STOCHASTIC AND DETERMINISTIC ANALYSIS OF SIS HOUSEHOLD EPIDEMICS

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Abstract

We analyse SIS epidemics among populations partitioned into households. The analysis considers both the stochastic and deterministic models and, unlike in previous analyses, we consider general infectious period distributions. For the deterministic model, we prove the existence of an endemic equilibrium for the epidemic if and only if the threshold parameter, R_*, is greater than 1. Furthermore, by utilising Markov chains we show that the total number of infectives converges to the endemic equilibrium as $t \to \infty$. For the stochastic model, we prove a law of large numbers result for the convergence, to the deterministic limit, of the mean number of infectives per household. This is followed by the derivation of a Gaussian limit process for the fluctuations of the stochastic model.

Keywords: Stochastic model; deterministic model; SIS epidemic; household model; endemic equilibrium; Gaussian process

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1. Introduction

The household epidemic model, which models the spread of an epidemic among a community of households, has recently received considerable attention; see, for example, [6], [4], [2], and [3]. In all the above examples, closed-population SIR (susceptible → infective → removed) epidemics are considered and, therefore, endemic behaviour is not possible. The simplest epidemic model which can exhibit endemic behaviour is the closed-population SIS (susceptible → infective → susceptible) epidemic model. That is, infectives at the end of their infectious period return to the susceptible state and therefore can be reinfected. The study of homogeneously mixing closed-population SIS epidemic models goes back to [16]; see also [11] and [9] for stochastic analyses. However, it is only recently, in [1] and [10], that the extension to a household epidemic model has been considered. The aim of the current work is to study closed-population SIS household epidemic models further.

In [1, Section 2] the initial stages of the epidemic process were considered, that is, when there are initially a few infectives in an otherwise susceptible population. In such circumstances, by considering a sequence of epidemics indexed by the total number of households, n, as $n \to \infty$, a branching process approximation for the epidemic can be derived. The branching process approximation can be used to answer the question of whether or not the SIS epidemic can exhibit endemic behaviour. The results of [1, Section 2] apply to a very general SIS epidemic model allowing for unequally sized households and general infectious periods. Therefore, we shall focus on the endemic behaviour or, more specifically, the trajectory of the total number of infectives per household. In this respect, we extend the work of [1, Section 3] by taking a

novel approach. In [1, Section 3] the special case of equally sized households (i.e. in which there exists an $m \geq 2$ such that all households contain m individuals) and exponentially distributed infectious periods was considered. This enabled the derivation of a system of differential equations defining the deterministic SIS epidemic model; see [1, Equation (10)]. The differential equations can then, in principle, be solved to determine the progress of the epidemic over time. Moreover, results of [12] and [13] can be utilised to prove convergence (suitably normalised) of the stochastic epidemic model to the deterministic limit and to derive a Gaussian limit process for the fluctuations of the epidemic model about the deterministic limit. Finally, for equally sized households of size 2 in [1], the endemic behaviour of the deterministic model was considered, and it was shown that if the initial proportion of the population which is infectious is positive, then the distribution of the total number of infectives within the households converges to the endemic equilibrium, given that it exists, as $t \to \infty$.

In [10] the SIS household epidemic model was analysed using methods from statistical physics, namely self-consistent field methods. The analysis was essentially deterministic, and self-consistent field theory was utilised to consider the individual household epidemics as independent epidemics, subjected to a 'mean-field' global infection. We shall also utilise a construction which considers the individual household epidemics as conditionally independent given the total amount of global infection. However, our approach is rather different to that of [10], and we provide rigorous mathematical justification for our construction of the model.

The methods and results of [1] and [10] have two major drawbacks. Firstly, for $m \geq 1$ and $0 \leq i \leq m$, it is necessary to keep track of the total number of households of size m with i infectives. Therefore, for $m \geq 1$ we require m separate differential equations for households of size m and, so, for unequally sized household epidemics the system of differential equations rapidly grows in complexity. Secondly, it is required that each infectious period, the length of time from an individual becoming infected until they return to the susceptible state, be exponentially distributed. In order to surmount these problems we focus on a single quantity, the total number of infectives or, more precisely, the mean number of infectives per household. This requires a radically different approach to analysing the model, a full description of which is given in Section 2. Although our methods can be used with very general choices of infectious period, it is again necessary to restrict attention to exponentially distributed infectious periods to obtain explicit results. This is primarily due to difficulties in obtaining explicit expressions for the deterministic model for general choices of infectious period.

The paper is structured as follows. In Section 2 the household epidemic model is described in full detail. Since we are considering asymptotic results, we define a sequence of epidemic processes $\{E_n\}$, indexed by the total number of households, n, as $n \to \infty$. Then, in Section 3, a weak law of large numbers result is derived for the convergence of the mean number of infectives per household to a deterministic limit. In Section 4 we study the deterministic limit in some detail in the case where the infectious periods are exponentially distributed. In particular, we extend [1, Theorem 3.1] to a very general household structure and thereby prove an associated conjecture (see [1, p. 64]). These results establish necessary and sufficient conditions for the existence of an endemic equilibrium and show that, as $t \to \infty$, the epidemic converges to the endemