected by a typical infected household in an otherwise uninfected population, $R_*^V(p)$ say, is given by

$$R_*^V(p) = (1-p)\mu_G \left(1 + \sum_{j=1}^{n-1} \binom{n-1}{j} (1-p)^j p^{n-1-j} \mu_H^{(j+1)}\right).$$

The corresponding critical vaccination coverage p_C is found by solving $R_*^V(p) = 1$ numerically and R_V then follows using (17). The leaky-vaccine-associated reproduction number R_{VL} may be computed by noting that if the entire population is vaccinated with a leaky vaccine having efficacy $\mathcal{E}$ then after vaccination the model behaves as $\mathscr{E}^H(n, (1-\mathcal{E})\mu_G, (1-\mathcal{E})\lambda_H)$, so a

post-vaccination reproduction number, $R_*^{VL}(\mathcal{E})$ say, is easily calculated. The critical efficacy $\mathcal{E}_C$ is found by solving $R_*^{VL}(\mathcal{E}) = 1$ numerically and R_{VL} is then given by (18).

Turning to the exponential-growth-associated reproduction number R_r and its approximation $\widetilde{R}_r$, the real-time growth rate r for the Markov SIR households model $\mathscr{E}^H(n, \mu_G, \lambda_H)$ may be computed using the matrix method described in Pellis et al. [21], Section 4.2. The infectivity profile of a typical infective in $\mathscr{E}^H(n, \mu_G, \lambda_H)$ is given by (23), with $T_I \sim \text{Exp}(1)$. Hence, $W_G \sim \text{Exp}(1)$, so $\mathcal{M}_{W_G}(\theta) = (1+\theta)^{-1}$ $(\theta > -1)$ and, recalling (20), $R_r = 1 + r$. As explained just after (23), $\widetilde{W}_G \sim \text{Exp}(1 + \lambda_H)$, so $\mathcal{M}_{\widetilde{W}_G}(\theta) = \frac{1+\lambda_H}{1+\lambda_H+\theta}$ $(\theta > -(1+\lambda_H))$. It follows that $\widetilde{R}_r = 1 + \tilde{r}$, where $\tilde{r}$ solves (25).

Figures 3 to 5 show the various reproduction numbers as functions of the within-household infection rate λ_H for various combinations of household size n and overall global infection rate μ_G. The parameters and format are the same as in Figure 1 of Goldstein et al. [11], though the range of values for λ_H is reduced. Note that in this model all of the reproduction numbers, except R_r and $\widetilde{R}_r$, are invariant to the introduction of a latent period into the model. Figure 3 compares all of the reproduction numbers except R_{VL}, R_r and $\widetilde{R}_r$. Observe that they are all ordered in accordance with Theorem 1*(b)* and that the conjectured comparison between R_0 and R_2 is also satisfied. Moreover, $R_I = R_0 = R_2$ $(= R_V$ in a growing epidemic) when $n = 2$, as expected. In particular, $R_0 \leq R_V \leq R_I$ in a growing epidemic. Note that generally, in a growing epidemic, R_* is appreciably greater than R_I and is a poor approximation to R_V. (Recall, though, that in the present setting, when all households have the same size, R_* gives the correct critical vaccination coverage if households are either fully vaccinated or fully unvaccinated.) Also, in a growing epidemic, R_{HI} is generally a noticeably worse lower bound to R_V than R_2. Indeed R_2 and R_0 are very close and, as is the case in most of the figures, R_0 is very close to R_V. Note that less knowledge of the epidemic model is required to compute R_2 than to compute R_0.

Figure 4 compares the reproduction numbers R_I, R_{VL}, R_V, R_0 and R_2. Recall that, in our notation, Goldstein et al. [11] proved that, in a growing epidemic, $\bar{R}_{HI} \leq R_V \leq R_{VL} \leq R_*$ so, using Theorem 1*(b)*, $R_0 \leq R_V \leq R_{VL}$, as is clearly seen in Figure 4. Note that although R_I and R_{VL} cannot be ordered in general (see the graphs when $n = 8$ and $\mu_G = 10$), R_{VL} is generally appreciably larger than R_I, unless the within-household infection rate is small.

Figure 5 compares the exponential-growth-associated reproduction number R_r and its variant $\widetilde{R}_r$ with R_I, R_V and R_0. Goldstein et al. [11] noted that in most plausible parameter regions $R_r \geq R_V$ and this is seen in Figure 5. However, R_r is usually an appreciably coarser upper bound than R_I for R_V, though, as seen from the graphs when $n = 8$ and $\mu_G = 10$, it is not possible to order R_r and R_I in general. As a particular case of Theorem 2*(c)*, for the Markov SIR model, in all growing epidemics $R_0 \leq \widetilde{R}_r \leq R_r$ and, for $n = 2$, $R_r = \widetilde{R}_r$ since $\widetilde{W}_G$ gives the correct infection interval for local infection between the primary and secondary case in a household. Also note that, when $n = 2$, $R_r = R_{VL}$. This is proved in Appendix E, where it is shown that R_r and R_{VL} cannot in general be ordered.

We now add a latent period to the above model. Specifically we assume that infectives have independent latent periods, each distributed as $\text{Exp}(\delta)$, so the mean latent period is δ^{-1}. The latent periods are also independent of all the other random quantities used to

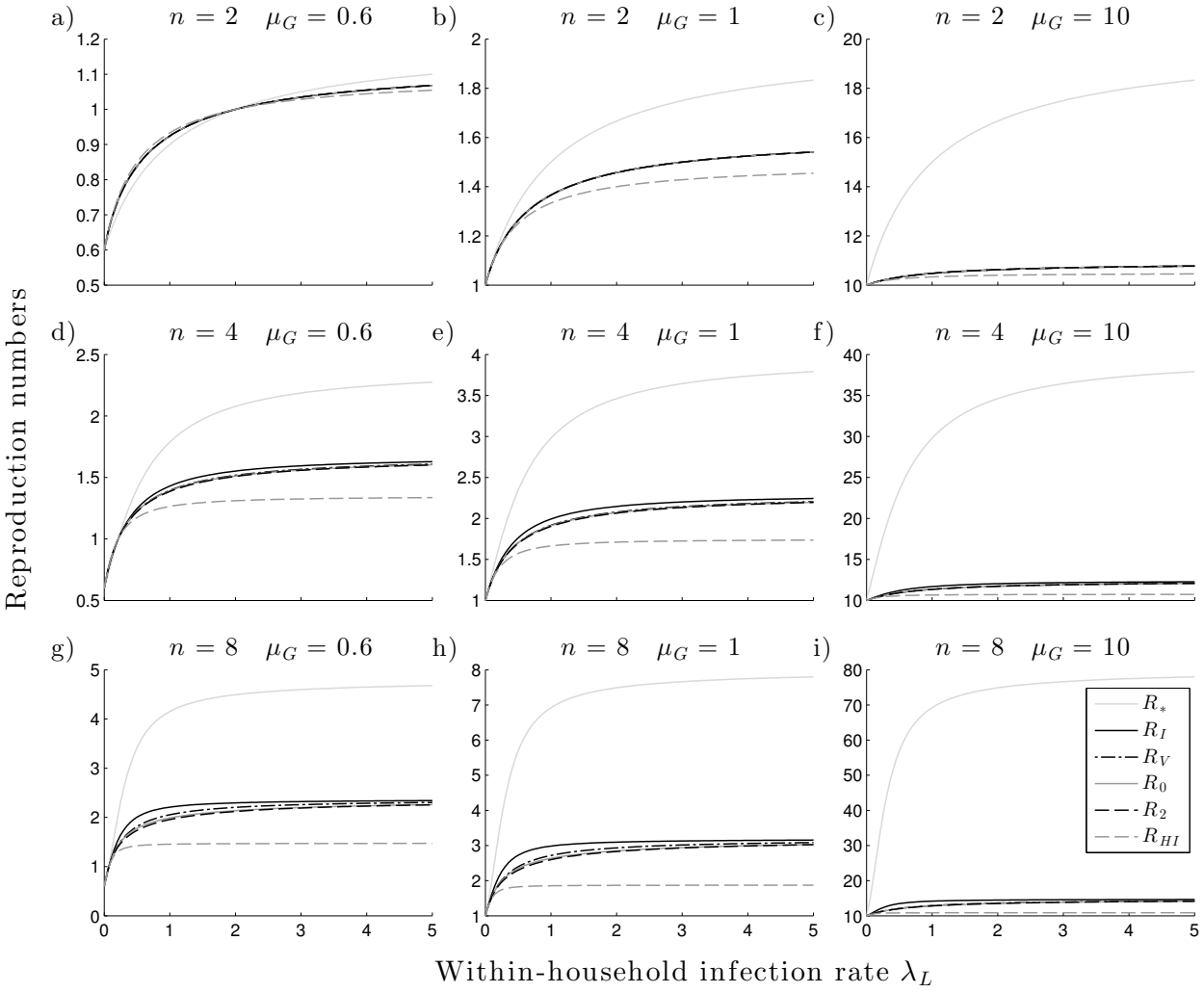

Figure 3: Reproduction numbers R_*, R_I, R_V, R_0, R_2 and R_{HI} for the Markov SIR households model $\mathscr{E}^H(n, \mu_G, \lambda_H)$.

define the model. Thus the model is now a Markov SEIR households epidemic model and is identical to one used by Goldstein et al. [11] in their numerical illustrations. As noted previously, the introduction of a latent period changes only the reproduction numbers R_r and $\widetilde{R}_r$.

Denote the above model by $\mathscr{E}^H(n, \mu_G, \lambda_H, \delta)$. Goldstein et al. [11] determined the real-time growth rate r for $\mathscr{E}^H(n, \mu_G, \lambda_H, \delta)$ by linearising a system of differential equations that describe the evolution of the relative numbers of households in different states (when the total population size N is large), where the state of a household is given by the number of infected, latent and susceptible individuals it contains, and determining the corresponding largest eigenvalue. We determine r by extending the matrix method in Pellis et al. [21], Section 4.2, to incorporate a latent period. The infectivity profile of a typical infective in

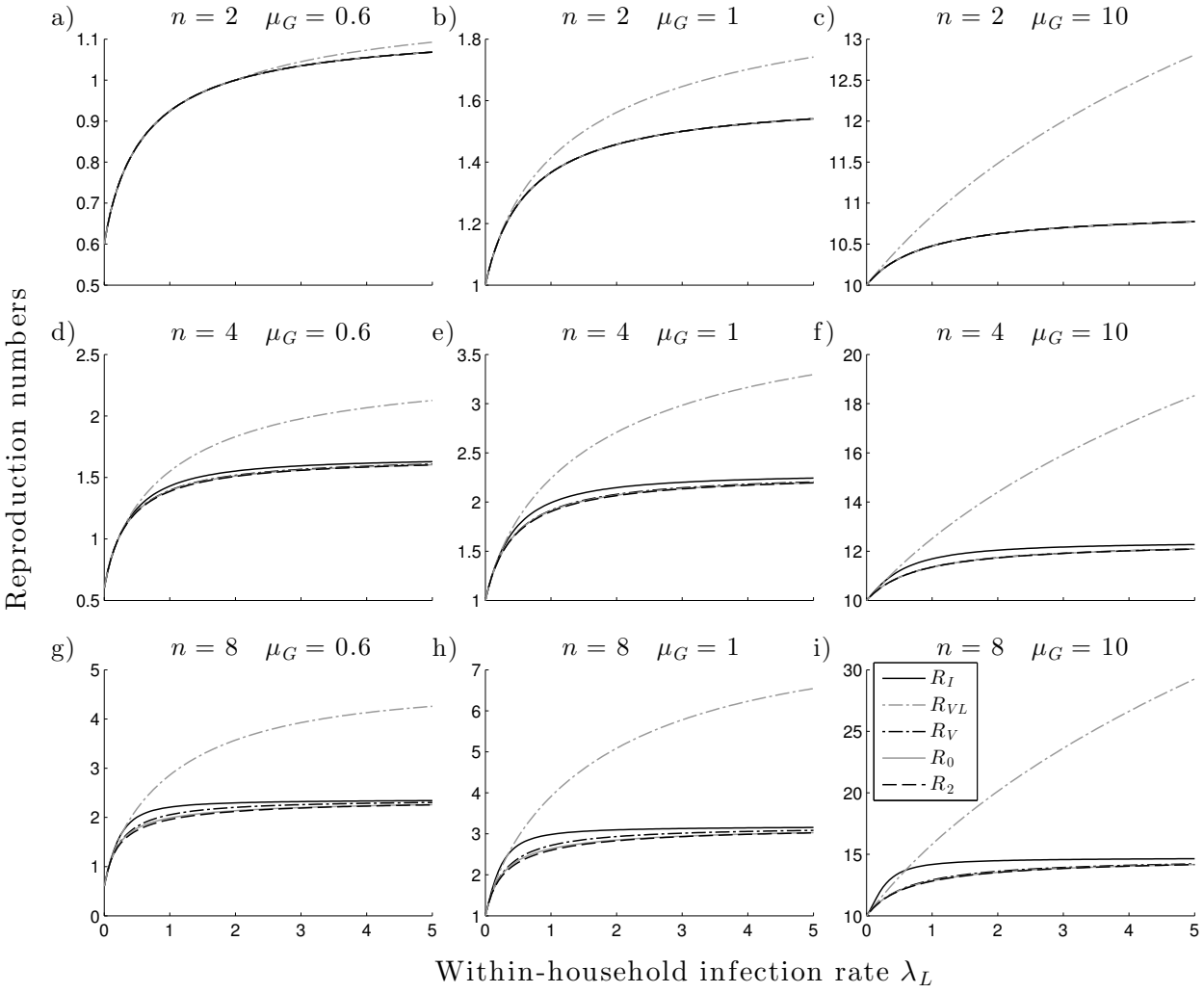

Figure 4: Reproduction numbers R_I, R_{VL}, R_V, R_0 and R_2 for the Markov SIR households model $\mathscr{E}^H(n, \mu_G, \lambda_H)$.

$\mathscr{E}^H(n, \mu_G, \lambda_H, \delta)$ is given by

$$\mathcal{I}(t) = \begin{cases} 1 & \text{if } T_E \le t \le T_E + T_I, \\ 0 & \text{otherwise}, \end{cases}$$

where $T_E \sim \text{Exp}(\delta)$ and $T_I \sim \text{Exp}(1)$ are independent random variables giving the latent and infectious periods of a typical infective. It is then readily verified that

$$\mathcal{M}_{W_G}(\theta) = \frac{\delta}{(\delta + \theta)(1 + \theta)} \qquad (\theta > -\min(1, \delta)).$$

Note that $W_G = \Psi_0 + T_E$, where Ψ_0 is the infectious contact interval for $\mathscr{E}^H(n, \mu_G, \lambda_H)$, and

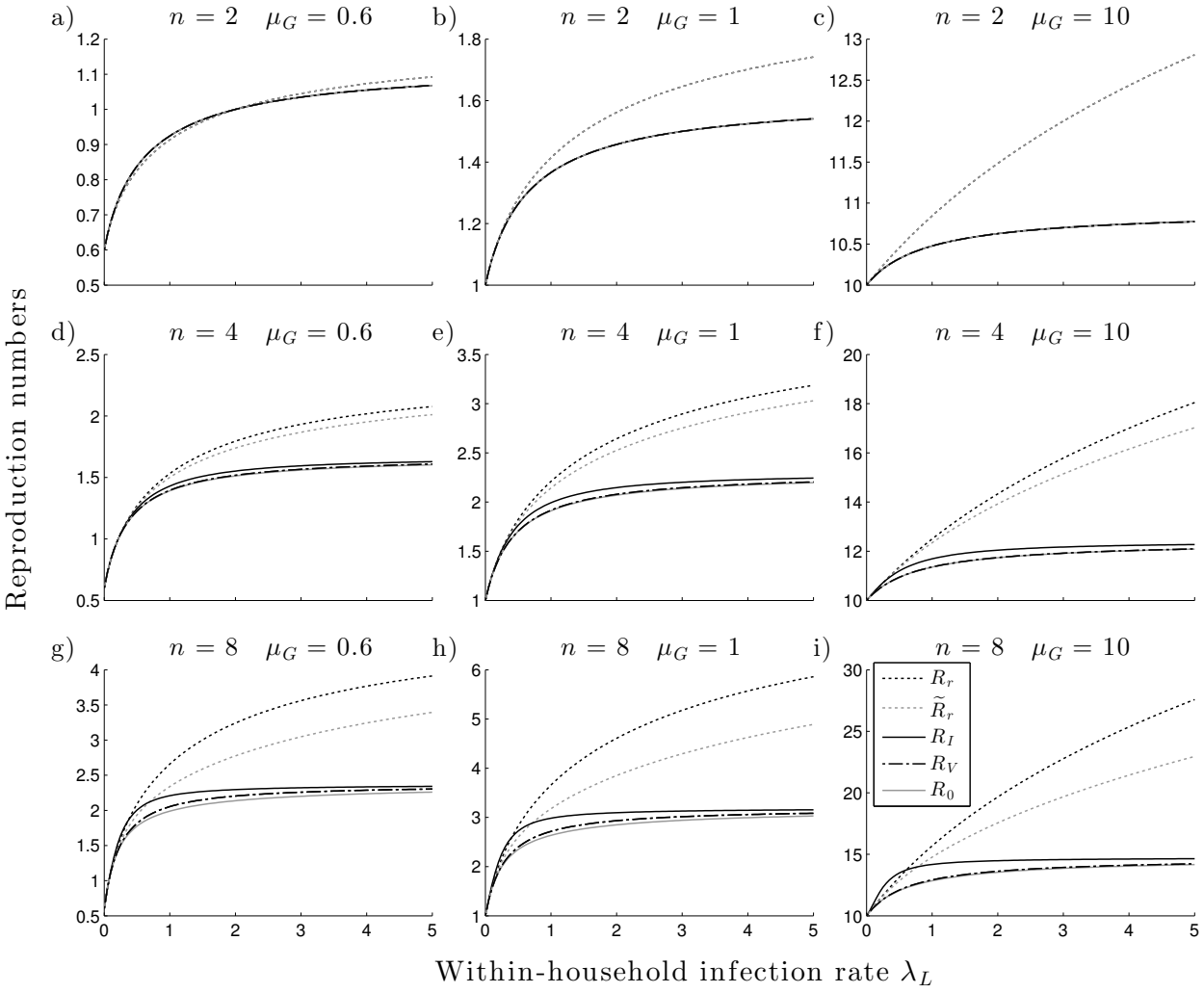

Figure 5: Reproduction numbers $R_r, \widetilde{R}_r, R_I, R_V$ and R_0 for the Markov SIR households model $\mathscr{E}^H(n, \mu_G, \lambda_H)$.

Ψ_0 and T_E are independent. Further, in an obvious notation, $\widetilde{W}_G = \Phi_0 + T_E$, whence

$$\mathcal{M}_{\widetilde{W}_G}(\theta) = \frac{\delta}{\delta + \theta} \frac{1 + \lambda_H}{1 + \lambda_H + \theta} \qquad (\theta > -\min(1 + \lambda_H, \delta)).$$

Thus, given r, both R_r and $\widetilde{R}_r$ are easily calculated.

Figure 6 shows the exponential-growth-associated reproduction numbers R_r and $\widetilde{R}_r$, and also R_I, R_{VL}, R_V and R_0, as functions of the mean latent period δ^{-1}. For the case $n = 2$, $R_r = \widetilde{R}_r$, as with the SIR model, and $R_0 = R_V = R_I$, agreeing with Theorem 1*(b)*. Further, $\widetilde{R}_r \neq R_0$, since W_G and $\widetilde{W}_G$ have different distributions. Note that R_r is decreasing in δ^{-1} and converges to R_0 as $\delta^{-1} \to \infty$. When $n = 3$, a similar picture emerges except that $R_0 = R_V < R_I$ and $R_r > \widetilde{R}_r$, though both R_r and $\widetilde{R}_r$ converge to R_0 $(= R_V)$ as $\delta^{-1} \to \infty$.

Observe that neither R_r nor $\widetilde{R}_r$ can be ordered with R_I. The main differences between the cases $n = 3$ and $n = 4$ is that when $n = 4$, $R_0 < R_V$ and the exponential-growth-associated reproduction numbers R_r and $\widetilde{R}_r$ tend to different limits as $\delta^{-1} \to \infty$, though the discrepancy is difficult to see as R_0 and R_V are very close. It is much clearer in the case when $n = 8$. Observe that $\widetilde{R}_r \to R_0$ as $\delta^{-1} \to \infty$, whilst R_r converges to a limit lying strictly between R_0 and R_V. The fact that $R_r < R_V$ for very long latent periods when $n \geq 4$ is noted in Goldstein et al. [11], though the proof in Appendix B of that paper, which in our terminology shows that $R_r \to R_0$ as the latent periods become infinitely long, does not hold for the Markov SEIR households model. This is explored further in Appendix F, where it is proved that for the Markov SEIR households model, in the limit as $\delta^{-1} \to \infty$, if the maximum household size $n_H \leq 3$ then $R_r = \widetilde{R}_r = R_0$ $(= R_V)$, whilst if $n_H \geq 4$ then $R_r > \widetilde{R}_r = R_0$. Further, when $n_H = 4$, we show that $R_V > R_r > R_0$, though we do not have a proof for $n_H \geq 5$. Although such long latent periods do not occur in real-life infections, we let the mean latent period δ^{-1} in Figures 6 and 9 run up to 10^4 times the mean infectious period to illustrate the limiting behaviour of the reproduction numbers as $\delta^{-1} \to \infty$.

6.2 Households model with non-random infectivity profile

We now assume that the infectivity profile of an individual is non-random. Specifically, following Fraser [10] and Goldstein et al. [11], we assume that the infectious contact interval W_G follows a gamma distribution, with parameters $\alpha > 0$ and $\gamma > 0$. Thus $\mathcal{I}(t) = w_G(t)$ $(t \geq 0)$, where

$$w_G(t) = \frac{\gamma^\alpha t^{\alpha-1} \mathrm{e}^{-\gamma t}}{\Gamma(\alpha)} \tag{44}$$

and $\Gamma(\alpha) = \int_0^\infty t^{\alpha-1}\mathrm{e}^{-t}\mathrm{d}t$ is the gamma function. Similar to Section 2.8, we assume that, t time units after he/she was infected, an infectious individual makes global contacts at overall rate $\mu_G w_G(t)$ and, additionally, he/she contacts any given susceptible in his/her household at rate $\lambda_H w_G(t)$. Thus, since $\int_0^\infty w_G(t)\mathrm{d}t = 1$, a given infective infects locally other members of its household independently, each with probability $p = 1 - \mathrm{e}^{-\lambda_H}$. It follows that the mean generation sizes $\mu_1^{(n)}, \mu_2^{(n)}, \cdots, \mu_{n-1}^{(n)}$ for a single size-n household epidemic coincide with those of a Reed-Frost model with escape probability $q = 1 - p$ and hence may be computed using the algorithm in Appendix A of Pellis et al. [22]. This enables all of the reproduction numbers, except for R_r and $\widetilde{R}_r$, to be computed in a similar fashion as for the Markov SIR model. (Again $\mu_H^{(n)}$ may be computed more directly using Ball [3], Equations (2.25) and (2.26).) Note that, except for R_r and $\widetilde{R}_r$, all of the reproduction numbers are independent of the parameters (α, γ) of the gamma distribution that describes the infectivity profile; indeed they are independent of the infectivity profile, provided it is non-random.

To calculate R_r, the real-time growth rate r is required, for which we are not aware of any exact method of calculation. Goldstein et al. [11] used stochastic simulations, involving an approximate discrete-time model having a small time step, to estimate the mean infectivity profile $\beta_H(t)$ $(t \geq 0)$ of a single-household epidemic. We use a simulation method, based on a Sellke [25] construction and described in Appendix G, to estimate the Laplace transform

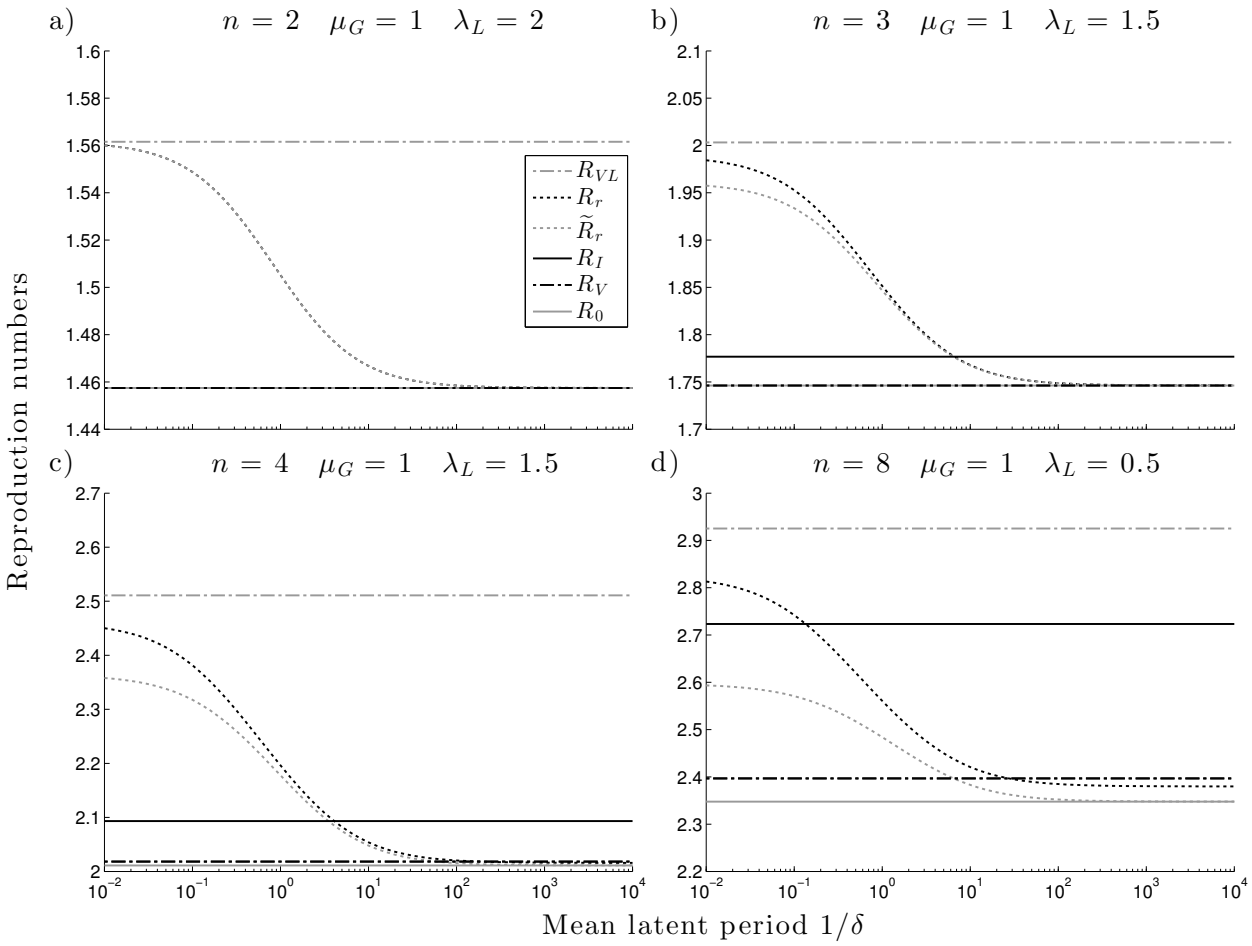

Figure 6: Reproduction numbers $R_r, \widetilde{R}_r, R_{VL}, R_I, R_V$ and R_0 for the Markov SEIR households model $\mathscr{E}^H(n, \mu_G, \lambda_H, \delta)$.

$\mathcal{L}_{\beta_H}(\theta)$ of $\beta_H(t)$, whence r is obtained by solving $\mathcal{L}_{\beta_H}(r) = 1$ numerically. The reproduction number R_r then follows, using (20) with $\mathcal{M}_{W_G}(r) = \left(\frac{\gamma}{\gamma+r}\right)^{\alpha}$. In the present model there is no closed-form expression for $\mathcal{M}_{\widetilde{W}_G}(\theta)$, so we do not consider $\widetilde{R}_r$.

For brevity we present results only for the case when all households are of size 8 and $\mu_G = 1$. In Figure 7a, the reproduction numbers R_*, R_I, R_V, R_0, R_2 and R_{HI} are plotted against the within-household infection probability p. These reproduction numbers satisfy $R_{HI} < R_0 < R_V < R_I < R_*$ and $R_{HI} < R_2 < R_I$, as predicted by Theorem 1*(b)*, and the conjecture $R_2 < R_0$. As $p \to 1$, so $\lambda_H \to \infty$, the mean generation sizes become $\mu_1 = 7$ and $\mu_k = 0$ $(k = 2, 3, \cdots, 7)$, and the corresponding limiting values of the reproduction numbers are easily obtained. Note that unless p is small, i.e. unless there is very little enhanced spread of infection within households, R_* is a coarse upper bound for R_V and R_{HI} is a coarse lower bound. Further, R_0 is a good approximation to R_V across the full range of values for

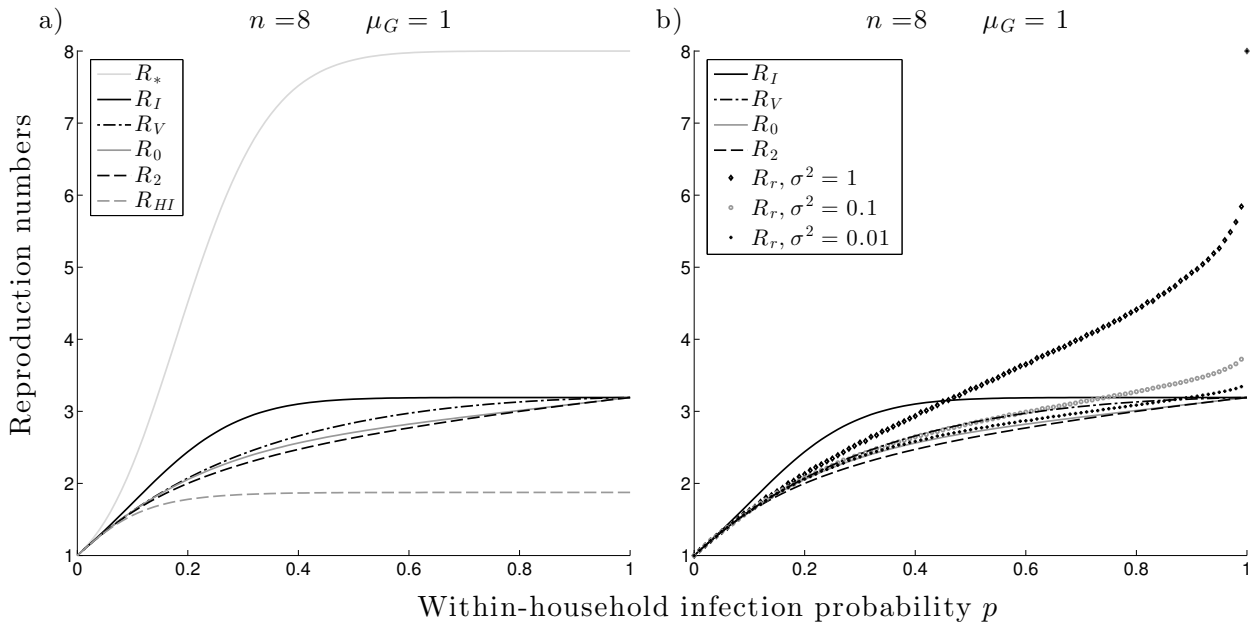

Figure 7: a) Reproduction numbers R_*, R_I, R_V, R_0, R_2 and R_{HI} for a households model with a non-random infectivity profile; and b) reproduction numbers R_I, R_V, R_0, R_2 and R_r (with $\sigma^2 = 1, 0.1$ and 0.01) for a households model with a non-random infectivity profile which follows a gamma distribution with mean 1.

p, though it is an underestimate.

Figure 7b shows the reproduction numbers R_2, R_0, R_V, R_I and R_r as functions of p. Note that R_r depends on the parameters of the gamma distribution describing the non-random infectivity profile. When W_G has probability density function given by (44), $\mathbb{E}[W_G] = \frac{\alpha}{\gamma}$ and $\sigma^2 = \mathrm{Var}(W_G) = \frac{\alpha}{\gamma^2}$. In Figure 7b, we assume that $\mathbb{E}[W_G] = 1$, so $\alpha = \gamma$, and show R_r when $\sigma^2 = 1$ ($\alpha = 1$), $\sigma^2 = 0.1$ ($\alpha = 10$) and $\sigma^2 = 0.01$ ($\alpha = 100$). Each graph for R_r is estimated from $10,000$ simulations of the corresponding single-household epidemic. Observe that, for fixed p, the exponential-growth-associated reproduction number R_r is a decreasing function of σ^2. As σ^2 decreases to 0 the epidemic model becomes more and more like a Reed-Frost type model, for which $R_r = R_0$. The accuracy of R_r as an approximation to R_V depends on both the variance of the infectious contact interval W and on how infectious the disease is within households. Generally, the approximation is good when p is small, since then there is little spread within households, and improves as σ^2 decreases. Normally, R_r overestimates R_V but when the infectious contact interval is highly peaked it may be a slight underestimate, as is illustrated in the graph when $\sigma^2 = 0.01$.

6.3 Markov SIR and SEIR households-workplaces models

The Markov SIR households model described in Section 6.1 is readily generalised to incorporate workplaces. For simplicity, we assume that all households have common size n_H and all workplaces have common size n_W. During his/her infectious period, which is distributed as Exp(1), a typical infective makes global contacts at overall rate μ_G, infects any given susceptible in his/her household at rate λ_H and any susceptible in his/her workplace at rate λ_W. The mean generation sizes for within-household and within-workplace epidemics may be evaluated using the methods described for the Markov SIR households model, so, apart from R_r and $\widetilde{R}_r$, the reproduction numbers are readily computed.

To compute the exponential-growth-associated reproduction number R_r, consider first a single-household epidemic and let $S(t)$ and $I(t)$ be respectively the numbers of susceptible and infectives at time t. Then, at time t, new infections occur in this household at rate $\lambda_H S(t)I(t)$, so, in the notation of Section 4.7, $\xi_H(t) = \lambda_H \mathbb{E}[S(t)I(t)]$ ($t \geq 0$). Hence

$$\mathcal{L}_{\xi_H}(\theta) = \int_0^\infty \lambda_H \mathbb{E}[S(t)I(t)]\mathrm{e}^{-\theta t}\mathrm{d}t,$$

which can be evaluated numerically using the matrix method described in Pellis et al. [21], Section 4.3. The Laplace transform $\mathcal{L}_{\xi_W}(\theta)$ may be computed similarly. The real-time growth rate r may be computed by solving (38) numerically (recall that $\mathcal{M}_{W_G}(\theta) = (1+\theta)^{-1}$) and R_r is then given by $R_r = 1 + r$. Note that, in the notation of (43) $\mathcal{M}_{\widetilde{W}_G^H}(r) = \frac{1+\lambda_H}{1+\lambda_H+r}$ and $\mathcal{M}_{\widetilde{W}_G^W}(r) = \frac{1+\lambda_W}{1+\lambda_W+r}$, thus enabling $\tilde{r}$ to be computed, whence $\widetilde{R}_r = 1 + \tilde{r}$.

Figure 8 is for a model in which $n_H = 5$ and $n_W = 15$. Figure 8a shows graphs of the reproduction numbers R_H, R_W, R_I, R_V and R_0 against λ_H when $\mu_G = 0.1$ and $\lambda_W = 0.5$. For these parameter values, R_H and R_W are distinct, though their difference is small and both are useless as approximations to R_V (R_*, not shown as it is so large, is even worse). This is

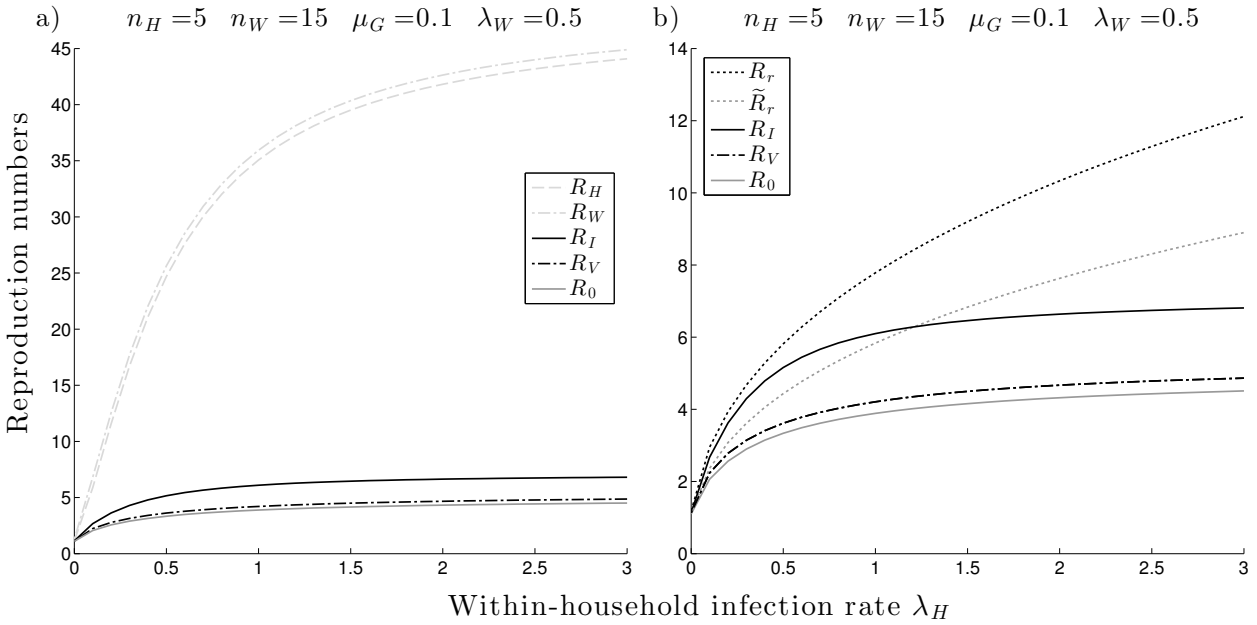

Figure 8: a) Reproduction numbers R_H, R_W, R_I, R_V and R_0 and b) reproduction numbers $R_r, \widetilde{R}_r, R_I, R_V$ and R_0 for a Markov SIR households-workplaces model.

because of the large within-workplace epidemic sizes. Note that the reproduction numbers satisfy the inequalities proved in Theorem 3*(b)*. In Figure 8b, the reproduction numbers $R_r, \widetilde{R}_r, R_I, R_V$ and R_0 are plotted against λ_H when $\mu_G = 0.5$ and $\lambda_W = 0.1$. Observe that $R_0 < \widetilde{R}_r < R_r$ for $\lambda_H > 0$, in accordance with Theorem 3*(c)*, and that neither R_r nor $\widetilde{R}_r$ can be ordered with R_I. Unless λ_H is small, R_r is not a good approximation to R_V. Note that in Figure 8, R_0 is a close approximation to R_V for all values of λ_H.

Finally, we consider the Markov SEIR version of the above model, which incorporates a latent period having an Exp(δ) distribution. Again, apart from R_r and $\widetilde{R}_r$, the reproduction numbers are unchanged by the inclusion of a latent period. The method described above for computing the real-time growth rate r is easily extended to the present model. Note that $\mathcal{M}_{W_G}(\theta)$ is the same as in the above Markov SEIR households model, $\mathcal{M}_{\widetilde{W}_G^H}(\theta) = \frac{\delta}{\delta+\theta}\frac{1+\lambda_H}{1+\lambda_H+\theta}$ $(\theta > -\min(1+\lambda_H, \delta))$ and $\mathcal{M}_{\widetilde{W}_G^W}(\theta) = \frac{\delta}{\delta+\theta}\frac{1+\lambda_W}{1+\lambda_W+\theta}$ $(\theta > -\min(1+\lambda_W, \delta))$, thus enabling R_r and $\widetilde{R}_r$ to be computed.

Figure 9a shows the dependence of the reproduction numbers $R_r, \widetilde{R}_r, R_I, R_V$ and R_0 on the mean latent period δ^{-1} when $n_H = n_W = 3$, $\mu_G = 0.5, \lambda_H = 0.5$ and $\lambda_W = 0.4$. Note that $R_V = R_0 < R_I$, as predicted by Theorem 3*(b)*, and that both R_r and $\widetilde{R}_r$ converge down to R_0 as $\delta^{-1} \to \infty$. Figure 9b shows the same reproduction numbers when $n_H = 4$ and $n_W = 15$. The values of μ_G and λ_H are as before and λ_W is now 0.1, in view of the larger workplace size. Now, $R_0 < R_V < R_I$, again as predicted by Theorem 3*(b)*, and $\widetilde{R}_r \to R_0$ as $\delta^{-1} \to \infty$, whereas R_r tends to a limit lying strictly between R_0 and R_V. The limiting case when $\delta^{-1} \to \infty$ is analysed in Appendix F, where similar results as for the households

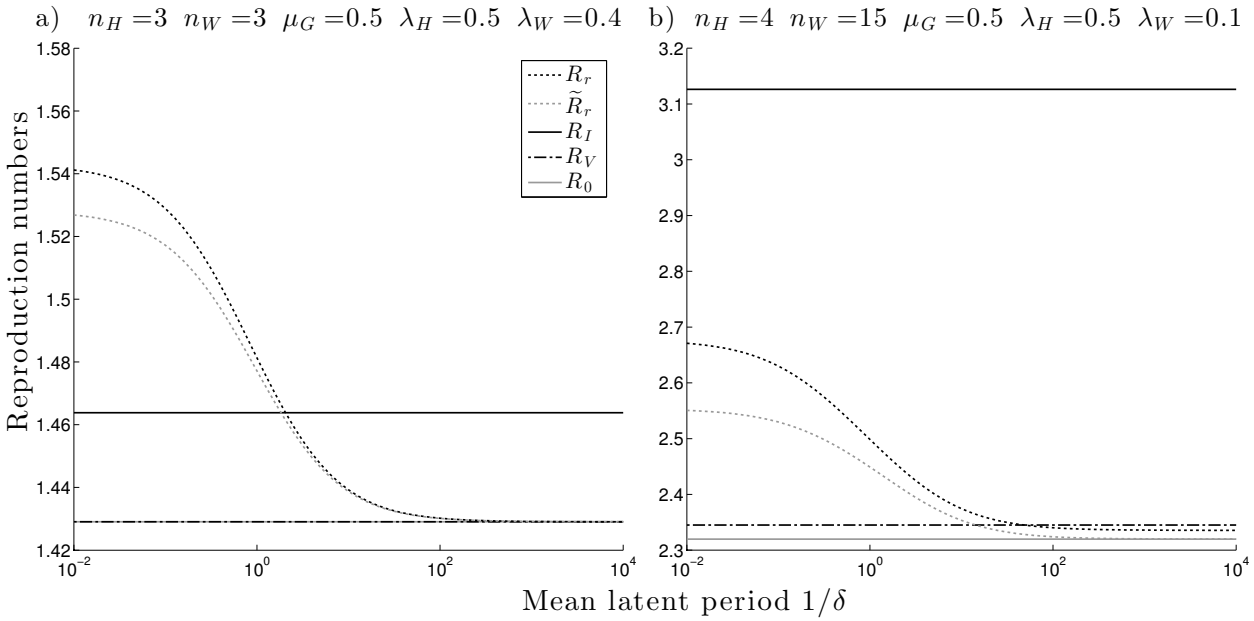

Figure 9: Reproduction numbers $R_r, \widetilde{R}_r, R_I, R_V$ and R_0 for a Markov SEIR households-workplaces model.

model are proved. Note that in Figure 9b, R_I is appreciably greater than R_r, owing in part to the effect of large workplaces.

7 Proofs

We define sign(x) to be -1, 0 and 1, for $x < 0$, $x = 0$ and $x > 0$, respectively.

7.1 Proof of Theorem 1

To shorten the exposition of the proof, we use the notation $\overset{n}{\geq}$ to denote that there is equality if the population contains no household with size strictly larger than n and the inequality is strict if the population contains households with size strictly larger than n. With this notation, the statement of Theorem 1 is as follows.

Theorem 1

(a) $R_* = 1 \iff R_I = 1 \iff R_0 = 1 \iff R_2 = 0 \iff R_{HI} = 1 \implies R_V = 1.$

(b) In a growing epidemic,

$$R_* > R_I \overset{2}{\geq} R_V \overset{3}{\geq} R_0 > R_{HI} > 1 \quad \textit{and} \quad R_I \overset{2}{\geq} R_2 > R_{HI} > 1,$$

and in a declining epidemic

$$R_* < R_I \overset{2}{\leq} R_0 < R_{HI} < 1 \quad \textit{and} \quad R_I \overset{2}{\leq} R_2 < R_{HI} < 1.$$

Proof. We first prove *(a)*. Note from (5) and (8) that

$$g_0(1) = g_I(1) = 1 - \mu_G(1 + \mu_H).$$

Recalling (13), note that $1 - a^{(n)} = 1/(1 + \mu_H^{(n)})$ $(n = 1, 2, \cdots, n_H)$, so

$$g_{HI}(1) = 1 - \mu_G \sum_{n=1} n_H \pi_n (1 + \mu_H^{(n)}) = 1 - \mu_G(1 + \mu_H).$$

Similarly, recalling (16), $1 - b^{(n)} = \mu_1^{(n)}/\mu_H^{(n)}$ $(n = 2, 3, \cdots, n_H)$, so

$$g_2(1) = 1 - \mu_G \sum_{n=2} n_H \pi_n (1 + \mu_H^{(n)}) = 1 - \mu_G(1 + \mu_H).$$

Recall that $R_* = \mu_G(1 + \mu_H)$. Now g_0 and g_I are strictly increasing on $(0, \infty)$, g_{HI} is strictly increasing on (a, ∞) and g_2 is strictly increasing on (b, ∞), so

$$\text{sign}(g_0(1)) = \text{sign}(g_I(1)) = \text{sign}(g_{HI}(1)) = \text{sign}(g_2(1)) = \text{sign}(1 - R_*),$$

since R_0, R_I, R_{HI} and R_2 are the unique roots of g_0, g_I, g_{HI} and g_2, respectively. Thus

$$R_* = 1 \iff R_I = 1 \iff R_0 = 1 \iff R_{HI} = 1 \iff R_2 = 1,$$

as required. By definition, $R_V = 1$ if $R_* = 1$.

To prove *(b)*, we first note that the above argument shows that the reproductions numbers R_*, R_I, R_0, R_{HI} and R_2 are all strictly greater than 1 in a growing epidemic and strictly smaller than 1 in a declining epidemic. We consider now each of the comparisons in turn.

(i) *R_* and R_I.*

Suppose that $R_* > 1$. From (8),

$$g_I(R_*) = 1 - \frac{\mu_G}{R_*} - \frac{\mu_H \mu_G}{R_*^2} > 1 - \frac{\mu_G}{R_*} - \frac{\mu_H \mu_G}{R_*} = 0,$$

since $R_* = \mu_G(1 + \mu_H)$. Thus $R_I < R_*$, since g_I is increasing in $(0, \infty)$ and R_I is the unique root of g_I in $(0, \infty)$. A similar argument shows that $R_* < R_I$ when $R_* < 1$.

(ii) *R_I and R_V*

Suppose that $R_I > 1$ and a fraction p of the population is vaccinated with a perfect vaccine. Then μ_G is reduced to $\mu_G(p) = (1 - p)\mu_G$ and μ_H is reduced to $\mu_H(p)$, for which we now obtain a simple upper bound. Consider the epidemic graph $\mathcal{G}^{(n)}$ defined in Section 2.1. For $i = 1, 2, \cdots, n - 1$, let $\chi_i^{(n)}$ denote the event that individual i

becomes infected in the single household epidemic (i.e. if in $\mathcal{G}^{(n)}$ there is a chain of directed edges from 0 to i) and let $(\chi_i^{(n)})^{\mathcal{C}}$ denote its complement. Then the mean size of the single household epidemic (not including the primary case) is given by $\mu_H^{(n)} = \sum_{i=1}^{n-1} \mathbb{P}(\chi_i^{(n)})$. Now keep the same realisation of $\mathcal{G}^{(n)}$, vaccinate each initial susceptible independently with probability p, and hence obtain a realisation of the single-household epidemic with vaccination. For $i = 1, 2, \cdots, n-1$, let $\chi_i^{(n)}(p)$ be the event that individual i is infected by the epidemic in the vaccinated population and let $(\chi_i^{(n)}(p))^{\mathcal{C}}$ be its complement. Clearly, for $p > 0$, if $\chi_i^{(n)}(p)$ occurs, then so does $\chi_i^{(n)}$ and i is not vaccinated. Hence, if $p > 0$, $\mathbb{P}(\chi_i^{(n)}(p)) \overset{2}{\leq} (1-p)\mathbb{P}(\chi_i^{(n)})$, since vaccination is independent of $\mathcal{G}^{(n)}$. (Note that $\chi_1^{(2)}(p)$ occurs if and only if $\chi_1^{(2)}$ occurs and 1 is not vaccinated, so $\mathbb{P}(\chi_1^{(2)}(p)) = (1-p)\mathbb{P}(\chi_1^{(2)})$. However, for $n > 2$, given that individual 1 is not vaccinated, it does not necessarily follow that he/she is infected in the vaccinated epidemic if he/she is infected in the unvaccinated epidemic, since all chains from from individual 0 to individual 1 may still be broken by vaccination.) This inequality implies, in obvious notation, that $\mu_H^{(n)}(p) \overset{2}{\leq} (1-p)\mu_H^{(n)}$, and taking expectations with respect to the size-biased household size distribution (π_n) then gives $\mu_H(p) \overset{2}{\leq} (1-p)\mu_H$. Let $R_I(p)$ denote the post-vaccination version of R_I. Then, as at (8), $R_I(p)$ is the unique solution of $g_{I,p}(\lambda) = 0$ in $(0, \infty)$, where

$$g_{I,p}(\lambda) = 1 - \frac{\mu_G(p)}{\lambda} - \frac{\mu_H(p)\mu_G(p)}{\lambda^2}.$$

Now, for $R_I > 1$ and $p > 0$,

$$\begin{aligned} g_{I,p}((1-p)R_I) &= 1 - \frac{\mu_G(p)}{(1-p)R_I} - \frac{\mu_H(p)\mu_G(p)}{(1-p)^2 R_I^2} \\ &\overset{2}{\geq} 1 - \frac{\mu_G}{R_I} - \frac{\mu_H \mu_G}{R_I^2} = 0, \end{aligned}$$

by the definition of R_I. It follows that $R_I(p) \overset{2}{\leq} (1-p)R_I$ and, in particular, if $p = 1 - R_I^{-1}$ then $R_I(p) \overset{2}{\leq} 1$. Hence, $p_C \overset{2}{\leq} 1 - R_I^{-1}$ and, using (17), $R_V \overset{2}{\leq} R_I$.

(iii) *R_V and R_0*

Suppose that $R_0 > 1$ and a fraction p of the population is vaccinated with a perfect vaccine. Then, cf. (5), the post-vaccination basic reproduction number, $R_0(p)$ say, is given by the unique solution in $(0, \infty)$ of $g_{0,p}(\lambda) = 0$, where

$$g_{0,p}(\lambda) = 1 - \sum_{k=0}^{n_H - 1} \frac{\nu_k(p)}{\lambda^{k+1}},$$

with $\nu_k(p) = \mu_k(p)\mu_G(p)$. Here, $\mu_G(p) = (1-p)\mu_G$ (as above) and, for $k = 0, 1, \cdots$, $\mu_k(p)$ is the post-vaccination mean size of the kth generation in a typical single-household epidemic with one initial infective (who is not vaccinated, so $\mu_0(p) = 1$). We

now obtain a lower bound for $\mu_k(p)$ $(k = 1, 2, \cdots)$. Consider again the epidemic graph $\mathcal{G}^{(n)}$. For $k, i = 1, 2, \cdots, n-1$, let $\chi_{k,i}^{(n)}$ be the event that individual i is a generation-k infective and let $(\chi_{k,i}^{(n)})^{\mathcal{C}}$ be its complement. Then the mean size of the kth generation is given by $\mu_k^{(n)} = \sum_{i=1}^{n-1} \mathbb{P}(\chi_{k,i}^{(n)})$. Now construct a realisation of the post-vaccination single-household epidemic as above, and define $\mu_k^{(n)}(p)$ and $\chi_{k,i}^{(n)}(p)$ in the obvious fashion. Then, fix generation k and suppose that individual i is a generation-k infective in the unvaccinated epidemic. Then $\chi_{k,i}^{(n)}$ occurs and in $\mathcal{G}^{(n)}$ there exists at least one chain of directed arcs of length k from the initial infective to individual i, and there is no shorter such chain connecting those individuals. Fix such a path of length k. If all k members of that path avoid vaccination, which happens with probability $(1-p)^k$ independently of $\mathcal{G}^{(n)}$, then $\chi_{k,i}^{(n)}(p)$ occurs. Therefore, $\mathbb{P}(\chi_{k,i}^{(n)}(p)|\chi_{k,i}^{(n)}) \geq (1-p)^k$, whence

$$\begin{aligned}\mathbb{P}(\chi_{k,i}^{(n)}(p)) &= \mathbb{P}(\chi_{k,i}^{(n)})\mathbb{P}(\chi_{k,i}^{(n)}(p)|\chi_{k,i}^{(n)}) + \mathbb{P}((\chi_{k,i}^{(n)})^{\mathcal{C}})\mathbb{P}(\chi_{k,i}^{(n)}(p)|(\chi_{k,i}^{(n)})^{\mathcal{C}}) \\ &\geq \mathbb{P}(\chi_{k,i}^{(n)})(1-p)^k,\end{aligned}$$

which implies that $\mu_k^{(n)}(p) \geq (1-p)^k \mu_k^{(n)}$ and hence that $\mu_k(p) \geq (1-p)^k \mu_k$. Note that for households of size $n \leq 3$, $\mu_k^{(n)}(p) = (1-p)^k \mu_k$ $(k = 0, 1, \cdots, n-1)$, since there can be at most one chain of length k linking an individual to the initial susceptible, but for $n \geq 4$ and $p > 0$ the inequality $\mu_k^{(n)}(p) \geq (1-p)^k \mu_k^{(n)}$ is strict for at least one k, as two or more chains may link an individual to the initial infective.

Clearly $R_V = 1$ if $R_0 = 1$. Suppose that $R_0 > 1$ and let $p_C' = 1 - R_0^{-1}$. Then,

$$\begin{aligned}g_{0,p_C'}(1) &= 1 - \sum_{k=0}^{n_H-1} \nu_k (p_C') \\ &\overset{3}{\leq} 1 - \sum_{k=0}^{n_H-1} (1-p_C')^{k+1} \mu_G \mu_k = 1 - \sum_{k=0}^{n_H-1} \frac{\nu_k}{R_0^{k+1}} = 0,\end{aligned}$$

as R_0 satisfies (5). Hence, $R_0(p_C') \overset{3}{\geq} 1$, since $R_0(p_C')$ is the unique positive solution of $g_{0,p_C'}(\lambda) = 0$. Thus $p_C \overset{3}{\geq} 1 - R_0^{-1}$ and, recalling (17), $R_V \overset{3}{\geq} R_0$.

(iv) *R_0 and R_I*

For a growing epidemic, we know that both R_0 and R_I are strictly greater than 1, and we have proved above that $R_I \overset{2}{\geq} R_V \overset{3}{\geq} R_0$, so we need consider only a declining epidemic. If $R_I < 1$, then it follows from (8) and (5) that $g_0(R_I) \overset{2}{\leq} g_I(R_I) = 0$, whence $R_0 \overset{2}{\geq} R_I$.

(v) *R_0 and R_{HI}.*

Let $h_0(\lambda) = g_{HI}(\lambda) - g_0(\lambda)$. We show that, for $\lambda > a$, $\text{sign}(h_0(\lambda)) = \text{sign}(\lambda - 1)$. It then follows that in a growing epidemic $R_0 > R_{HI}$ and in a declining epidemic $R_0 < R_{HI}$,

since g_0 and g_{HI} are each strictly increasing on their respective domains. Note that, since $g_0(\lambda) = \sum_{n=1}^{n_H} \pi_n g_0^{(n)}(\lambda)$ and $g_{HI}(\lambda) = \sum_{n=1}^{n_H} \pi_n g_{HI}^{(n)}(\lambda)$, it is sufficient to show, for each $n = 2, 3, \cdots, n_H$, that $\text{sign}(h_0(\lambda)) = \text{sign}(\lambda - 1)$ when all the households have size n. (It is easily verified that $g_0^{(1)}(\lambda) = g_{HI}^{(1)}(\lambda) = 1 - \mu_G/\lambda$, so households of size 1 do not contribute to $h_0(\lambda)$.) Thus we now assume that all households have size n, where $n \geq 2$. To ease the exposition, we suppress the explicit dependence on n.

It follows directly from (5) and (12) that

$$\begin{aligned} h_0(\lambda) &= \frac{\mu_G}{\lambda - a} \left\{ \left[\sum_{k=0}^{n-1} \frac{\mu_k(\lambda - a)}{\lambda^{k+1}} \right] - 1 \right\} \\ &= \frac{\mu_G}{\lambda(\lambda - a)} \left\{ \left[\sum_{k=1}^{n-1} \frac{\mu_k - a\mu_{k-1}}{\lambda^{k-1}} \right] - \frac{a\mu_{n-1}}{\lambda^n} \right\} \\ &= -\frac{\mu_G}{\lambda(\lambda - a)} f(\lambda^{-1}), \end{aligned} \tag{45}$$

where f is the polynomial of degree $n - 1$ given by $f(x) = \sum_{k=0}^{n-1} c_k x^k$, with

$$c_k = a\mu_k - \mu_{k+1} \text{ for } k = 0, 1, \cdots, n-2 \qquad \text{and} \qquad c_{n-1} = a\mu_{n-1}.$$

Now $f(1) = a \sum_{k=0}^{n-1} \mu_k - \sum_{k=1}^{n-1} \mu_k = a(1 + \mu_H) - \mu_H = 0$, so

$$f(x) = (x - 1)\tilde{f}(x), \tag{46}$$

where $\tilde{f}(x)$ is a polynomial of degree $n - 2$, say

$$\tilde{f}(x) = \sum_{k=0}^{n-2} \tilde{c}_k x^k. \tag{47}$$

Substituting (47) into (46) yields, after equating coefficients of powers of x, that, for $k = 0, 1, \cdots, n-2$,

$$\tilde{c}_k = \sum_{j=k+1}^{n-1} c_j = a \sum_{j=k+1}^{n-1} \mu_j - \sum_{j=k+2}^{n-1} \mu_j, \tag{48}$$

where the final sum is zero if $k = n - 2$.

Let $n_0 = \max(k : \mu_k > 0)$ and note that $n_0 \geq 1$, since otherwise $\mu_H = 0$. Then $\tilde{c}_{n_0-1} = a\mu_{n_0} > 0$ and $\tilde{c}_k = 0$ for $k \geq n_0$. Thus, to complete the proof we show that $\tilde{c}_k \geq 0$ $(k = 0, 1, \cdots, n_0 - 2)$, since then (45), (46) and (47) imply that

$$\text{sign}(h_0(\lambda)) = \text{sign}(\lambda - 1).$$

Recall that $a = \sum_{j=1}^{n-1} \mu_j / (1 + \sum_{j=1}^{n-1} \mu_j)$, which on substituting into (48) shows that, for $i = 0, 1, \cdots, n-3$, $\tilde{c}_i > 0$ if and only if

$$\sum_{j=k+2}^{n-1} \mu_j < \mu_{k+1} \sum_{j=1}^{n-1} \mu_j. \tag{49}$$

To prove (49), construct a realisation of a single-household epidemic using the epidemic graph $\mathcal{G}^{(n)}$. Let $Y_0, Y_1, \cdots, Y_{n-1}$ denote the sizes of the successive generations of infectives. Then, for $k = 0, 1, \cdots, n_0 - 2$,

$$\begin{aligned}\sum_{j=k+2}^{n-1} \mu_j &= \mathbb{E}\left[\sum_{j=k+2}^{n-1} Y_j\right] \\ &= \mathbb{E}\left[\mathbb{E}\left[\sum_{j=k+2}^{n-1} Y_j | Y_0, Y_1, \cdots, Y_{k+1}\right]\right] \\ &\leq \mathbb{E}[Y_{k+1}\mathbb{E}[\Upsilon_{k+1}|Y_0, Y_1, \cdots, Y_{k+1}]], \end{aligned} \tag{50}$$

where Υ_{k+1} is the total number of infectives in generations $k+2, k+3, \cdots, n-1$ that are descended from (i.e. in the epidemic graph have chain of directed edges from) a typical generation-$(k+1)$ infective. Note that an infective in generation $j > k+1$ may be descended from more than one generation-$(i+1)$ infective, hence the inequality in (50). Further, $\Upsilon_{k+1}|Y_0, Y_1, \cdots, Y_{k+1}$ is distributed as the total number of infectives, Υ say, in generations $1, 2, \cdots, n-2-k$ of a single-household epidemic with initially 1 infective and $n - (Y_0 + Y_1 + \cdots + Y_{k+1})$ susceptibles. Now Υ is stochastically strictly less than the total number of infectives in generations $1, 2, \cdots, n-2-k$ of such an epidemic with initially 1 infective and $n-1$ susceptibles, so

$$\mathbb{E}[\Upsilon_{k+1}|Y_0, Y_1, \cdots, Y_{k+1}] < \sum_{j=1}^{n-2-k} \mu_j,$$

and (50) yields

$$\sum_{j=k+2}^{n-1} \mu_j < \mathbb{E}\left[Y_{k+1} \sum_{j=1}^{n-2-k} \mu_j\right] = \mu_{k+1}\left(\sum_{j=1}^{n-2-k} \mu_j\right) \leq \mu_{k+1} \sum_{j=1}^{n-1} \mu_j, \tag{51}$$

proving (49).

(vi) *R_I and R_2.*

Let $h_I(\lambda) = g_2(\lambda) - g_I(\lambda)$. From (8) and (4),
$g_I(\lambda) = 1 - \frac{\mu_G}{\lambda}\left(1 + \sum_{n=2}^{n_H} \pi_n \frac{\mu_H^{(n)}}{\lambda}\right)$, whence, recalling (16),

$$\begin{aligned} h_I(\lambda) &= \frac{\mu_G}{\lambda} \sum_{n=2}^{n_H} \pi_n \left(\frac{\mu_H^{(n)}}{\lambda} - \frac{\mu_1^{(n)}}{\lambda - b^{(n)}}\right) \\ &= \mu_G \frac{\lambda - 1}{\lambda^2} \sum_{n=2}^{n_H} \pi_n \frac{\mu_H^{(n)} - \mu_1^{(n)}}{\lambda - b^{(n)}}, \end{aligned}$$

since $b^{(n)} = 1 - \left(\mu_1^{(n)}/\mu_H^{(n)}\right)$. Now $\mu_H^{(2)} = \mu_1^{(2)}$ so, if $n_H = 2$, then $h_I(\lambda) \equiv 0$ and $R_I = R_2$. If $n_H > 2$, then $\text{sign}(h_I(\lambda)) = \text{sign}(\lambda - 1)$ for $\lambda > b = \max\left(b^{(2)}, b^{(3)}, \cdots, b^{(n_H)}\right)$, since $\mu_H > \mu_1$, and, similar to the comparison of R_0 and R_{HI}, it follows that in a growing epidemic $R_I > R_2$ and in a declining epidemic $R_I < R_2$.

(vii) *R_2 and R_{HI}.*

Let $h_2(\lambda) = g_{HI}(\lambda) - g_2(\lambda)$. As in the proof of the comparison of R_0 and R_{HI}, it is sufficient to assume that all households have size n, where $n \geq 2$, and show that $\text{sign}(h_2(\lambda)) = \text{sign}(\lambda - 1)$ for $\lambda > \max(a, b)$. Equations (12) and (15) imply that, for $\lambda > \max(a, b)$,

$$\begin{aligned} h_2(\lambda) &= \mu_G \left[\frac{1}{\lambda} + \frac{\mu_1}{\lambda(\lambda - b)} - \frac{1}{\lambda - a} \right] \\ &= \frac{\mu_G}{\lambda(\lambda - a)(\lambda - b)} \left[\lambda(\mu_1 - a) - a(\mu_1 - b) \right]. \end{aligned} \tag{52}$$

It follows from (12) and (15) that $g_{HI}(1) = g_2(1) = 1 - R_*$, so $h_2(1) = 0$, whence $\mu_1 - a = a(\mu_1 - b)$. (The latter is easily checked directly using the definitions of a and b.) Setting $i = 0$ in (49), recalling that $a = \sum_{k=1}^{n-1} \mu_k / (1 + \sum_{k=1}^{n-1} \mu_k)$ and rearranging shows that $\mu_1 > a$. (Note that this implies $b < \mu_1$, as claimed after (14).) Substituting $\mu_1 - a = a(\mu_1 - b)$ into (52) then shows that, for $\lambda > \max(a, b))$, $\text{sign}(h_2(\lambda) = \text{sign}(\lambda - 1)$, which completes the proof.

□

7.2 Proof of Theorem 2

In this subsection we prove Theorem 2, which we restate here.

Theorem 2 *(a) For all choices of infectivity profile $\mathcal{I}(t)$ $(t \geq 0)$,*

$$R_r = 1 \iff \widetilde{R}_r = 1 \iff R_0 = 1.$$

(b) If $\mathcal{I}(t) = J w_G(t)$ $(t \geq 0)$, where J is a non-negative random variable, then in a growing epidemic,

$$R_r \geq R_0 > 1,$$

and in a declining epidemic,

$$R_r \leq R_0 < 1.$$

(c) If $\mathcal{I}(t) = f(t)\mathbb{1}(T_I > t)$ $(t \geq 0)$, where $f(t)$ is a deterministic function and T_I a non-negative random variable, then in a growing epidemic,

$$R_r \geq \widetilde{R}_r \geq R_0 > 1,$$

and in a declining epidemic,

$$R_r \leq \widetilde{R}_r \leq R_0 < 1.$$

The above results still hold if a latent period independent of the remainder of the infectivity profile is added.

Proof. To prove part *(a)* of Theorem 2, note that

$$\mathcal{L}_{\beta_H}(0) = \widetilde{\mathcal{L}}_{\beta_H}(0) = \mathcal{L}^{(0)}_{\beta_H}(0) = \mu_G(1+\mu_H) = R_*. \tag{53}$$

Let $r, \tilde{r}$ and $r^{(0)}$ be the unique real solutions of

$$\mathcal{L}_{\beta_H}(\theta) = 1, \quad \widetilde{\mathcal{L}}_{\beta_H}(\theta) = 1 \quad \text{and} \quad \mathcal{L}^{(0)}_{\beta_H}(\theta) = 1, \tag{54}$$

respectively. Then,

$$R_r = \frac{1}{\mathcal{M}_{W_G}(r)}, \quad \widetilde{R}_r = \frac{1}{\mathcal{M}_{W_G}(\tilde{r})} \quad \text{and} \quad R_0 = \frac{1}{\mathcal{M}_{W_G}(r^{(0)})}. \tag{55}$$

The functions $\mathcal{L}_{\beta_H}(\theta), \widetilde{\mathcal{L}}_{\beta_H}(\theta)$ and $\mathcal{L}^{(0)}_{\beta_H}(\theta)$ are each strictly decreasing in θ, so (53) implies that

$$\text{sign}(r) = \text{sign}(\tilde{r}) = \text{sign}(r^{(0)}) = \text{sign}(R_* - 1),$$

so, since $\mathcal{M}_{W_G}(\theta)$ is strictly decreasing in θ and $\mathcal{M}_{W_G}(0) = 1$,

$$\text{sign}(R_r - 1) = \text{sign}(\widetilde{R}_r - 1) = \text{sign}(R_0 - 1) = \text{sign}(R_* - 1).$$

This proves part *(a)* and shows also that $R_r, \widetilde{R}_r, R_0$ and R_* are all strictly greater than 1 in a growing epidemic and strictly less than 1 in a declining epidemic.

For ease of presentation, we assume first that all households have the same size n and we drop the explicit dependence of $\lambda_H^{(n)}$ on n. We further assume $n \geq 2$ in order to avoid trivial cases. We outline at the end of the proof how it extends to variable household sizes.

Consider a local epidemic started by a single initial infective. Label the individuals $0, 1, \cdots, n-1$, with individual 0 being the initial infective in the household. Construct the augmented random graph derived from $\mathcal{G}^{(n)}$ as described in Section 2.1. For future reference we refer to this augmented graph as $\tilde{\mathcal{G}}^{(n)}$. Recall that $t_{ii'}$ denotes the time of this first contact (since i's infection) to i'; we refer to $t_{ii'}$ as the real infection interval for i to infect i'. For $i = 1, 2, \cdots, n-1$, if individual i is infected by the local epidemic, then his/her time of infection, denoted by T_i, is given by the minimum of the sums of the real infection intervals between every pair of linked individuals along all directed paths from the initial infective to i; if i is not infected by the local epidemic then we set $T_i = \infty$. We set $T_0 = 0$. This fully specifies the real-time construction of the epidemic.

The overall expected household infectivity profile $\beta_H(t)$ can be decomposed as $\sum_{i=0}^{n-1} \beta_{H,i}(t)$, where $\beta_{H,i}(t) = \mu_G \, \mathbb{E}\left[\mathcal{I}_i(t - T_i)\right]$ is the contribution from individual i and $\mathcal{I}_i(t)$ is his/her infectivity profile (with $\mathcal{I}_i(t) = 0$ if $t < 0$). Now, $\int_0^\infty e^{-\theta t}\mathcal{I}_i(t - T_i)\mathrm{d}t = e^{-\theta T_i}\int_0^\infty e^{-\theta t}\mathcal{I}_i(t)\mathrm{d}t$

for $T_i < \infty$, while the integral is 0 for $T_i = \infty$. Therefore, noting that T_i and $\{\mathcal{I}_i(t) : t \geq 0\}$ are independent, we have

$$\begin{aligned}
\mathcal{L}_{\beta_H}(\theta) &= \int_0^\infty \beta_H(t)\mathrm{e}^{-\theta t}\mathrm{d}t = \sum_{i=0}^{n-1}\int_0^\infty \beta_{H,i}(t)\mathrm{e}^{-\theta t}\mathrm{d}t \\
&= \sum_{i=0}^{n-1}\mathbb{E}\left[\mathrm{e}^{-\theta T_i}\right]\int_0^\infty \mu_G\,\mathbb{E}[\mathcal{I}_i(t)]\mathrm{e}^{-\theta t}\mathrm{d}t \\
&= \mu_G\mathcal{M}_{W_G}(\theta)\sum_{i=0}^{n-1}\mathbb{E}\left[\mathrm{e}^{-\theta T_i}\right], \qquad (56)
\end{aligned}$$

since $\int_0^\infty \mathbb{E}[\mathcal{I}_i(t)]\mathrm{e}^{-\theta t}\mathrm{d}t = \mathcal{M}_{W_G}(\theta)$. Let $\chi_k(i)$ be the event that individual i is in generation k $(i, k = 0, 1, \cdots n-1)$. Then,

$$\sum_{i=1}^{n-1}\mathbb{E}[\mathrm{e}^{-\theta T_i}] = \sum_{i=1}^{n-1}\sum_{k=1}^{n-1}\mathbb{P}(\chi_k(i))\,\mathbb{E}[\mathrm{e}^{-\theta T_i}|\chi_k(i)] = \sum_{k=1}^{n-1}\mu_k\,\mathbb{E}[\mathrm{e}^{-\theta T_1}|\chi_k(1)], \qquad (57)$$

since $\mathbb{E}[\mathrm{e}^{-\theta T_i}|\chi_k(i)]$ is independent of i and $\mu_k = \sum_{i=1}^{n-1}\mathbb{P}(\chi_k(i))$. Hence, using (56), and recalling that $T_0 = 0$,

$$\mathcal{L}_{\beta_H}(\theta) = \mu_G\mathcal{M}_{W_G}(\theta)\left\{1 + \sum_{k=1}^{n-1}\mu_k\,\mathbb{E}[\mathrm{e}^{-\theta T_1}|\chi_k(1)]\right\}. \qquad (58)$$

Suppose that an individual, i say, is in household generation k. Then there exists at least one path of length k, and no shorter path, from the initial case in the household to i. Consider one such path and relabel the individuals so that the successive individuals in that path are $0, 1, \cdots, k$, so our given individual now has label k. Let $\hat{T}_k = \sum_{i'=0}^{k-1} t_{i',i'+1}$ and observe that, since $\hat{T}_k$ is defined using the "length" of a specific path and T_k is the minimum length over a collection of possible paths, we have

$$T_k \leq \hat{T}_k. \qquad (59)$$

Consider case *(b)* of Theorem 2, in which $\mathcal{I}(t) = Jw_G(t)$ $(t \geq 0)$, where J is a non-negative random variable. In this case the augmented random graph $\tilde{\mathcal{G}}^{(n)}$ may be constructed by independently for each individual, i say, first sampling J_i according to J and then, conditional on J_i, letting $N_{ii'}$ $(i' \neq i)$ be independent Poisson random variables having mean J_i. The random variable $N_{ii'}$ gives the number of infectious contacts individual i makes towards individual i'. If $N_{ii'} > 0$ then the times of these contacts, relative to i's time of infection are given by $w_G^{(ii')}(1), w_G^{(ii')}(2), \cdots, w_G^{(ii')}(N_{ii'})$, which are mutually independent realisations of the random variable W_G. Suppose that i makes infectious contact with i', so $N_{ii'} > 0$. Then $t_{ii'} = \min\left(w_G^{(ii')}(1), w_G^{(ii')}(2), \cdots, w_G^{(ii')}(N_{ii'})\right)$ and, in particular, $t_{ii'} \leq w_G^{(ii')}(1)$. Since

$w_G^{(ii')}(m)$ $(i \neq i', m = 1, 2, \cdots, N_{ii'})$ are mutually independent it follows that

$$\hat{T}_k \overset{st}{\leq} \sum_{l=0}^{k-1} \Psi_l, \tag{60}$$

where $\Psi_0, \Psi_1, \cdots, \Psi_{k-1}$ are independent and identically distributed copies of W_G. Thus, if $\theta > 0$, then (58), (59) and (60) imply that

$$\mathcal{L}_{\beta_H}(\theta) \geq \mu_G \mathcal{M}_{W_G}(\theta) \left\{ 1 + \sum_{k=1}^{n-1} \mu_k \mathcal{M}_{W_G}(\theta)^k \right\} = \mathcal{L}_{\beta_H}^{(0)}(\theta), \tag{61}$$

where $\mathcal{L}_{\beta_H}^{(0)}$ is defined at (22), with the opposite inequality holding if $\theta < 0$.

Suppose that the epidemic is growing, so $R_* > 1$. Then, (61) states that, for $\theta > 0$,

$$\mathcal{L}_{\beta_H}(\theta) \geq \mathcal{L}_{\beta_H}^{(0)}(\theta),$$

so, since $\mathcal{L}_{\beta_H}(\theta)$ and $\mathcal{L}_{\beta_H}^{(0)}(\theta)$ are strictly decreasing in θ and $\mathcal{L}_{\beta_H}(0) = \mathcal{L}_{\beta_H}^{(0)}(0) = R_*$ it follows that $0 < r^{(0)} \leq r$, whence, since $\mathcal{M}_{W_G}(\theta)$ is strictly decreasing in θ, (55) implies that $R_r \geq R_0 > 1$. A similar argument shows that $R_r \leq R_0 < 1$ in a declining epidemic.

Turn now to case *(c)* of Theorem 2, in which $\mathcal{I}(t) = f(t)\mathbb{1}(T_I > t)$ $(t \geq 0)$, where $f(t)$ is a deterministic function and T_I a non-negative random variable. For $m = 0, 1, \cdots, n-1$, let the random variable Φ_m be distributed as the time of the first infectious contact between two given individuals (say from i to i'), given that there is at least one such contact and that i does not contact m other given individuals. Note that the condition that i does not contact 0 other given individuals is necessarily satisfied, so Φ_0 has the same distribution as the random variable $\widetilde{W}_G$ defined in Section 2.8.

Observe that if we know that an individual is in household generation k, then there exists at least one path of length k, and no shorter path, from the initial case in the household to that individual. If we know one path of length k and we condition on knowing all edges in the epidemic generating graph in the household, not starting at one of the individuals in that path, then we know that a contact is made from an individual to the next individual in the path and some other contacts are not made (namely contacts which would lead to paths of shorter length than k, e.g. a contact from an individual to an individual more than one place further along the path). We call the latter contacts "forbidden" (see Figure 10).

Suppose that an individual, i say, is in household generation k. Select a path of length k from the initial case to individual i and, as above, relabel the individuals so that the successive individuals in that path are $0, 1, \cdots, k$. Denote the configuration, in the epidemic graph, of all edges not emanating from any node in the path *plus* all those in the path itself by Ξ (the solid arrows in Figure 10) and let $m(i') = m(i', \Xi)$, $(i' = 0, 1, \cdots, k-1)$ be the number of forbidden contacts from individual i' under configuration Ξ. (In Figure 10, $m(0) = 3$, $m(1) = 1$ and $m(2) = 0$.) Recall that $\hat{T}_k$ is the time it takes for individual k to be infected along this path. Then, as contacts emanating from different individuals are

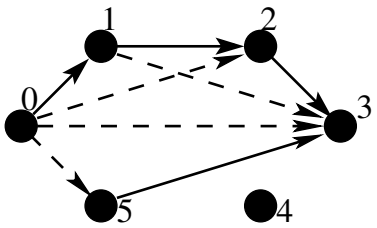

Figure 10: Epidemic graph, with relevant contacts represented by solid arrows. We consider the path from 0 to 3 (via 1 and 2). The forbidden contacts, which would make the path from 0 to 3 shorter are represented by dashed arrows. In this Figure, there are 3 forbidden contacts emanating from individual 0 and 1 from individual 1.

independent,

$$\mathbb{E}\left[\mathrm{e}^{-\theta\hat{T}_k}\right] = \mathbb{E}_\Xi\left[\prod_{i'=0}^{k-1}\mathbb{E}\left[\mathrm{e}^{-\theta\Phi_{m(i')}}|\Xi\right]\right], \qquad \theta\in(-\infty,\infty). \tag{62}$$

(The notation $\mathbb{E}_\Xi$ denotes that the expectation is with respect to the distribution of Ξ. Since the path of length k is fixed, the randomness in Ξ is contained in the distribution of edges in the epidemic graph that emanate from nodes not in the path.) We now show that

$$\Phi_m \overset{st}{\leq} \widetilde{W}_G \quad \text{for all } m=1,2,\cdots,n-1. \tag{63}$$

For $m=0,1,\cdots,n-1$, let $\mathcal{D}_m$ be the event that there is at least one contact between two given individuals (say i and i') and m other specified individuals are not contacted by i. Let $\mathcal{D}$ be the event that there is at least one contact between two given individuals, so $\mathcal{D}=\mathcal{D}_0$. Note that the probability of $\mathcal{D}_m$ depends on the infectious profile $\mathcal{I}_i$ $(=\{\mathcal{I}_i(t):t\geq 0\})$. By the definition of conditional expectation and noting that $\mathcal{P}(\mathcal{D}_m)=\mathbb{E}_\mathcal{I}[\mathbb{1}(\mathcal{D}_m)]$, we have that, for $m=0,1,\cdots,n-1$,

$$\mathbb{P}(\Phi_m\leq t)=\mathbb{E}_\mathcal{I}\left[\mathbb{1}(\mathcal{D}_m)\frac{\int_0^t \mathrm{e}^{-\int_0^s\lambda_H\mathcal{I}(x)\mathrm{d}x}\mathcal{I}(s)\mathrm{d}s}{\int_0^\infty \mathrm{e}^{-\int_0^s\lambda_H\mathcal{I}(x)\mathrm{d}x}\mathcal{I}(s)\mathrm{d}s}\right]/\mathbb{E}_\mathcal{I}[\mathbb{1}(\mathcal{D}_m)] \qquad (t\geq 0). \tag{64}$$

Making the substitution $u(t)=\int_0^t\mathcal{I}(x)\mathrm{d}x$ we obtain

$$\int_0^t \mathrm{e}^{-\int_0^s\lambda_H\mathcal{I}(x)\mathrm{d}x}\mathcal{I}(s)\mathrm{d}s=\int_0^t \mathrm{e}^{-\lambda_H u(s)}\frac{\mathrm{d}u(s)}{\mathrm{d}s}\mathrm{d}s=1-\mathrm{e}^{-\lambda_H u(t)}=1-\mathrm{e}^{-\lambda_H\int_0^t\mathcal{I}(s)\mathrm{d}s}$$

and similarly $\int_0^\infty \mathrm{e}^{-\int_0^s\lambda_H\mathcal{I}(x)\mathrm{d}x}\mathcal{I}(s)ds=1-\mathrm{e}^{-\lambda_H\int_0^\infty\mathcal{I}(s)\mathrm{d}s}$. Furthermore, $\mathcal{D}_m\subseteq\mathcal{D}$ and

$$\mathbb{P}(\mathcal{D}_m|\int_0^\infty\mathcal{I}(s)\mathrm{d}s)=\mathrm{e}^{-m\lambda_H\int_0^\infty\mathcal{I}(s)\mathrm{d}s}.$$

Combining these observations yields that, for $m = 0, 1, \cdots, n-1$, (64) can be rewritten as

$$\mathbb{P}(\Phi_m \le t) = \frac{\mathbb{E}_{\mathcal{I}|\mathcal{D}}\left[\mathrm{e}^{-m\lambda_H \int_0^\infty \mathcal{I}(s)\mathrm{d}s} \frac{1-\mathrm{e}^{-\lambda_H \int_0^t \mathcal{I}(s)\mathrm{d}s}}{1-\mathrm{e}^{-\lambda_H \int_0^\infty \mathcal{I}(s)\mathrm{d}s}} | \mathcal{D}\right]}{\mathbb{E}_{\mathcal{I}|\mathcal{D}}[\mathrm{e}^{-m\lambda_H \int_0^\infty \mathcal{I}(s)\mathrm{d}s}|\mathcal{D}]} \qquad (t \ge 0). \tag{65}$$

(The notation $\mathbb{E}_{\mathcal{I}|\mathcal{D}}$ denotes that the expectation is with respect to the distribution of the infectivity profile $\mathcal{I} = \{\mathcal{I}(t) : t \ge 0\}$ of an infective given that that infective makes at least one contact with a given individual.) The distribution function of $\widetilde{W}_G$ may be obtained by setting $m = 0$ in (65). Hence, $\Phi_m \overset{st}{\le} \widetilde{W}_G$ if and only if, for all $t > 0$,

$$\mathbb{E}_{\mathcal{I}|\mathcal{D}}\left[\mathrm{e}^{-m\lambda_H \int_0^\infty \mathcal{I}(s)\mathrm{d}s} \frac{1-\mathrm{e}^{-\lambda_H \int_0^t \mathcal{I}(s)\mathrm{d}s}}{1-\mathrm{e}^{-\lambda_H \int_0^\infty \mathcal{I}(s)\mathrm{d}s}} | \mathcal{D}\right]$$
$$\ge \mathbb{E}_{\mathcal{I}|\mathcal{D}}\left[\mathrm{e}^{-m\lambda_H \int_0^\infty \mathcal{I}(s)\mathrm{d}s}|\mathcal{D}\right] \mathbb{E}_{\mathcal{I}|\mathcal{D}}\left[\frac{1-\mathrm{e}^{-\lambda_H \int_0^t \mathcal{I}(s)\mathrm{d}s}}{1-\mathrm{e}^{-\lambda_H \int_0^\infty \mathcal{I}(s)\mathrm{d}s}}|\mathcal{D}\right]. \tag{66}$$

Recall Chebychev's 'other' inequality (also referred to as Harris' inequality) (Hardy [13], p. 168), which states that if $f_1(x)$ and $f_2(x)$ are both increasing or both decreasing functions and X is a random variable, then

$$\mathbb{E}[f_1(X)f_2(X)] \ge \mathbb{E}[f_1(X)]\mathbb{E}[f_2(X)]. \tag{67}$$

From the proof of this inequality it follows immediately that the inequality is strict if both $f_1(X)$ and $f_2(X)$ have strictly positive variance, which is the case if (i) both functions are strictly increasing or both functions are strictly decreasing and (ii) $\mathrm{Var}(X) > 0$. We now apply Chebychev's 'other' inequality to conditional expectations. In case *(c)* of Theorem 2, for $t \in (0, \infty]$ we have $\int_0^t \mathcal{I}(s)\mathrm{d}s = \int_0^{\min(T_I, t)} f(s)\mathrm{d}s$ and we observe that both

$$f_1(x) = \mathrm{e}^{-m\lambda_H \int_0^x \mathcal{I}(s)\mathrm{d}s}$$

and

$$f_2(x) = \frac{1-\mathrm{e}^{-\lambda_H \int_0^{\min(x,t)} \mathcal{I}(s)\mathrm{d}s}}{1-\mathrm{e}^{-\lambda_H \int_0^x \mathcal{I}(s)\mathrm{d}s}} = \mathbb{1}(x < t) + \mathbb{1}(x \ge t)\frac{1-\mathrm{e}^{-\lambda_H \int_0^t \mathcal{I}(s)\mathrm{d}s}}{1-\mathrm{e}^{-\lambda_H \int_0^x \mathcal{I}(s)\mathrm{d}s}}$$

are decreasing in x. Thus by (66) and (67) we have $\Phi_m \overset{st}{\le} \widetilde{W}_G$.

It follows from (63) that $\mathcal{M}_{\Phi_m}(r) \ge \mathcal{M}_{\widetilde{W}_G}(r)$ if $r > 0$ and $\mathcal{M}_{\Phi_m}(r) \le \mathcal{M}_{\widetilde{W}_G}(r)$ if $r < 0$. It then follows using (58), (59) and (62) that, if $r > 0$, then

$$\mathcal{L}_{\beta_H}(r) \ge \mu_G \mathcal{M}_{W_G}(r)\left\{1 + \sum_{k=1}^{n-1} \mu_k \mathcal{M}_{\widetilde{W}_G}(r)^k\right\} = \widetilde{\mathcal{L}}_{\beta_H}(r), \tag{68}$$

where $\widetilde{\mathcal{L}}_{\beta_H}$ is defined at (24), with the opposite inequality holding if $r < 0$. Arguing as for case *(b)* above, shows that $R_r \ge \widetilde{R}_r > 1$ in a growing epidemic and $R_r \le \widetilde{R}_r < 1$ in a declining epidemic.

To compare $\widetilde{R}_r$ and R_0, we need to show that

$$\mathcal{M}_{\widetilde{W}_G}(\theta) \geq \mathcal{M}_{W_G}(\theta) \text{ if } \theta > 0 \quad \text{and} \quad \mathcal{M}_{\widetilde{W}_G}(\theta) \leq \mathcal{M}_{W_G}(\theta) \text{ if } \theta < 0. \tag{69}$$

Recall from Section 2.8 that $\mathcal{M}_{W_G}(\theta) = \int_0^\infty \mathrm{e}^{-\theta t}\mathbb{E}[\mathcal{I}(t)]\mathrm{d}t$. From the definition of $\widetilde{W}_G$ we see that

$$\mathbb{P}(\widetilde{W}_G \leq t) = \frac{\mathbb{E}_{\mathcal{I}}\left[\int_0^t \mathrm{e}^{-\int_0^s \lambda_H \mathcal{I}(x)\mathrm{d}x}\lambda_H \mathcal{I}(s)\mathrm{d}s\right]}{\mathbb{E}_{\mathcal{I}}\left[\int_0^\infty \mathrm{e}^{-\int_0^s \lambda_H \mathcal{I}(x)\mathrm{d}x}\lambda_H \mathcal{I}(s)\mathrm{d}s\right]}, \qquad t \geq 0. \tag{70}$$

After first differentiating (70) to obtain the density of $\widetilde{W}_G$, we obtain (using the dominated convergence theorem for a fully rigorous argument) that

$$\mathcal{M}_{\widetilde{W}_G}(\theta) = \frac{\int_0^\infty \mathrm{e}^{-\theta t}\mathbb{E}_{\mathcal{I}}\left[\mathrm{e}^{-\int_0^t \lambda_H \mathcal{I}(x)\mathrm{d}x}\mathcal{I}(t)\right]\mathrm{d}t}{\mathbb{E}_{\mathcal{I}}\left[\int_0^\infty \mathrm{e}^{-\int_0^s \lambda_H \mathcal{I}(x)\mathrm{d}x}\mathcal{I}(s)\mathrm{d}s\right]}, \qquad \theta \in (-\infty, \infty).$$

Now using that $\mathcal{I}(t) = f(t)\mathbb{1}(T_I > t)$ for some random variable T_I gives that for all real θ, $\mathcal{M}_{W_G}(\theta) = \int_0^\infty \mathrm{e}^{-\theta t} f(t)\mathbb{P}[T_I > t]\mathrm{d}t$ and

$$\begin{aligned}
\mathcal{M}_{\widetilde{W}_G}(\theta) &= \frac{\int_0^\infty \mathrm{e}^{-\theta t}\mathbb{E}_{T_I}\left[\mathrm{e}^{-\int_0^t \lambda_H f(x)\mathrm{d}x} f(t)\mathbb{1}(T_I > t)\right]\mathrm{d}t}{\mathbb{E}_{T_I}\left[\int_0^\infty \mathrm{e}^{-\int_0^s \lambda_H f(x)\mathrm{d}x} f(s)\mathbb{1}(T_I > s)\mathrm{d}s\right]} \\
&= \frac{\int_0^\infty \mathrm{e}^{-\theta t}\mathrm{e}^{-\int_0^t \lambda_H f(x)\mathrm{d}x} f(t)\mathbb{P}[T_I > t]\mathrm{d}t}{\int_0^\infty \mathrm{e}^{-\int_0^s \lambda_H f(x)\mathrm{d}x} f(s)\mathbb{P}[T_I > s]\mathrm{d}s}.
\end{aligned}$$

Note that $f(t)\mathbb{P}[T_I > t] = \mathbb{E}[\mathcal{I}(t)] = w_G(t)$, which is the density of W_G. Using this definition of W_G, we obtain that

$$\mathcal{M}_{W_G}(\theta) = \mathbb{E}\left[\mathrm{e}^{-\theta W_G}\right] \qquad \text{and} \qquad \mathcal{M}_{\widetilde{W}_G}(\theta) = \frac{\mathbb{E}\left[\mathrm{e}^{-\theta W_G}\mathrm{e}^{-\int_0^{W_G} \lambda_H f(x)\mathrm{d}x}\right]}{\mathbb{E}\left[\mathrm{e}^{-\int_0^{W_G} \lambda_H f(x)\mathrm{d}x}\right]}.$$

For $\theta > 0$, the inequality $\mathcal{M}_{\widetilde{W}_G}(\theta) \geq \mathcal{M}_{W_G}(\theta)$ now follows from applying Chebychev's 'other' inequality (inequality (67)) to the functions $f_1(x) = \mathrm{e}^{-\theta x}$ and $f_2(x) = \mathrm{e}^{-\int_0^x \lambda_H f(s)\mathrm{d}s}$. The result for $\theta < 0$ is proved in the same way, using $f_1(x) = -\mathrm{e}^{-\theta x}$ instead. It follows using (22) and (24) that $\widetilde{\mathcal{L}}_{\beta_H}(\theta) \geq \mathcal{L}^{(0)}_{\beta_H}(\theta)$ if $\theta > 0$ and $\widetilde{\mathcal{L}}_{\beta_H}(\theta) \leq \mathcal{L}^{(0)}_{\beta_H}(\theta)$ if $\theta < 0$, which implies that $\widetilde{R}_r \geq R_0$ in a growing epidemic and $\widetilde{R}_r \leq R_0$ in a declining epidemic.

Note that in case *(b)* of Theorem 2 (i.e. when $\mathcal{I}(t) = Jw_G(t)$, with J random and $w_G(t)$ ($t \geq 0$) non-random), $\Phi_m \overset{st}{\leq} \widetilde{W}_G$ does not necessarily hold, because conditioning on the absence of some edges leads to relatively low realisations of J, which implies fewer infectious contacts even if there is at least one contact between given individuals, which in turn implies later first contacts. So, here we cannot conclude that, for example, $R_r \geq \widetilde{R}_r$ in a growing epidemic.

Note that in the variable household size setting (58) becomes

$$\mathcal{L}_{\beta_H}(\theta) = \mu_G \mathcal{M}_{W_G}(\theta) \left\{ 1 + \sum_{n=2}^{n_H} \pi_n \sum_{k=1}^{n-1} \mu_k^{(n)} \, \mathbb{E}[\mathrm{e}^{-\theta T_1^{(n)}} | \chi_k(1)] \right\}, \tag{71}$$

where $T_1^{(n)}$ is the time that individual 1 is infected in a local epidemic in a household having size n. The expectations are conditioned on individual 1 being in generation k. The arguments leading to (60) show that

$$\mathbb{E}[\mathrm{e}^{-\theta T_1^{(n)}} | \chi_k(1)] \geq [\mathcal{M}_{W_G}(\theta)]^k \qquad \text{for } \theta > 0, \tag{72}$$

and

$$\mathbb{E}[\mathrm{e}^{-\theta T_1^{(n)}} | \chi_k(1)] \leq [\mathcal{M}_{W_G}(\theta)]^k \qquad \text{for } \theta < 0. \tag{73}$$

It then follows using (3) that, if $\theta > 0$, inequality (61) holds, with the opposite inequality holding if $\theta < 0$. Case *(b)* of Theorem 2 now follows as before.

Turning to case *(c)*, recall that if $\lambda_H^{(n)}$ varies with n then so does the distribution of $\widetilde{W}_G^{(n)}$. In that case recall that $\widetilde{W}_G^{(n)}$ is a random variable distributed as $\widetilde{W}_G$ for a size-n household and, for $m = 0, 1, \cdots n-1$, let $\Phi_m^{(n)}$ be a random variable distributed as Φ_m, again for a size-n household. (Note that, cf. (71), the distribution of W_G is determined purely by the distribution of the infectivity profile $\{\mathcal{I}(t) : t \geq 0\}$ and hence it is independent of household size n.) Arguing as before shows that $\Phi_m^{(n)} \overset{st}{\leq} W_G$ $(n = 2, 3, \cdots, n_H; m = 0, 1, \cdots, n-1)$ and using obvious extensions of (59) and (62) to the variable household size setting it follows from (71) that, if $r > 0$, then (68) holds with $\widetilde{\mathcal{L}}_{\beta_H}(r)$ defined at (27), and if $r < 0$, then $\mathcal{L}_{\beta_H}(r) \leq \widetilde{\mathcal{L}}_{\beta_H}(r)$. As in the case when all households have the same size, this implies that $R_r \geq \widetilde{R}_r > 1$ in a growing epidemic and $R_r \leq \widetilde{R}_r < 1$ in a declining epidemic. Finally the previous argument shows that for $n = 2, 3, \cdots n_H$, $\mathcal{M}_{\widetilde{W}_G^{(n)}}(\theta) \geq \mathcal{M}_{W_G}(\theta)$ if $\theta > 0$ and $\mathcal{M}_{\widetilde{W}_G^{(n)}}(\theta) \leq \mathcal{M}_{W_G}(\theta)$ if $\theta < 0$. The comparison between $\widetilde{R}_r$ and R_0 then follows on noting that $\mathcal{L}_{\beta_H}^{(0)}(r)$ is obtained by replacing $\mathcal{M}_{\widetilde{W}_G^{(n)}}(r)$ by $\mathcal{M}_{W_G}(r)$ in equation (27).

□

Remark 6 *Note that if $w_G(t)$ is a proper density function, i.e. $w_G(t) < \infty$ for all $t \geq 0$, then the inequality in* (61) *is strict, so in that case the inequalities in Theorem 2(b) are strict. Note that for the infectivity profile considered in Theorem 2(c), the random variable W_G necessarily has a proper density function, so the application of Chebychev's other inequality leads to strict inequalities in* (69)*. Thus, in this case, we have $\widetilde{R}_r > R_0$ in a growing epidemic and $\widetilde{R}_r < R_0$ in a declining epidemic.*

We have already observed that $\mathcal{L}_{\beta_H}(\theta) = \widetilde{\mathcal{L}}_{\beta_H}(\theta)$ and therefore $\widetilde{R}_r = R_r$ for $n_H \leq 2$, since there is only one possible path from the initial infective to the other individual in a household of size 2. In households of size 3, it depends on the distribution of T_I, whether the (real) time needed for the epidemic to traverse an infection path of length 2 might be shorter than the time needed to traverse an infection path of length 1. If this is impossible, then $\widetilde{R}_r = R_r$ for

$n_H = 3$, otherwise $\widetilde{R}_r \neq R_r$ unless they are both one. In households of size 4 or larger, it is possible that there are two disjoint paths of length 2 from the initial infective in the household to an individual in generation 2, so in this case, $\mathcal{L}_{\beta_H}(\theta) = \widetilde{\mathcal{L}}_{\beta_H}(\theta)$, for all $\theta \in (-\infty, \infty)$, if and only if $\mathrm{Var}(\widetilde{W}_G) = 0$. Thus, for $n_H \geq 4$, unless they are both one, $\widetilde{R}_r = R_r$ if and only if $\mathrm{Var}(\widetilde{W}_G) = 0$.

7.3 Proof of Theorem 3

Where relevant, we now use the notation $\overset{n}{\geq}$ to denote that the inequality is strict if and only if $\max(n_H, n_W) > n$, so the statement of Theorem 3 is as follows.

Theorem 3 *(a)* $R_* = 1 \iff R_H = 1 \iff R_I = 1 \iff R_0 = 1 \Longrightarrow R_V = 1$.

(b) In a growing epidemic,

$$R_* > R_H > R_I \overset{2}{\geq} R_V \overset{3}{\geq} R_0 > 1,$$

and in a declining epidemic

$$R_* < R_H < R_I \overset{2}{\leq} R_0 < 1.$$

(c) Theorem 2 holds also for the households-workplaces model.

Proof. We first prove *(a)*. Let

$$f_{HW}(\mu_G, \mu_H, \mu_W) = \mu_G(1+\mu_H)(1+\mu_W) + \mu_H\mu_W, \tag{74}$$

and note from (34) that $R_* = 1$ if and only if $f_{HW}(\mu_G, \mu_H, \mu_W) = 1$. Observe from (36) and (37) that $g_H(1) = g_I^{(HW)}(1) = 1 - f_{HW}(\mu_G, \mu_H, \mu_W)$, so $R_* = 1 \iff R_H = 1 \iff R_I = 1$.

Turning to R_0, note that

$$\mu_H\mu_W = \left(\sum_{\ell=1}^{n_H-1} \mu_\ell^H\right)\left(\sum_{\ell'=1}^{n_W-1} \mu_{\ell'}^W\right) = \sum_{k=1}^{n_H+n_W-3}\left(\sum_{\ell=\max(1,k-n_W+2)}^{\min(k,n_H-1)} \mu_\ell^H \mu_{k+1-\ell}^W\right)$$

and

$$\begin{aligned}(1+\mu_H)(1+\mu_W) &= \left(\sum_{\ell=0}^{n_H-1} \mu_\ell^H\right)\left(\sum_{\ell'=0}^{n_W-1} \mu_{\ell'}^W\right) \\ &= \sum_{k=0}^{n_H+n_W-2}\left(\sum_{\ell=\max(0,k-n_W+1)}^{\min(k,n_H-1)} \mu_\ell^H \mu_{k-\ell}^W\right).\end{aligned}$$

Thus

$$f_{HW}(\mu_G, \mu_H, \mu_W) = \sum_{k=0}^{n_H+n_W-2} c_k, \tag{75}$$

where c_k is defined in (33) ($c_0 = \mu_G$) and, using (32), $g_0^{(HW)}(1) = 1 - f_{HW}(\mu_G, \mu_H, \mu_W)$. Hence, $R_0 = 1 \iff R_* = 1$. By definition, $R_V = 1$ if $R_* = 1$.

To prove *(b)*, we first note that (34) and (74) imply that

$$\text{sign}(R_* - 1) = \text{sign}(f_{HW}(\mu_G, \mu_H, \mu_W) - 1). \tag{76}$$

Thus, since the functions $g_H, g_I^{(HW)}$ and $g_0^{(HW)}$ are all strictly increasing on $(0, \infty)$, it follows that the reproduction numbers R_*, R_H, R_I and R_0 are all strictly greater than 1 in a growing epidemic and all strictly smaller than 1 in a declining epidemic. We consider now each of the comparisons in turn.

(i) *R_* and R_H.*

Suppose that $R_* > 1$. Clearly, $R_* > R_H$ if $R_* = \infty$, so suppose that $R_* < \infty$. An elementary calculation shows that

$$g_H(R_*) = \frac{\mu_H}{\mu_G(1+\mu_H)^2} \left(f_{HW}(\mu_G, \mu_H, \mu_W) - 1\right),$$

whence, using (76), $g_H(R_*) > 0$. It follows that $R_H < R_*$, since g_H is strictly increasing on $(0, \infty)$ and $g_H(R_H) = 0$. A similar argument shows that $R_H > R_*$ if $R_* < 1$.

(ii) *R_H and R_I*

Elementary algebra gives

$$g_I^{(HW)}(\lambda) - g_H(\lambda) = (\lambda - 1)\left[\frac{\mu_H(\mu_G + \mu_W)}{\lambda^2} + \frac{\mu_G\mu_H\mu_W}{\lambda^3}\right],$$

so, for $\lambda > 0$,

$$\text{sign}\left(g_I^{(HW)}(\lambda) - g_H(\lambda)\right) = \text{sign}(\lambda - 1). \tag{77}$$

Recall that R_H and R_I are the unique roots in $(0, \infty)$ of g_H and $g_I^{(HW)}$, respectively. Suppose that $R_H > 1$. Then, since $g_H(R_H) = 0$, (77) implies that $g_I^{(HW)}(R_H) > 0$, whence $R_I < R_H$, since $g_I^{(HW)}(R_I) = 0$ and $g_I^{(HW)}$ is increasing on $(0, \infty)$. A similar argument shows that $R_I > R_H$ if $R_H < 1$.

(iii) *R_I and R_V*

Suppose that $R_I > 1$ and a fraction p of individuals is vaccinated with a perfect vaccine. Then, as in the households model, μ_G, μ_H and μ_W are reduced to $\mu_G(p), \mu_H(p)$ and $\mu_W(p)$, respectively, where

$$\mu_G(p) = (1-p)\mu_G, \mu_H(p) \overset{2}{\leq} (1-p)\mu_H \qquad \text{and} \qquad \mu_W(p) \overset{2}{\leq} (1-p)\mu_W,$$

and R_I is reduced to $R_I(p)$, which is given by the unique solution of $g_{I,p}^{(HW)}(\lambda) = 0$ in $(0, \infty)$, where

$$g_{I,p}^{(HW)}(\lambda) = 1 - \frac{\mu_G(p)}{\lambda} - \frac{\mu_G(p)\mu_H(p) + \mu_G(p)\mu_W(p) + \mu_H(p)\mu_W(p)}{\lambda^2} - \frac{\mu_G(p)\mu_H(p)\mu_W(p)}{\lambda^3}.$$

Suppose that $p > 0$. Then, the above inequalities imply that

$$g_{I,p}^{(HW)}((1-p)R_I) \overset{2}{\geq} 1 - \frac{\mu_G}{R_I} - \frac{\mu_G\mu_H + \mu_G\mu_W + \mu_H\mu_W}{R_I^2} - \frac{\mu_G\mu_H\mu_W}{R_I^3} = 0,$$

since $g_I^{(HW)}(R_I) = 0$. Hence, since $g_{I,p}^{(HW)}(R_I(p)) = 0$ and $g_{I,p}^{(HW)}$ is strictly increasing on $(0, \infty)$, $R_I(p) \overset{2}{\leq} (1-p)R_I$. In particular, $R_I(1 - R_I^{-1}) \overset{2}{\leq} 1$, whence $p_C \overset{2}{\leq} 1 - R_I^{-1}$ and, using (17), $R_V \overset{2}{\leq} R_I$.

(iv) *R_V and R_0*

Recall that R_0 is given by the unique root in $(0, \infty)$ of $g_0^{(HW)}$ defined at (32). Suppose that $R_0 > 1$ and a fraction p of the population is vaccinated with a perfect vaccine. Then the post-vaccination basic reproduction number, $R_0(p)$ say, is given by the unique root in $(0, \infty)$ of the function $g_{0,p}^{(HW)}$ defined by

$$g_{0,p}^{(HW)}(\lambda) = 1 - \sum_{k=0}^{n_H+n_W-2} \frac{c_k(p)}{\lambda^k},$$

where $c_0(p) = \mu_G(p)$ and, for $k = 1, 2, \cdots, n_H + n_W - 2$,

$$c_k(p) = \mu_G(p) \left(\sum_{\ell=\max(0,k-n_W+1)}^{\min(k,n_H-1)} \mu_\ell^H(p)\mu_{k-\ell}^W(p) \right) + \sum_{\ell=\max(1,k-n_W+2)}^{\min(k,n_H-1)} \mu_\ell^H(p)\mu_{k+1-\ell}^W(p),$$

$\mu_G(p) = (1-p)\mu_G$, and, for $\ell = 0, 1, \cdots, \mu_\ell^H(p)$ (respectively $\mu_\ell^W(p)$) is the post-vaccination mean size of the ℓth generation in a typical single-household (respectively single-workplace) epidemic with one (unvaccinated) initial infective; the second sum in the expression for $c_k(p)$ is zero when $k = n_H + n_W - 2$.

As in the proof of Theorem 1,

$\mu_\ell^H(p) \geq (1-p)^\ell \mu_\ell^H$ $(\ell = 0, 1, \cdots, n_H - 1)$ and $\mu_{\ell'}^W(p) \geq (1-p)^{\ell'} \mu_{\ell'}^W$ $(\ell' = 0, 1, \cdots, n_W - 1)$,

whence $c_k(p) \geq (1-p)^{k+1} c_k$ $(k = 1, 2, \cdots, n_H + n_W - 2)$. Moreover, these inequalities are all equalities if $\max(n_H, n_W) \leq 3$, otherwise at least one of them is strict. Arguing exactly as in the proof of Theorem 1 shows that $R_V \overset{3}{\geq} R_0$.

(v) *R_I and R_0*

We need to consider only a declining epidemic, since for a growing epidemic comparison of R_I and R_0 follows from (iii) and (iv) above. It is convenient to express (74) and (75) as

$$\mu_G + \mu_G\mu_H + \mu_G\mu_W + \mu_G\mu_H\mu_W + \mu_H\mu_W = \sum_{k=0}^{n_H+n_W-2} c_k. \tag{78}$$

Note that $c_0 = \mu_G$ and that, in (78), the contributions to $\mu_G\mu_H\mu_W$ come from elements of the sums in $c_2, c_3, \cdots, c_{n_H+n_W-2}$ (and not c_1). Thus, we may write

$$\mu_G\mu_H + \mu_G\mu_W + \mu_H\mu_W = \sum_{k=1}^{n_H+n_W-2} c_k^{(1)} \quad \text{and} \quad \mu_G\mu_H\mu_W = \sum_{k=2}^{n_H+n_W-2} c_k^{(2)},$$

where $c_1^{(1)} = c_1$ and, for k=$2, 3, \cdots, n_H + n_W - 2$, $c_k = c_k^{(1)} + c_k^{(2)}$ with both $c_k^{(1)}$ and $c_k^{(2)}$ being positive. Now, from (32),

$$g_0^{(HW)}(\lambda) = 1 - \frac{\mu_G}{\lambda} - \sum_{k=1}^{n_H+n_W-2} \frac{c_k^{(1)}}{\lambda^{k+1}} - \sum_{k=2}^{n_H+n_W-2} \frac{c_k^{(2)}}{\lambda^{k+1}}.$$

Suppose that $R_I < 1$. Then,

$$\begin{aligned} g_0^{(HW)}(R_I) &= 1 - \frac{\mu_G}{R_I} - \sum_{k=1}^{n_H+n_W-2} \frac{c_k^{(1)}}{R_I^{k+1}} - \sum_{k=2}^{n_H+n_W-2} \frac{c_k^{(2)}}{R_I^{k+1}} \\ &\leq 1 - \frac{\mu_G}{R_I} - \frac{1}{R_I^2} \sum_{k=1}^{n_H+n_W-2} c_k^{(1)} - \frac{1}{R_I^3} \sum_{k=2}^{n_H+n_W-2} c_k^{(2)} \\ &= 1 - \frac{\mu_G}{R_I} - \frac{\mu_G\mu_H + \mu_G\mu_W + \mu_H\mu_W}{R_I^2} - \frac{\mu_G\mu_H\mu_W}{R_I^3} \\ &= g_I^{(HW)}(R_I) \\ &= 0, \end{aligned} \tag{79}$$

by the definition of R_I. Hence, $R_0 \geq R_I$, since $g_0^{(HW)}(R_0) = 0$ and $g_0^{(HW)}$ is increasing on $(0, \infty)$. If $n_H = n_W = 2$ then $c_1 = \mu_G\mu_H + \mu_G\mu_W + \mu_H\mu_W$ and $c_2 = \mu_G\mu_H\mu_W$, whence $g_0^{(HW)} = g_I^{(HW)}$ and $R_0 = R_I$. If $n_H > 2$ or $n_W > 2$ then it is readily seen using (33) that $c_3^{(2)} > 0$, as $n_H + n_W - 2 \geq 3$, which implies that the inequality (79) is strict, whence $R_0 \overset{2}{\geq} R_I$.

Finally, we prove *(c)*. For $\theta \in (-\infty, \infty)$, let

$$F_{HW}(\theta) = \mu_G \mathcal{M}_{W_G}(\theta)(\mathcal{L}_{\xi_H}(\theta)+1)(\mathcal{L}_{\xi_W}(\theta)+1) + \mathcal{L}_{\xi_H}(\theta)\mathcal{L}_{\xi_W}(\theta),$$

and define $\widetilde{F}_{HW}(\theta)$ and $F^{(0)}_{HW}(\theta)$ similarly, using $\widetilde{\mathcal{L}}_{\xi_H}(\theta)$ and $\widetilde{\mathcal{L}}_{\xi_W}(\theta)$ (recall (41) and (42)) for $\widetilde{F}_{HW}(\theta)$, and $\mathcal{L}^{(0)}_{\xi_H}(\theta)$ and $\mathcal{L}^{(0)}_{\xi_W}(\theta)$ (recall (39) and (40)) for $F^{(0)}_{HW}(\theta)$. Then, recalling (38), the real-time growth rate r, and its approximations $\tilde{r}$ and $r^{(0)}$ under the two approximate models, are given by the unique real solutions of

$$F_{HW}(r) = 1, \quad \widetilde{F}_{HW}(\tilde{r}) = 1 \quad \text{and} \quad F^{(0)}_{HW}(r^{(0)}) = 1. \tag{80}$$

Note that $\mathcal{M}_{W_G}(0)=1$, $\mathcal{L}_{\xi_H}(0)=\widetilde{\mathcal{L}}_{\xi_H}(0)=\mathcal{L}^{(0)}_{\xi_H}(0)=\mu_H$ and $\mathcal{L}_{\xi_W}(0)=\widetilde{\mathcal{L}}_{\xi_W}(0)=\mathcal{L}^{(0)}_{\xi_W}(0)=\mu_W$, so, recalling (74),

$$F_{HW}(0) = \widetilde{F}_{HW}(0) = F^{(0)}_{HW}(0) = f_{HW}(\mu_G, \mu_H, \mu_W).$$

Thus, using part *(a)* and its proof,

$$\begin{aligned} R_0 = 1 \iff R_* = 1 &\iff f_{HW}(\mu_G, \mu_H, \mu_W) = 1 \\ &\iff F_{HW}(0) = \widetilde{F}_{HW}(0) = F^{(0)}_{HW}(0) = 1. \end{aligned}$$

Hence, using (80),

$$R_* = 1 \iff r = \tilde{r} = r^{(0)} = 0,$$

and part *(a)* of Theorem 2 holds for the households-workplaces model, since $\mathcal{M}_{W_G}(0) = 1$.

Turning to part *(b)* of Theorem 2, applied to the households-workplaces model, suppose first that all households have size n. Then an analogous argument to the derivation of (58) yields, using the same notation,

$$\mathcal{L}_{\xi_H}(\theta) = \sum_{i=1}^{n-1} \mathbb{E}\left[\mathrm{e}^{-\theta T_i}\right] = \sum_{k=1}^{n-1} \mu_k^H \, \mathbb{E}[\mathrm{e}^{-\theta T_1} | \chi_k(1)].$$

Arguing as for the households model then gives that $\mathcal{L}_{\xi_H}(\theta) \geq \mathcal{L}^{(0)}_{\xi_H}(\theta)$ if $\theta > 0$, while if $\theta < 0$, then $\mathcal{L}_{\xi_H}(\theta) \leq \mathcal{L}^{(0)}_{\xi_H}(\theta)$, and further that these inequalities hold also in the unequal household size setting, which, together with analogous inequalities for $\mathcal{L}_{\xi_W}(\theta)$ and $\mathcal{L}^{(0)}_{\xi_W}(\theta)$, imply that $F_{HW}(\theta) \geq F^{(0)}_{HW}(\theta)$ if $\theta > 0$ and $F_{HW}(\theta) \leq F^{(0)}_{HW}(\theta)$ if $\theta < 0$. Using (80), it follows that $0 < r^{(0)} \leq r$ in a growing epidemic and $r \leq r^{(0)} < 0$ in a declining epidemic. Part *(b)* of Theorem 2 now follows for the households-workplaces model, since $\mathcal{M}_{W_G}(\theta)$ strictly decreases with θ. The proof of part *(c)* of Theorem 2 for the households-workplaces model is omitted since it exploits arguments used in the corresponding proof for the households model in exactly the same way as is done above for part *(b)*. □

8 Conclusions

In this paper, we focus on an SIR model for a directly transmissible infection spreading in a fully susceptible population, socially structured into households, or households and workplaces. However, most of our results extend readily to SEIR models. We collect together most of the reproduction numbers that have been defined in the literature (see Tables 1 and 3) and we show how they relate to each other. Particular emphasis is placed on the basic reproduction number R_0, for which we provide a simpler and more elegant method for its calculation than that introduced in the companion paper of this [22]. Extending the work of Goldstein et al. [11], we add other reproduction numbers (namely $\hat{R}_2$, R_I and R_0) to the ones they already discuss, and we provide new definitions for the reproduction numbers R_{HI} and R_2 in a way that is more satisfactory when households have variable size: see (13) and (16), respectively.

We extend the inequalities discussed in Goldstein et al. [11] (Table 2) and, by doing so, we provide significantly sharper bounds for the vaccine-associated reproduction number R_V than previously available, a result that holds consistently also for the network-households and households-workplaces models.

More precisely, Goldstein et al. [11] proved that R_*, R_r , R_V , R_{VL} and (if all households have the same size) $\bar{R}_{HI}$ share the same threshold at 1 and $R_* \geq R_{VL} \geq R_V \geq \bar{R}_{HI}$ in a growing epidemic. They noted also that in most cases R_r fits into the inequalities as

$$R_* \geq R_{VL} \geq R_r \geq R_V \geq \bar{R}_{HI}.$$

Although R_r may sometimes represent a practically useful upper bound for R_V, which is usually the quantity of interest for public health purposes, it can be excessively large at times (e.g. see Figure 5) and it requires knowledge of the generation-time distribution w_G. In general, R_{VL} cannot be computed easily from the model parameters, so this leaves R_* and $\bar{R}_{HI}$ as the only generally valid, time-independent and easy-to-calculate (from the basic model parameters) bounds for R_V, but R_* is often excessively large and $\bar{R}_{HI}$ is not a threshold parameter when households are not all of the same size.

Although a proof is still to be found, we conjecture that $R_0 \geq R_2$ in a growing epidemic, with the opposite inequality holding in a declining epidemic. Assuming this to be true, we have that, in a growing epidemic

$$R_* \geq R_I \geq R_V \geq R_0 \geq R_2 \geq R_{HI} > 1$$

and, in a declining epidemic,

$$R_* \leq R_I \leq R_0 \leq R_2 \leq R_{HI} < 1.$$

Note that, even if the conjecture about R_2 does not hold, R_I and R_0 provide sharper bounds for R_V than R_* and R_{HI}. Moreover, the numerical illustrations in Section 6 demonstrate that the improvement can be appreciable. This provides useful information for bracketing the critical vaccination coverage within an interval which does not depend on the fine

details of the person-to-person contact process and is therefore robust to poor estimates of complex model components, such as the generation-time distribution.

Turning to the spread in real-time, R_r cannot always be related with R_0, although for virtually all models considered in the literature (including the standard SIR model and models with a deterministic time-varying infectivity profile) we have $R_r \geq R_0$ in a growing epidemic. Further, we have shown that R_r and R_{VL} cannot be ordered in general. A further reproduction number $\widetilde{R}_r$ has also been introduced, which in the case of the standard SIR model (and extensions to non-constant infection rates), approximates R_0 better than R_r.

Other models with a different social structure have also been studied. These models all share the same qualitative construction of R_0 as presented in our previous paper [22]. As far as the network-households model is concerned, the relationships between R_*, R_I, R_V and R_0 are the same as in the households model, although inequalities involving R_0, R_2 and R_{HI} are more complex. Also, for the model with households and workplaces, the relationships between R_*, R_I, R_V and R_0 are the same, with the additional presence of the household and workplace reproduction numbers as in Theorem 3.

Although our results stress how R_V is bracketed between R_I and R_0, we still believe that each of the reproduction numbers discussed have their own merit: R_* carries a simple interpretation, is easiest to calculate, and in the households model gives the critical vaccination coverage when whole households are vaccinated uniformly at random; R_V and R_{VL} are important for practical reasons; R_r is useful as r can generally be estimated in new epidemics; R_0 represents a fundamental concept in epidemic models; R_2 is usually very close to R_0, but requires less knowledge about the epidemic model to be computed (in addition to μ_G, only μ_1 and the mean size of within-household epidemics) and might be easier to estimate from households studies, especially when within-household generations quickly overlap; and R_{HI} requires even less knowledge than R_2, but is a coarser bound for R_V. For the households-workplaces model, in addition to the simple construction of R_* and the bounds that R_I and R_0 provide for R_V, R_H still carries a simple interpretation, unlike R_0 is always finite and is informative about the control effort required when vaccination target entire households [20].

Finally, much effort has been placed in studying the properties of R_r, in particular in relationship with R_0. As already mentioned above, it is not possible to order them in general, although in most of the models commonly considered in the literature $R_r \geq R_0$ in a growing epidemic (see Theorem 2). However, on a more speculative but practically relevant note, consider the case of a non-random infectivity profile $w_G(t)$ and assume that w_G is unimodal, with small variance and mean significantly larger than 0. Then, if instead of the true generations we deal with the computationally much more tractable rank generations (approximating process T_k by $\hat{T}_k$ in Section 7.2, c.f. equation (59)) the errors involved are small because generations do not easily overlap, in particular for realistically small household sizes. Furthermore, if we approximate the relative time at which real infections are made with that at which infections contacts are made (approximating $\hat{T}_k$ by $\sum_{m=0}^{k-1} \Psi_m$, c.f. equation (60)), the errors are also minor, because repeated infectious contacts between the same pair of individuals are likely to be all gathered around the mode of w_G. Therefore, the quantitative values of R_r and R_0 are very similar to each other, thus suggesting that R_0, the individual

generation time distribution w_G and the real-time growth rate r are approximately related as in the case of simple homogeneously mixing models. Given that many infections lead to infectivity profiles of the type described above (e.g. influenza and SARS), this intuitive argument increases confidence in the estimates of R_0 obtained in the literature using models that ignore the household structure.

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A Comparison of R_0 and R_2

In this appendix we discuss the conjecture concerning the comparison of R_0 and R_2. Recall that R_0 is given by the unique root in $(0, \infty)$ of the function g_0 defined at (5) and R_2 is given by the unique root in (b, ∞) of the function g_2 defined at (16). Recall also that $g_0(\lambda) = \sum_{n=1}^{n_H} \pi_n g_0^{(n)}(\lambda)$ and $g_2(\lambda) = \sum_{n=1}^{n_H} \pi_n g_2^{(n)}(\lambda)$, where $g_0^{(n)}$ and $g_2^{(n)}$ are defined at (6) and (15), respectively.

Observe that $g_0^{(n)} = g_2^{(n)}$ for $n = 1, 2$, so $R_0 = R_2$ if $n_H \leq 2$. We aim to show that if $n \geq 3$ then $\text{sign}(g_2^{(n)}(\lambda) - g_0^{(n)}(\lambda)) = \text{sign}(\lambda - 1)$ for all $\lambda > b^{(n)}$. This implies that if $n_H \geq 3$ then $\text{sign}(g_2(\lambda) - g_0(\lambda)) = \text{sign}(\lambda - 1)$ for all $\lambda > b$. It would then follow, as in the proof of the comparison between R_0 and R_{HI} in Theorem 1, that if $R_0 > 1$ then $R_0 > R_2$ and if $R_0 < 1$ then $R_0 < R_2$.

We now fix $n \geq 3$ and suppose that all households have size n, so $g_0^{(n)} = g_0$ and $g_2^{(n)} = g_2$.

Then, for any $\lambda > b = 1 - \mu_1/\mu_H$,

$$\begin{aligned} g_2(\lambda) - g_0(\lambda) &= \mu_G \left[\sum_{k=1}^{n-1} \frac{\mu_k}{\lambda^{k+1}} - \frac{\mu_1}{\lambda(\lambda - b)} \right] \\ &= \frac{\mu_G}{\lambda - b} \left[\sum_{k=1}^{n-1} \frac{(\lambda - b)\mu_k}{\lambda^{k+1}} - \frac{\mu_1}{\lambda} \right] \\ &= \frac{\mu_G}{\lambda - b} \left[\sum_{k=2}^{n-1} \frac{\mu_k}{\lambda^k} - b \sum_{k=1}^{n-1} \frac{\mu_k}{\lambda^{k+1}} \right] \\ &= \frac{\mu_G}{\lambda^2(\lambda - b)} f_n(\lambda^{-1}), \end{aligned} \tag{81}$$

where f_n is the polynomial of degree $n-2$ given by $f_n(x) = \sum_{j=0}^{n-2} c_j x^j$, with $c_j = \mu_{j+2} - b\mu_{j+1}$ $(j = 0, 1, \cdots, n-3)$ and $c_{n-2} = -b\mu_{n-1}$. Note that $f_n(1) = 0$. Thus, as at (46),

$$f_n(x) = (x - 1)\tilde{f}_n(x), \tag{82}$$

where

$$\tilde{f}_n(x) = \sum_{j=0}^{n-3} \tilde{c}_j x^j, \tag{83}$$

with $\tilde{c}_j = \sum_{l=j+1}^{n-2} c_l$ $(j = 0, 1, \cdots, n-3)$. Thus,

$$\tilde{c}_j = \sum_{l=j+3}^{n-1} \mu_l - b \sum_{l=j+2}^{n-1} \mu_l \qquad (j = 0, 1, \cdots, n-4)$$

and $\tilde{c}_{n-3} = -b\mu_{n-1}$. It follows from (81) and (83) that $\text{sign}(g_2(\lambda) - g_0(\lambda)) = \text{sign}(\lambda - 1)$ if $\tilde{c}_j \leq 0$ $(j = 0, 1, \cdots, n-3)$ and at least one of these inequalities is strict.
Now $\tilde{c}_{n-3} = -b\mu_{n-1} < 0$[8], so a sufficient condition for $\text{sign}(g_2(\lambda) - g_0(\lambda)) = \text{sign}(\lambda - 1)$, and hence for the conjectured comparisons between R_0 and R_2, is that

$$\frac{\sum_{l=j+3}^{n-1} \mu_l}{\sum_{l=j+2}^{n-1} \mu_l} \leq b \quad (j = 0, 1, \cdots, n-4)$$

or equivalently that

$$\frac{1}{\mu_j} \sum_{l=j+1}^{n-1} \mu_l \leq \frac{1}{\mu_1} \sum_{l=2}^{n-1} \mu_l \quad (j = 2, 3, \cdots, n-2). \tag{84}$$

When $n = 3$, the condition (84) is vacuous, so the conjectured comparison between R_0 and R_2 holds when $n_H = 3$. We do not have a proof that (84) holds in general.

[8]This assumes that $\mu_{n-1} > 0$, which is the case for most models studied in the literature. If $\mu_{n-1} = 0$ then the ensuing discussion may be modified in the obvious fashion.

Suppose that household generation sizes are the same as for a Reed-Frost model, as is the case when individuals have a non-random infectivity profile. Let p be the probability that a given infective infects a given susceptible household member. Suppose that $n = 4$. The mean generation sizes are obtained easily using probabilities of different chains of infection (see e.g. Bailey [2], Table 14.3) and are given by

$$\mu_1 = 3p, \quad \mu_2 = 3p^2(1-p)(2-p^2) \quad \text{and} \quad \mu_3 = 6p^3(1-p)^3.$$

Thus,

$$\frac{\mu_3}{\mu_2} = \frac{2p(1-p)^2}{2-p^2} \quad \text{and} \quad \frac{\mu_2+\mu_3}{\mu_1} = p(1-p)(2-p^2+2p(1-p)^2),$$

whence, for $p \in [0,1]$,

$$\begin{aligned} \frac{\mu_3}{\mu_2} \leq \frac{\mu_2+\mu_3}{\mu_1} &\iff \frac{2(1-p)}{2-p^2} \leq 2-p^2+2p(1-p)^2 \\ &\iff 2+6p(1-p)^2-4p^3+5p^4-2p^5 \geq 0. \end{aligned}$$

Let $\varphi(p) = 4p^3-5p^4+2p^5$. Then $\varphi'(p) = 2p^2(1+5(1-p)^2) \geq 0$, so $0 \leq \varphi(p) \leq 1$ for $p \in [0,1]$, whence $\frac{\mu_3}{\mu_2} \leq \frac{\mu_2+\mu_3}{\mu_1}$ and (84) holds for $n = 4$, proving the conjectured comparison between R_0 and R_2 in this case. The expressions for the mean generation sizes become increasing unwieldy as n increases. However, numerical investigation using the recursive method for computing the mean generation sizes described in Appendix A of Pellis et al. [22] did not find any violation of (84) for $n = 5, 6, \cdots, 20$ and $p = 0.001, 0.002, \cdots, 0.999$, suggesting that the conjectured comparison between R_0 and R_2 holds generally for the Reed-Frost model. A similar investigation for the Markov model in which a typical infective contacts any given household member at rate λ_H during an infectious period that has an Exp(1) distribution did not find any violation of (84) for $n = 4, 5, \cdots, 20$ and $\lambda_H = 0.01, 0.02, \cdots, 10.00$, suggesting that the comparison between R_0 and R_2 holds generally for this model too.

B Comparison of R_I and R_{VL}

In this appendix we give an example which demonstrates that, for the households model, the reproduction numbers R_I and R_{VL} cannot in general be ordered. We consider an SIR epidemic among a population of households, all of which have size 3. The infectious period is assumed to be constant and equal to one. The individual to individual local infection rate is λ_H. Suppose that the entire population is vaccinated with a leaky vaccine having efficacy $\mathcal{E}$ and let $R_I(\mathcal{E})$ denote the post-vaccination version of R_I. Then $R_I(\mathcal{E})$ is the largest eigenvalue of

$$M_I(\mathcal{E}) = \begin{bmatrix} \mu_G(\mathcal{E}) & \mu_H(\mathcal{E}) \\ \mu_G(\mathcal{E}) & 0 \end{bmatrix},$$

where $\mu_G(\mathcal{E}) = (1-\mathcal{E})\mu_G$ and $\mu_H(\mathcal{E})$ is the mean size of a single-household epidemic, with one initial infective and two initial susceptibles, both of whom are vaccinated. We assume

throughout this appendix that $R_I > 1$. By considering the characteristic polynomial of $M_I(\mathcal{E})$ and arguing as for the comparison of R_I and R_V in the proof of Theorem 1, it is readily seen that $\text{sign}(R_{VL} - R_I) = \text{sign}(\mu_H(\mathcal{E}) - (1-\mathcal{E})\mu_H)$, with $\mathcal{E} = 1 - R_I^{-1}$.

The definition of the leaky vaccine action implies that $\mu_H(\mathcal{E})$ is given by mean size of the single-household epidemic with λ_H replaced by $\lambda_H(1-\mathcal{E})$. Direct calculation shows that for the present population

$$\mu_H(\mathcal{E}) = 2 - 4\mathrm{e}^{-2\lambda_H(1-\mathcal{E})} + 2\mathrm{e}^{-3\lambda_H(1-\mathcal{E})}.$$

Thus, if we let $x = 1 - \mathcal{E}$, then

$$\text{sign}(\mu_H(\mathcal{E}) - (1-\mathcal{E})\mu_H) = \text{sign}(u_1(x) - u_2(x)),$$

where

$$u_1(x) = 2 - 4\mathrm{e}^{-2\lambda_H x} + 2\mathrm{e}^{-3\lambda_H x} \text{ and } u_2(x) = x(2 - 4\mathrm{e}^{-2\lambda_H} + 2\mathrm{e}^{-3\lambda_H}).$$

Now

$$u_1'(x) = 8\lambda_H\mathrm{e}^{-2\lambda_H x} - 6\lambda_H\mathrm{e}^{-3\lambda_H x} \text{ and } u_2'(x) = 2 - 4\mathrm{e}^{-2\lambda_H} + 2\mathrm{e}^{-3\lambda_H},$$

so, since $u_1(0) = u_2(0) = 0$, $u_1(x) - u_2(x) > 0$ (respectively < 0) for all sufficiently small $x > 0$ if $v(\lambda_H) > 0$ (respectively < 0), where

$$v(\lambda_H) = 2\lambda_H - 2 + 4\mathrm{e}^{-2\lambda_H} - 2\mathrm{e}^{-3\lambda_H}.$$

Further,

$$v'(\lambda_H) = 2 - 8\mathrm{e}^{-2\lambda_H} + 6\mathrm{e}^{-3\lambda_H} \text{ and } v''(\lambda_H) = 16\mathrm{e}^{-2\lambda_H} - 18\mathrm{e}^{-3\lambda_H}.$$

Thus $\text{sign}(v''(\lambda_H)) = \text{sign}(\lambda_H - \log(9/8))$ and elementary calculus shows that $v(\lambda_H) = 0$ has a unique solution, λ_H^* say, in $(0, \infty)$ and that

$$\text{sign}(v(\lambda_H)) = \text{sign}(\lambda_H - \lambda_H^*) \qquad \text{for } \lambda_H \in (0, \infty).$$

(Numerical calculation shows that $\lambda_H^* \approx 0.4219$.) It follows that if $\lambda_H \in (0, \lambda_H^*)$ then $u_1(x) < u_2(x)$ for all sufficiently small $x > 0$, whilst if $\lambda_H \in (\lambda_H^*, \infty)$ then $u_1(x) > u_2(x)$ for all sufficiently small $x > 0$. Recall that $x = 1 - \mathcal{E}$, where $\mathcal{E} = 1 - R_I^{-1}$, so $x = R_I^{-1}$. Also, note that R_I increases with μ_G for fixed λ_H. Hence, if $\lambda_H \in (0, \lambda_H^*)$, then there exists $\mu_G^* > 0$ such that $R_I > R_{VL}$ for all $\mu_G > \mu_G^*$, whilst if $\lambda_H \in (\lambda_H^*, \infty)$, then there exists $\mu_G^\dagger > 0$ such that $R_I < R_{VL}$ for all $\mu_G > \mu_G^\dagger$. Thus the reproduction numbers R_I and R_{VL} cannot in general be ordered.

C Comparisons between R_0, R_{HI}, $\hat{R}_{HI}$ and $\bar{R}_{HI}$

In this appendix, we discuss the orderings of the individual reproduction numbers $R_0, R_{HI}, \hat{R}_{HI}$ and $\bar{R}_{HI}$.

Recall from Section 2.5 that $a^{(n)} = \mu_H^{(n)}/(1+\mu_H^{(n)})$ and that R_{HI} is the unique positive solution of g_{HI} (defined at (13)) in (a,∞), with $a = \max\left(a^{(n)}, n = 1, 2, \cdots n_H\right)$. Further, with $\hat{a} = \mu_H/(1+\mu_H)$, it follows from (10) that $\hat{R}_{HI}$ is the unique root in $(\hat{a},\infty)$ of

$$\hat{g}_{HI}(\lambda) = 1 - \frac{\mu_G}{\lambda - \hat{a}} \qquad (\lambda > \hat{a}),$$

and, with $\bar{a} = \sum_{n=1}^{n_H} \pi_n a^{(n)}$, it follows from (11) that $\bar{R}_{HI}$ is the unique root in $(\bar{a},\infty)$ of

$$\bar{g}_{HI}(\lambda) = 1 - \frac{\mu_G}{\lambda - \bar{a}} \qquad (\lambda > \bar{a}).$$

First, we compare R_{HI} and $\bar{R}_{HI}$. For fixed $\lambda > 0$, define the function $\bar{f}_\lambda$ by

$$\bar{f}_\lambda(x) = 1 - \frac{\mu_G}{\lambda - x} \qquad (x < \lambda).$$

Now $\bar{f}''_\lambda(x) = -2\mu_G(\lambda - x)^{-3} < 0$ for $x < \lambda$, so $\bar{f}_\lambda$ is concave and by Jensen's inequality,

$$g_{HI}(\lambda) = \sum_{n=1}^{n_H} \pi_n \bar{f}_\lambda(a^{(n)}) \le \bar{f}_\lambda(\bar{a}) = \bar{g}_{HI}(\lambda) \qquad (\lambda > a),$$

whence $\bar{R}_{HI} \le R_{HI}$ always, with equality only if $\mu_H^{(n)}$ is constant for all n with $\pi_n > 0$. (Note that, as $\mu_H^{(1)} = 0$, if $\pi_1 > 0$ this condition is satisfied only in the trivial cases where $n_H = 1$ or there is no transmission within the household.) In particular, in a growing epidemic, Theorem 1*(b)* leads to

$$R_0 > R_{HI} \ge \bar{R}_{HI},$$

but note that $\bar{R}_{HI}$, which is not a threshold parameter, might be smaller than 1 while the other two are larger than 1. Exploiting this fact, we now prove that the inequality between R_0 and $\bar{R}_{HI}$ is not necessarily reversed in a declining epidemic. Suppose that $n_H = 2$ and further that $\pi_1 > 0, \pi_2 > 0$ and $\mu_H^{(2)} > \mu_H^{(1)} = 0$. Then, there exists $\mu_G > 0$ such that $\bar{R}_{HI} < R_{HI} = R_0 = 1$. Now, $\bar{R}_{HI}, R_{HI}$ and R_0 all depend continuously on μ_G, so reducing μ_G slightly gives a declining epidemic for which $\bar{R}_{HI} < R_0$. However, for a common household size, $\bar{R}_{HI} = R_{HI}$ and Theorem 1*(b)* implies that $\bar{R}_{HI} > R_0$ in a declining epidemic. Thus, in general, $\bar{R}_{HI}$ and R_0 cannot be ordered in a declining epidemic.

Now we compare R_{HI} and $\hat{R}_{HI}$. First, note that

$$\begin{aligned} g_{HI}(\lambda) &= 1 - \mu_G \sum_{n=1}^{n_H} \frac{\pi_n}{\lambda - a^{(n)}} \\ &= 1 - \mu_G \sum_{n=1}^{n_H} \pi_n \frac{1}{\lambda - \frac{\mu_H^{(n)}}{1+\mu_H^{(n)}}} \\ &= 1 - \mu_G \sum_{n=1}^{n_H} \pi_n \frac{1+\mu_H^{(n)}}{\lambda + (\lambda-1)\mu_H^{(n)}}. \end{aligned}$$

For fixed $\lambda > 0$, define the function $\hat{f}_\lambda$ by

$$\hat{f}_\lambda(x) = \frac{1+x}{\lambda + (\lambda-1)x} \qquad (x \neq \lambda/(1-\lambda)),$$

so $\hat{f}''_\lambda(x) = -2(\lambda-1)/(\lambda+(\lambda-1)x)^3$. Thus, if $\lambda > 1$ then $\hat{f}_\lambda$ is strictly concave on $[0,\infty)$ so, using Jensen's inequality,

$$\begin{aligned} g_{HI}(\lambda) &= 1 - \mu_G \sum_{n=1}^{n_H} \pi_n \hat{f}_\lambda(\mu_H^{(n)}) \\ &\geq 1 - \mu_G \hat{f}_\lambda(\mu_H) = \hat{g}_{HI}(\lambda), \end{aligned}$$

and it follows that $R_{HI} \leq \hat{R}_{HI}$ in a growing epidemic.

Suppose that $\lambda < 1$. Then $\hat{f}_\lambda$ is strictly convex on $[\,0, \lambda/(1-\lambda)\,)$. Recall from (13) that $g_{HI}(\lambda)$ is defined for $\lambda > a = \max\left(a^{(n)} : n = 1, 2, \cdots, n_H\right)$, where $a^{(n)} = \mu_H^{(n)} / \left(1 + \mu_H^{(n)}\right)$. Thus, for each n, $\mu_H^{(n)} < \lambda/(1-\lambda)$ and applying Jensen's inequality as above yields that $g_{HI}(\lambda) \leq \hat{g}_{HI}(\lambda)$ $(\lambda > a)$. It follows that $R_{HI} \geq \hat{R}_{HI}$ in a declining epidemic. These inequalities are strict except again in the case when $\mu_H^{(n)}$ is constant for all n with $\pi_n > 0$.

Finally, we give an example which demonstrates that the reproduction numbers R_0 and $\hat{R}_{HI}$ cannot in general be ordered if the population contains households of different sizes. We use notation analogous to that in the comparison between R_0 and R_{HI} in the proof of Theorem 1. Suppose that the population contains only households of sizes 1 and 3, so $\pi_3 = 1 - \pi_1$. Then $\mu_0 = 1, \mu_1 = \pi_3 \mu_1^{(3)}$ and $\mu_2 = \pi_3 \mu_2^{(3)}$, so, using (11), $\hat{R}_{HI} = \mu_G + \hat{a}$, with $\hat{a} = \pi_3(\mu_1^{(3)} + \mu_2^{(3)})/(1 + \pi_3(\mu_1^{(3)} + \mu_2^{(3)}))$. Let $\hat{h}_0(\lambda) = \hat{g}_{HI}(\lambda) - g_0(\lambda)$. Then, arguing as in (45) to (48), shows that

$$\begin{aligned} \hat{h}_0(\lambda) &= -\frac{\mu_G}{\lambda(\lambda - \hat{a})}(\lambda^{-1} - 1)\tilde{f}(\lambda^{-1}) \\ &= \frac{\mu_G(\lambda - 1)}{\lambda^2(\lambda - \hat{a})}\tilde{f}(\lambda^{-1}), \end{aligned} \tag{85}$$

where

$$\tilde{f}(x) = \hat{a}(\mu_1 + \mu_2) - \mu_2 + \hat{a}\mu_2 x. \tag{86}$$

(In the notation of (48), it is easily shown that $\tilde{c}_0 = \hat{a}(\mu_1 + \mu_2) - \mu_2$ and $\tilde{c}_1 = \hat{a}\mu_2$.) Substituting the above expressions for μ_1, μ_2 and $\hat{a}$ into (86) yields that, for $x > 0$,

$$\tilde{f}(x) < 0 \iff \mu_2^{(3)} > \frac{\pi_3(\mu_1^{(3)} + \mu_2^{(3)})}{1 + \pi_3(\mu_1^{(3))} + \mu_2^{(3)})} \left[\mu_1^{(3)} + \mu_2^{(3)}(1+x)\right]. \tag{87}$$

Thus, for any $x > 0$, $\tilde{f}(x) < 0$ for all sufficiently small $\pi_3 \in (0,1)$.

Recall that R_0 is the unique root in $(0,\infty)$ of g_0. Suppose that $R_0 > 1$. Then, since $g_0(R_0) = 0$, it follows from (85) and (87) that, if $\pi_3 \in (0,1)$ is sufficiently small, then

$\hat{g}_{HI}(R_0) < 0$, whence $\hat{R}_{HI} > R_0$. A similar argument shows that, if $R_0 < 1$ and $\pi_3 \in (0,1)$ is sufficiently small, then $\hat{R}_{HI} < R_0$. Note that these inequalities are again the reverse of those proved for R_{HI}, and hence of those for the situation when all households have the same size, in which $R_{HI}, \hat{R}_{HI}$ and R_{HI} coincide. Thus, R_0 and $\hat{R}_{HI}$ cannot in general be ordered.

D Random infectivity profile

The proof of Theorem 2 in Section 7.2 already reveals that in order to show that $R_r \geq R_0$ (respectively $R_r \leq R_0$) does not generally hold in growing (respectively declining) epidemics, we should look for a model in which Φ_m is not stochastically smaller than $\widetilde{W}_G$. In particular this is the case if an individual with a large total infectivity makes its contacts relatively early after infection, while a an individual with a small total infectivity makes its contacts, long after infection. Here we provide a simple example in a household of size $n = 3$. As before the individuals are denoted by $i = 0$ (the initial infective in the household), $i = 1$ and $i = 2$ (the initial susceptibles).

Consider a random infectivity profile which either has its complete mass κ_a at time t_a or it has its complete mass κ_b at time t_b, both with probability 1/2. Thus, for $x > 0$,

$$\int_0^x \mathcal{I}(t)\mathrm{d}t = \begin{cases} \kappa_a \mathbb{1}(x \geq t_a) & \text{with probability } 1/2 \\ \kappa_b \mathbb{1}(x \geq t_b) & \text{with probability } 1/2 \end{cases}. \tag{88}$$

Here all parameters are non-negative. We assume further that

$$(\kappa_a - \kappa_b)(t_a - t_b) < 0. \tag{89}$$

Note that $\kappa_a + \kappa_b = 2$, since the infectivity profile necessarily satisfies $\int_0^\infty \mathbb{E}[\mathcal{I}(t)]dt = 1$. Furthermore, from the definition of W_G, we have that

$$\mathcal{M}_{W_G}(r) = \frac{\kappa_a \mathrm{e}^{-rt_a} + \kappa_b \mathrm{e}^{-rt_b}}{2} = \frac{\kappa_a \mathrm{e}^{-rt_a} + \kappa_b \mathrm{e}^{-rt_b}}{\kappa_a + \kappa_b}. \tag{90}$$

Define $p_a = 1 - \mathrm{e}^{-\lambda_H \kappa_a}$ and $p_b = 1 - \mathrm{e}^{-\lambda_H \kappa_b}$, and note that an infective individual that has total infectivity κ_a (respectively κ_b) infects each susceptible independently with probability p_a (respectively p_b) and all infections occur at time t_a (respectively t_b). Hence,

$$\mathcal{M}_{\widetilde{W}_G}(r) = \frac{p_a \mathrm{e}^{-rt_a} + p_b \mathrm{e}^{-rt_b}}{p_a + p_b}. \tag{91}$$

Straightforward algebra gives

$$\mathcal{M}_{W_G}(r) - \mathcal{M}_{\widetilde{W}_G}(r) = \frac{(p_b\kappa_a - p_a\kappa_b)(\mathrm{e}^{-rt_a} - \mathrm{e}^{-rt_b})}{2(p_a + p_b)}. \tag{92}$$

Furthermore, since for $\lambda_H, r > 0$, the function $(1 - \mathrm{e}^{-r\lambda_H x})/x$ is decreasing for $x > 0$, and $p_b\kappa_a - p_a\kappa_b > 0$ if and only if $p_b/\kappa_b > p_a/\kappa_a$, we obtain that $p_b\kappa_a - p_a\kappa_b > 0$ if and only if

$\kappa_a > \kappa_b$. Combining this with (89) we obtain that $\mathcal{M}_{W_G}(r) - \mathcal{M}_{\widetilde{W}_G}(r) > 0$ for $r > 0$. If $R_* > 1$, this implies that $R_0 > \widetilde{R}_r$ (cf. the end of the proof of Theorem 2*(b)*), while if $R_* < 1$ (and therefore $r < 0$), then $R_0 < \widetilde{R}_r$.

If we prove further that under the given conditions $\widetilde{R}_r > R_r$ in growing epidemics and $\widetilde{R}_r < R_r$ in declining epidemics, then we have constructed the desired counter example. Therefore, in what follows, we only compare the constructions from which $\widetilde{R}_r$ and R_r are deduced. In particular, we have to compare $\mathcal{L}_{\beta_H}(\theta)$ and $\widetilde{\mathcal{L}}_{\beta_H}(\theta)$, through which $\tilde{r}$ and r are defined by (54). In turn, $\tilde{r}$ and r are used to define $\widetilde{R}_r$ and R_r by (55).

Recall that $R_r = 1/\mathcal{M}_{W_G}(r)$, where r is the unique real value of θ which solves the first equation in (54), and $\widetilde{R}_r = 1/\mathcal{M}_{W_G}(\tilde{r})$, where $\tilde{r}$ is the unique real value of θ which solves the second equation in (54). Thus, cf. (58) and (24), we need to compare the pair of times (T_1, T_2) with the pair of times $(\sum_{l=0}^{k_1-1} \Phi_{l,1}, \sum_{l=0}^{k_2-1} \Phi_{l,2})$, where k_1 and k_2 are the generation numbers of individual 1 and 2, while the $\Phi_{l,1}$s and $\Phi_{l,2}$s are independent random variables all distributed as $\widetilde{W}_G$. Note that we assume that individual 0 is infected at time 0. For ease of reference, define $(\widetilde{T}_0, \widetilde{T}_1, \widetilde{T}_2) = (0, \sum_{l=0}^{k_1-1} \Phi_{l,1}, \sum_{l=0}^{k_2-1} \Phi_{l,2})$. We now compare

$$\sum_{i=0}^{2} \mathbb{E}\left[\mathrm{e}^{-rT_i}\right] = \mathbb{E}\left[\mathrm{e}^{-rT_0} + \mathrm{e}^{-rT_1} + \mathrm{e}^{-rT_2}\right] \tag{93}$$

and

$$\sum_{i=0}^{2} \mathbb{E}\left[\mathrm{e}^{-r\widetilde{T}_i}\right] = \mathbb{E}\left[\mathrm{e}^{-r\widetilde{T}_0} + \mathrm{e}^{-r\widetilde{T}_1} + \mathrm{e}^{-r\widetilde{T}_2}\right] \tag{94}$$

Since $T_0 = \widetilde{T}_0$ we only have to compare

$$\zeta(r) = \mathbb{E}\left[\mathrm{e}^{-rT_1} + \mathrm{e}^{-rT_2}\right] \qquad \text{and} \qquad \widetilde{\zeta}(r) = \mathbb{E}\left[\mathrm{e}^{-r\widetilde{T}_1} + \mathrm{e}^{-r\widetilde{T}_2}\right]. \tag{95}$$

After some algebra, we obtain

$$\zeta(r) = \left(p_a \mathrm{e}^{-rt_a} + p_b \mathrm{e}^{-rt_b}\right)\left(1 + \frac{p_a(1-p_a)\mathrm{e}^{-rt_a} + p_b(1-p_b)\mathrm{e}^{-rt_b}}{2}\right). \tag{96}$$

In order to compute $\widetilde{\zeta}(r)$, we compute explicitly the average number of cases in each generation, viz.

$$\mu_1 = p_a + p_b, \tag{97}$$

$$\mu_2 = (p_a + p_b)(p_a(1-p_a) + p_b(1-p_b))/2. \tag{98}$$

From the definition of $\widetilde{\zeta}(r)$ and from (91) we deduce

$$\widetilde{\zeta}(r) = \mu_1 \mathcal{M}_{\widetilde{W}_G}(r) + \mu_2 \left(\mathcal{M}_{\widetilde{W}_G}(r)\right)^2. \tag{99}$$

Straightforward but lengthy algebra shows that

$$\zeta(r) - \widetilde{\zeta}(r) \; = \frac{p_a p_b \left(p_a \mathrm{e}^{-rt_a} + p_b \mathrm{e}^{-rt_b}\right)}{2(p_a + p_b)} \left(p_b - p_a\right) \left(\mathrm{e}^{-rt_a} - \mathrm{e}^{-rt_b}\right), \tag{100}$$

from which we conclude that $\zeta(r) < \widetilde{\zeta}(r)$, and therefore $R_r < \widetilde{R}_r$, when

$$\left(p_b - p_a\right) \left(\mathrm{e}^{-rt_a} - \mathrm{e}^{-rt_b}\right) < 0,$$

which we assumed for growing epidemics in (89) since p_a is increasing in κ_a. This completes the counter example for growing epidemics.

If $R_* < 1$ (i.e. $r < 0$), the same counter example in this case leads to $R_r \geq \widetilde{R}_r > R_0$, showing that also in a declining epidemic R_0 and R_r cannot be ordered in general.

E Comparison of R_r and R_{VL}

In this appendix we give examples which demonstrate that, for the households model, R_r and R_{VL} cannot in general be ordered. We consider an SIR epidemic among a population of households, all of which have size 2. The infectious periods of infectives are independent, each distributed according to a random variable T_I having mean 1 and moment-generating function $\mathcal{M}_{T_I}(\theta) = \mathbb{E}[\mathrm{e}^{-\theta T_I}]$. Whilst infectious, the initial infective in a household contacts locally his/her other household member at the points of a Poisson process having rate λ_H.

Note that, since $\int_0^\infty \mathbb{P}(T_I \geq t)\mathrm{d}t = \mathbb{E}[T_I] = 1$, the mean infectivity profile of an infective is $w_G(t) = \mathbb{P}(T_I \geq t)$ $(t \geq 0)$, whence

$$\mathcal{M}_{W_G}(\theta) = (1 - \mathcal{M}_{T_I}(\theta))/\theta.$$

Consider a single household epidemic, label the initial infective 0 and the other household member 1. Let T_I denote individual 0's infectious period and X denote the time of the first local infectious contact of individual 1 by individual 0. Thus, $X \sim \mathrm{Exp}(\lambda_H)$ and 0 infects 1 locally if and only if $X < T_I$. Hence, the probability that 0 infects 1 locally is

$$\mathbb{E}_{T_I}[\mathbb{P}(X < I)] = \mathbb{E}_{T_I}[1 - \mathrm{e}^{-\lambda_H T_I}] = 1 - \mathcal{M}_{W_G}(\lambda_H),$$

which is also the household mean generation size μ_1. Note that, in the notation of Section 2.8, $\widetilde{W}_G$ is distributed as $(X|X < T_I)$, whence

$$\mathcal{M}_{\widetilde{W}_G}(\theta) = \frac{\lambda_H}{\lambda_H + \theta} \frac{1 - \mathcal{M}_{W_G}(\lambda_H + \theta)}{1 - \mathcal{M}_{W_G}(\lambda_H)}.$$

Further, since all households have size 2, $\mathcal{L}_{\beta_H}(r) = \widetilde{\mathcal{L}}_{\beta_H}(r)$ (see the observation at the end of Section 2.8) and, using (25), the real-time growth rate r is the unique solution of $F(r) = 1$, where

$$F(r) = \mu_G \mathcal{M}_{W_G}(r) \left(1 + \mu_1 \mathcal{M}_{\widetilde{W}_G}(r)\right),$$

which, using the above expressions for μ_1 and $\mathcal{M}_{\widetilde{W}_G}(\theta)$, may be written as

$$F(r) = \mu_G \mathcal{M}_{W_G}(r) \left(1 + \lambda_H \mathcal{M}_{W_G}(\lambda_H + r)\right). \tag{101}$$

Suppose that $r > 0$, so $R_r > 1$, and that the entire population is vaccinated with a leaky vaccine having efficacy $\mathcal{E} = 1 - R_r^{-1}$. Then, recalling (20), $1 - \mathcal{E} = \mathcal{M}_{W_G}(r)$. Hence, after vaccination, μ_G becomes $\mathcal{M}_{W_G}(r)\mu_G$ and λ_H becomes $\mathcal{M}_{W_G}(r)\lambda_H$, so, using (101), the post-vaccination real-time growth rate, $r_\mathcal{E}$ say, is given by the unique real solution of $F_\mathcal{E}(r_\mathcal{E}) = 1$, where

$$F_\mathcal{E}(r_\mathcal{E}) = \mu_G \mathcal{M}_{W_G}(r) \mathcal{M}_{W_G}(r_\mathcal{E}) \left[1 + \mathcal{M}_{W_G}(r)\lambda_H \mathcal{M}_{W_G}\left(\mathcal{M}_{W_G}(r)\lambda_H + r_\mathcal{E}\right)\right].$$

Now,

$$F_\mathcal{E}(0) = \mu_G \mathcal{M}_{W_G}(r) \left[1 + \mathcal{M}_{W_G}(r)\lambda_H \mathcal{M}_{W_G}\left(\mathcal{M}_{W_G}(r)\lambda_H\right)\right],$$

so, since $F(r) = 1$, it follows from (101) that

$$\text{sign}(F_\mathcal{E}(0) - 1) = \text{sign}(G(\lambda_H, r)),$$

where

$$G(\lambda_H, r) = \mathcal{M}_{W_G}(r) \mathcal{M}_{W_G}\left(\mathcal{M}_{W_G}(r)\lambda_H\right) - \mathcal{M}_{W_G}(\lambda_H + r).$$

Note that (i) if $G(\lambda_H, r) = 0$ then $r_\mathcal{E} = 0$, so the post-vaccination epidemic is critical and $R_{VL} = R_r$; (ii) if $G(\lambda_H, r) > 0$ then $r_\mathcal{E} > 0$, so the post-vaccination epidemic is supercritical and $R_{VL} > R_r$; and (iii) if $G(\lambda_H, r) < 0$ then $r_\mathcal{E} < 0$, so the post-vaccination epidemic is subcritical and $R_{VL} < R_r$.

Suppose that $T_I \sim \text{Exp}(1)$. Then $\mathcal{M}_{W_G}(\theta) = (1 + \theta)^{-1}$ and $G(\lambda_H, r) = 0$, whence $R_{VL} = R_r$, as noted in Section 6.1.

Suppose that T_I has probability density function $f_{T_I}(t) = 2te^{-2t}$ $(t \geq 0)$, i.e. T_I follows a gamma distribution with parameters $\alpha = \gamma = 2$ (see (44)). Then $\mathcal{M}_{T_I}(r) = \left(\frac{2}{2+r}\right)^2$, whence $\mathcal{M}_{W_G}(r) = \frac{4+r}{(2+r)^2}$. Lengthy algebra then yields that

$$G(\lambda_H, r) = \frac{\lambda_H r \left[(4+r)^2\lambda_H + (2+r)^2(8+r)\right]}{\left[(2+\lambda_H+r)\left(2(2+r)^2 + \lambda_H(4+r)\right)\right]^2} > 0,$$

since $r > 0$ and $\lambda_H > 0$. Thus, $R_{VL} > R_r$.

Suppose instead that T_I has probability density function

$$f_{T_I}(t) = \frac{1}{3}e^{-\frac{2}{3}t} + e^{-2t} \quad (t \geq 0),$$

so T_I is an equally weighted mixture of $\text{Exp}(\frac{2}{3})$ and $\text{Exp}(2)$. Then

$$\mathcal{M}_{T_I}(r) = \frac{1}{2+3r} + \frac{1}{2+r} \qquad \text{and} \qquad \mathcal{M}_{W_G}(r) = \frac{1}{2}\left(\frac{3}{2+3r} + \frac{1}{2+r}\right).$$

Lengthy algebra now yields that

$$G(\lambda_H, r) = -\frac{\lambda_H r(3r+8)\left[3(4+3r)\lambda_H + (2+3r)(6+3r)\right]}{H(\lambda_H, r)\left(2+\lambda_H+r\right)\left(2+3(\lambda_H+r)\right)},$$

where

$$H(\lambda_H, r) = \left[2(2+r)(2+3r) + \lambda_H(4+3r)\right]\left[2(2+r)(2+3r) + 3\lambda_H(4+3r)\right].$$

Hence $G(\lambda_H, r) < 0$, since $r > 0$ and $\lambda_H > 0$, so now $R_{VL} < R_r$. Thus R_r and R_{VL} cannot in general be ordered.

It is difficult to make general statements since there is no simple expression for $G(\lambda_H, r)$. However, note that in the above examples, $R_{VL} > R_r$ when the infectious period distribution is less variable than an exponential distribution and $R_{VL} < R_r$ when it is more variable.

F Infinitely long latent periods

We consider first a Markov SEIR households epidemic model, in which the latent and infectious periods follow exponential distributions with rates δ and 1, respectively, and whilst infectious a typical infective makes global contacts at overall rate μ_G and contacts any given susceptible in his/her household at rate λ_H. We study the limit of R_r as $\delta^{-1} \to \infty$, so the latent periods become infinitely long with all other parameters held fixed, and compare that limit with R_0 and R_V, which are both independent of δ. We restrict attention to a growing epidemic, i.e. when $R_0 > 1$.

For fixed δ, we may linearly rescale time by setting $t' = \delta t$ so that in the rescaled process the latent period is exponentially distributed with mean one. In the limit as $\delta^{-1} \to \infty$, in the rescaled process the infectious period of an infective is reduced to a single point in time. Note that the exponential-growth associated reproduction number R_r and the mean generation sizes $\mu_1, \mu_2, \cdots, \mu_{n_H-1}$ are each invariant to this rescaling ($\mu_1, \mu_2, \cdots, \mu_{n_H-1}$ are also invariant to δ). A similar rescaling is used in the proof of Lemma B.3.1 in Goldstein et al. [11] but the argument presented there assumes a constant latent period and hence does not apply to the Markov SEIR model.

Consider the limit of the rescaled process as $\delta^{-1} \to \infty$. In this process any infective makes all of his/her infectious contacts at the same time, i.e. at the end of his/her latent period, and the latent periods of distinct infectives are independent Exp(1) random variables. It follows that the infectious contact interval $W_G \sim \text{Exp}(1)$, whence $\mathcal{M}_{W_G}(r) = (1+r)^{-1}$. Suppose that all households have size n and that $n \leq 3$. Then in the epidemic graph $\mathcal{G}^{(n)}$ (see Section 2.1), for $k = 1, 2$, if an individual, i say, belongs to rank generation k, there is precisely one chain of directed edges from the initial infective to individual i that has length k. It follows that the real-time growth rate r satisfies $\mathcal{L}^{(0)}_{\beta_H}(r) = 1$, where $\mathcal{L}^{(0)}_{\beta_H}(r)$ is defined at (22). Note also that for this limiting process $\widetilde{W}_G \stackrel{D}{=} W_G$, where $\stackrel{D}{=}$ denotes equal in distribution. It then follows that, for the limiting process, $R_r = \widetilde{R}_r = R_0$. This conclusion

holds also in the case of unequal household sizes, provided the maximum household size n_H is at most 3.

Suppose now that all households have size $n = 4$. Then in the epidemic graph $\mathcal{G}^{(n)}$, when $k = 1, 3$, it is still true that for any individual, i say, belonging to rank generation k, there is precisely one chain of directed edges from the initial infective to individual i that has length k, but when $k = 2$ that is no longer the case. Recall that the individuals in $\mathcal{G}^{(4)}$ are labelled $0, 1, 2, 3$, where 0 is the initial infective. Suppose that individual 0 contacts individuals 1 and 2, but not individual 3, and that both individuals 1 and 2 contact individual 3. Thus there are two distinct paths of length 2 from individual 0 to individual 3. For $i = 0, 1, 2, 3$, let $T_E^{(i)}$ be the latent period of individual i (in the limiting rescaled process), so $T_E^{(i)} \sim \text{Exp}(1)$. Then individuals 1 and 2 are both infected at time $T_E^{(0)}$ and, for $i = 1, 2$, individual i attempts to infect individual 3 at time $T_E^{(0)} + T_E^{(i)}$, so individual 3 is infected at time $T_E^{(0)} + T'_E$, where $T'_E = \min(T_E^{(1)}, T_E^{(2)})$. Note that $T_E^{(0)}$ and T'_E are independent, and $T'_E \sim \text{Exp}(2)$, so $\mathcal{M}_{T'_E}(r) = 2/(2 + r)$.

Let the mean generation sizes μ_0, μ_1, μ_2 and μ_3 be defined as previously but now write $\mu_2 = \mu_{21} + \mu_{22}$, where, μ_{2j} is the mean number of generation 2 infectives that have precisely j paths of length 2 from the initial infective to them. Then,

$$\mathcal{L}_{\beta_H}(r) = \mu_G \mathcal{M}_{W_G}(r) \Big[1 + \mu_1 \mathcal{M}_{W_G}(r) + \mu_{21} (\mathcal{M}_{W_G}(r))^2 + \mu_{22} \mathcal{M}_{W_G}(r) \mathcal{M}_{T'_E}(r) + \mu_3 (\mathcal{M}_{W_G}(r))^3 \Big]. \tag{102}$$

Now $\mathcal{M}_{T'_E}(\theta) \geq \mathcal{M}_{W_G}(\theta)$, for $\theta > 0$, whence $r > r^{(0)}$, where $r^{(0)}$ solves $\mathcal{L}^{(0)}_{\beta_H}(r) = 1$, and it follows that $R_r > R_0$. Again, $\widetilde{R}_r = R_0$, since $\widetilde{W}_G \stackrel{D}{=} W_G$. Similar arguments show that $R_r > \widetilde{R}_r = R_0$ for any population with $n_H \geq 4$.

We now compare R_r with R_V. Recall from Theorem 1 that $R_0 = R_V$ when $n_H \leq 3$, whence $R_r = R_V$. Thus suppose that all households have size 4 and that a fraction $1 - R_r^{-1}$ of the population is vaccinated with a perfect vaccine. Then, using (20), the probability that a given individual is not vaccinated is $R_r^{-1} = \mathcal{M}_{W_G}(r)$. Hence, after vaccination, μ_G is reduced to $\mu_G^V = \mathcal{M}_{W_G}(r)\mu_G$ and, for $k = 1, 3$, μ_k is reduced to $\mu_k^V = (\mathcal{M}_{W_G}(r))^k \mu_k$, as prior to vaccination any individual in generation 1 or 3 has precisely one chain of the appropriate length linking them to the initial infective. Consider the situation described above, in which, prior to vaccination, individual 0 contacts individuals 1 and 2, but not individual 3, and that both individuals 1 and 2 contact individual 3. Individual 3 still has two chains linking them to the initial infective after vaccination if and only if individuals $1, 2$ and 3 are not vaccinated, which happens with probability $(\mathcal{M}_{W_G}(r))^3$. (Note that individual 0 is assumed to be unvaccinated, as μ_G is reduced to μ_G^V.) Thus, $\mu_{22}^V = (\mathcal{M}_{W_G}(r))^3 \mu_{22}$. In the above situation, individual 3 has precisely one chain linking them to individual 0 after vaccination if and only if individual 3 and exactly one of individuals 1 and 2 are not vaccinated, which occurs with probability $2(\mathcal{M}_{W_G}(r))^2(1 - \mathcal{M}_{W_G}(r))$. It follows that $\mu_{21}^V = (\mathcal{M}_{W_G}(r))^2 \mu_{21} + 2(\mathcal{M}_{W_G}(r))^2(1 - \mathcal{M}_{W_G}(r))\mu_{22}$. Hence, after vaccination, the growth

rate, r_V say, satisfies $\mathcal{L}^V_{\beta_H}(r_V) = 1$, where

$$\begin{aligned}\mathcal{L}^V_{\beta_H}(r_V) &= \mu_G \mathcal{M}_{W_G}(r_V) \Big[1 + \mu_1^V \mathcal{M}_{W_G}(r_V) + \mu_{21}^V (\mathcal{M}_{W_G}(r_V))^2 \\ &\quad + \mu_{22}^V \mathcal{M}_{W_G}(r_V) \mathcal{M}_{T'_E}(r_V) + \mu_3 (\mathcal{M}_{W_G}(r_V))^3 \Big].\end{aligned}$$

Now $\mathcal{M}_{W_G}(0) = \mathcal{M}_{T'_E}(0) = 1$ and $\mathcal{L}_{\beta_H}(r) = 1$, so

$$\begin{aligned}\mathcal{L}^V_{\beta_H}(0) &= \mu_G^V(1 + \mu_1^V + \mu_{21}^V + \mu_{22}^V + \mu_3^V) \\ &= \mu_G \mathcal{M}_{W_G}(r) \Big[1 + \mu_1 \mathcal{M}_{W_G}(r) + \mu_{21} (\mathcal{M}_{W_G}(r))^2 \\ &\quad + \mu_{22} \left(2(\mathcal{M}_{W_G}(r))^2 - (\mathcal{M}_{W_G}(r))^3 \right) + \mu_3 (\mathcal{M}_{W_G}(r))^3 \Big] \\ &= \mathcal{L}_{\beta_H^{(1)}}(r) + \mu_G (\mathcal{M}_{W_G}(r))^2 \mu_{22} \left[2\mathcal{M}_{W_G}(r) - (\mathcal{M}_{W_G}(r))^2 - \mathcal{M}_{T'_E}(r) \right] \\ &= 1 + \mu_G (\mathcal{M}_{W_G}(r))^2 \mu_{22} \frac{r}{(1+r)^2(2+r)} \\ &> 1, \end{aligned} \tag{103}$$

since $r > 0$. Hence $r_V > 0$, since $\mathcal{L}^V_{\beta_H}$ is a decreasing function and $\mathcal{L}^V_{\beta_H}(r_V) = 1$. Thus vaccinating a fraction $1 - R_r^{-1}$ of the population is insufficient to prevent a major outbreak, so $R_r < R_V$. Numerical evidence suggests that the same conclusion holds whenever $n_H \geq 4$. However, analytical progress is more difficult when $n_H > 4$ since then in the limiting rescaled process it is no longer the case that an individual's rank and true generations necessarily coincide.

Consider now the households-workplaces version of the above Markov SEIR model. Thus, whilst infectious, a typical infective makes global contacts at overall rate μ_G, contacts any given susceptible in his/her household at rate λ_H and any given susceptible in his/her workplace at rate λ_W. We use the same rescaling as in the households model and study the limit of the rescaled process as $\delta^{-1} \to \infty$. As previously, we restrict attention to a growing epidemic. Then, as at (38), the real-time growth rate r is given by the unique real solution of $F(r) = 1$, where

$$F(r) = \mu_G \mathcal{M}_{W_G}(r)(\mathcal{L}_{\beta_H}(r) + 1)(\mathcal{L}_{\beta_W}(r) + 1) + \mathcal{L}_{\beta_H}(r)\mathcal{L}_{\beta_W}(r),$$

and $\mathcal{M}_{W_G}(r) = (1+r)^{-1}$. The same arguments as used for the households model yield that, for $r \geq 0$,

$$\mathcal{L}_{\beta_H}(r) \overset{3}{\geq} \mathcal{L}_{\beta_H^{(2)}}(r) = \mathcal{L}_{\beta_H^{(3)}}(r) \quad \text{and} \quad \mathcal{L}_{\beta_W}(r) \overset{3}{\geq} \mathcal{L}_{\beta_W^{(2)}}(r) = \mathcal{L}_{\beta_W^{(3)}}(r),$$

whence

$$R_r \overset{3}{\geq} \widetilde{R}_r = R_0. \tag{104}$$

Turn now to the comparison of R_r and R_V. From Theorem 3 and (104), $R_r = R_V$ when $n_H \leq 3$ and $n_W \leq 3$. Suppose that $n_H = n_W = 4$ and that a fraction $1 - R_r^{-1}$ $(= 1 - \mathcal{M}_{W_G}(r)$,

where r is the real-time growth rate without vaccination) of the population is vaccinated with a perfect vaccine. Prior to vaccination,

$$\mathcal{L}_{\beta_H}(r) = \mu_1^H \mathcal{M}_{W_G}(r) + \mu_{21}^H (\mathcal{M}_{W_G}(r))^2 + \mu_{22}^H \mathcal{M}_{W_G}(r)\mathcal{M}_{T'_E}(r) + \mu_3^H (\mathcal{M}_{W_G}(r))^3,$$

where $\mu_1^H, \mu_{21}^H, \mu_{22}^H$ and μ_3^H are the mean generation sizes for a typical single-household epidemic (μ_2^H is decomposed into $\mu_{21}^H + \mu_{22}^H$ as above (102)), and $\mathcal{L}_{\beta_W}(r)$ is given by the same formula with $\mu_1^H, \mu_{21}^H, \mu_{22}^H$ and μ_3^H replaced by $\mu_1^W, \mu_{21}^W, \mu_{22}^W$ and μ_3^W, respectively. After vaccination, the real-time growth rate, r_V say, is given by the unique real solution of $F^V(r_V) = 1$, where

$$F^V(r_V) = \mu_G^V \mathcal{M}_{W_G}(r_V)(\mathcal{L}_{\beta_H}^V(r_V) + 1)(\mathcal{L}_{\beta_W}^V(r_V) + 1) + \mathcal{L}_{\beta_H}^V(r_V)\mathcal{L}_{\beta_W}^V(r_V),$$

where $\mu_G^V = \mathcal{M}_{W_G}(r)\mu_G$ and, for example,

$$\begin{aligned}\mathcal{L}_{\beta_H}^V(r_V) =& \mu_1^{HV} \mathcal{M}_{W_G}(r_V) + \mu_{21}^{HV} (\mathcal{M}_{W_G}(r_V))^2 + \mu_{22}^{HV} \mathcal{M}_{W_G}(r_V)\mathcal{M}_{T'_E}(r_V) \\ &+ \mu_3^{HV} (\mathcal{M}_{W_G}(r_V))^3,\end{aligned}$$

with

$$\begin{aligned}\mu_1^{HV} &= \mathcal{M}_{W_G}(r)\mu_1^H, \\ \mu_{21}^{HV} &= (\mathcal{M}_{W_G}(r))^2 \left(\mu_{21}^H + 2(1 - \mathcal{M}_{W_G}(r))\mu_{21}^H\right), \\ \mu_{22}^{HV} &= (\mathcal{M}_{W_G}(r))^3 \mu_{22}^H, \\ \mu_3^{HV} &= (\mathcal{M}_{W_G}(r))^3 \mu_3^H.\end{aligned}$$

Now,

$$\begin{aligned}\mathcal{L}_{\beta_H}^V(0) &= \mu_1^{HV} + \mu_{21}^{HV} + \mu_{22}^{HV} + \mu_3^{HV} \\ &= \mathcal{M}_{W_G}(r)\mu_1^H + (\mathcal{M}_{W_G}(r))^2 \mu_{21}^H + (\mathcal{M}_{W_G}(r))^2 (2 - \mathcal{M}_{W_G}(r))\mu_{22}^H \\ &\quad + (\mathcal{M}_{W_G}(r))^3 \mu_3^H \\ &= \mathcal{L}_{\beta_H}(r) + \mathcal{M}_{W_G}(r) \left[2\mathcal{M}_{W_G}(r) - (\mathcal{M}_{W_G}(r))^2 - \mathcal{M}_{T'_E}(r)\right] \mu_{22}^H \\ &> \mathcal{L}_{\beta_H}(r)\end{aligned}$$

(cf. (103)) and, similarly, $\mathcal{L}_{\beta_W}^V(0) > \mathcal{L}_{\beta_W}^V(r)$. It follows that $F^V(0) > F(r) = 1$. Thus $r_V > 0$, since F^V is a decreasing function, whence $R_r < R_V$. It is easily seen that the same conclusion holds if $n_H = 4$ and $n_W \leq 3$ or $n_W = 4$ and $n_H \leq 3$. We conjecture that it also holds whenever $\max(n_H, n_W) \geq 4$.

G Estimating r for households model with non-random infectivity profile

In this appendix we describe the simulation-based method used in Section 6.2 for determining the real-time growth rate for a households model with a non-random infectivity profile $\mathcal{I}(t) =$

$w_G(t)$ $(t \geq 0)$, where $\int_0^\infty w_G(t)\mathrm{d}t = 1$. For ease of exposition, we assume that all households have the same size n. The extension to unequal household sizes is straightforward. Recall that t time units after he/she was infected, an infectious individual makes global contacts at overall rate $\mu_G w_G(t)$ and, additionally, he/she contacts any given susceptible in his/her household at rate $\lambda_H w_G(t)$, where we have suppressed the dependence of λ_H on n. For ease of exposition, we assume that all households have the same size n. Our aim is to estimate the Laplace transform $\mathcal{L}_{\beta_H}(\theta) = \int_0^\infty \beta_H(t)\mathrm{e}^{-\theta t}\mathrm{d}t$ of the global infectivity profile of a household.

Consider n_{sim} independent simulations of a single-household epidemic, with initially one infective and $n-1$ susceptibles, under the above disease dynamics. For $s = 1, 2, \cdots, n_{sim}$, let $T_{s,0} = 0$, Z_s denote the size of the sth simulated epidemic, not counting the initial infective, and $T_{s,1}, T_{s,2}, \cdots, T_{s,Z_s}$ denote the corresponding infection times, assuming that the epidemic starts at time $t = 0$. Then the average global infectivity profile of the n_{sim} epidemics is

$$\hat{\beta}_H^{n_{sim}}(t) = \frac{1}{n_{sim}}\mu_G \sum_{s=1}^{n_{sim}} \sum_{i=0}^{Z_s} w_G(t - T_{s,i}) \quad (t \geq 0),$$

where $w_G(t) = 0$ if $t < 0$, whence an unbiased estimator of $\mathcal{L}_{\beta_H}(\theta)$ is

$$\hat{\mathcal{L}}_{\beta_H}^{n_{sim}}(\theta) = \frac{1}{n_{sim}}\mu_G \sum_{s=1}^{n_{sim}} \sum_{i=0}^{Z_s} \mathrm{e}^{-\theta T_{s,i}} \mathcal{M}_{W_G}(\theta) \quad (\theta > \theta_0),$$

where $\theta_0 = \inf\{\theta : \mathcal{M}_{W_G}(\theta) < \infty\}$. The real-time growth rate is estimated by solving $\hat{\mathcal{L}}_{\beta_H}^{n_{sim}}(r) = 1$ numerically, yielding $\hat{r}_{n_{sim}}$ say. Application of the strong law of large numbers yields that, for any $\theta > \theta_0$, $\hat{\mathcal{L}}_{\beta_H}^{n_{sim}}(\theta) \to \mathcal{L}_{\beta_H}(\theta)$ almost surely as $n_{sim} \to \infty$. This may be strengthened to (c.f. the Glivenko-Cantelli theorem) $\max_{\theta > \theta_1} |\hat{\mathcal{L}}_{\beta_H}^{n_{sim}}(\theta) - \mathcal{L}_{\beta_H}(\theta)| \to 0$ almost surely as $n_{sim} \to \infty$, for any $\theta_1 > \theta_0$. It follows that $\hat{r}_{n_{sim}} \to r$ almost surely as $n_{sim} \to \infty$.

Suppressing the suffix s, to simulate the size Z and the corresponding infection times $T_1, T_2, \cdots, T_{n-1}$ of a single-household epidemic we use the following generalisation of the construction of Sellke [25]. Label the individuals in the household $0, 1, \cdots, n-1$, where individual 0 is the initial infective. Let $Q_1, Q_2, \cdots, Q_{n-1}$ be independent and identically distributed $\mathrm{Exp}(\lambda_H)$ random variables. The random variable Q_i denotes individual i's critical exposure to infection. Let $Q_{(1)} \leq Q_{(2)} \leq \cdots \leq Q_{(n-1)}$ be the random variables $Q_1, Q_2, \cdots, Q_{n-1}$ arranged in increasing order, i.e. the order statistics of $Q_1, Q_2, \cdots, Q_{n-1}$. Note that, exploiting the lack-of-memory property of the exponential distribution, the random variables $Q_{(1)}, Q_{(2)} - Q_{(1)}, Q_{(3)} - Q_{(2)}, \cdots, Q_{(n-1)} - Q_{(n-2)}$ are mutually independent, $Q_{(1)} \sim \mathrm{Exp}\left((n-1)\lambda_H\right)$ and $Q_{(i)} - Q_{(i-1)} \sim \mathrm{Exp}\left((n-i)\lambda_H\right)$ $(i = 2, 3, \cdots, n-1)$.

The epidemic is constructed as follows. The initial infective becomes infected at time $T_0 = 0$. For $t \geq 0$, at time t, each individual accumulates exposure to infection from the initial infective at rate $w_G(t)$. For $i = 1, 2, \cdots, n-1$, individual i becomes infected if and when his/her accumulated exposure to infection reaches Q_i. Thus if $Q_{(1)} > 1$ then no susceptible is infected in the epidemic (recall that $\int_0^\infty w_G(t)\mathrm{d}t = 1$). Suppose that $Q_{(1)} < 1$ (note that $\mathbb{P}(Q_{(1)} = 1) = 0$ since $Q_{(1)}$ is a continuous random variable). Then the first infection

takes place at time T_1 given by $\int_0^{T_1} w_G(t)\mathrm{d}t = Q_{(1)}$. For $t > T_1$, at time t, each remaining susceptible accumulates exposure to infection at rate $w_G(t)$ from the initial infective and at rate $w_G(t-T_1)$ from the individual who was infected at time T_1. Thus, if $Q_{(2)} > 2$, there is no further spread of infection, whilst if $Q_{(2)} < 2$ the next infection occurs at time T_2 satisfying $\int_0^{T_2} w_G(t) + w_G(t-T_1)\mathrm{d}t = Q_{(2)}$. The construction of the epidemic continues in the obvious fashion. It is readily seen that $Z = \min(z : Q_{(z+1)} > z+1)$ and, for $i = 1, 2, \cdots, Z$, the ith infection time T_i is given implicitly by

$$\sum_{j=0}^{i-1} \int_{T_j}^{T_i} w_G(t-T_j)\mathrm{d}t = Q_{(i)}.$$

Note that for the example in Section 6.2 the infections times are easily simulated using MATLAB since the substitution $t' = \gamma t$ converts $\int_{T_j}^{T_i} w_G(t-T_j)\mathrm{d}t$ into an incomplete gamma function.

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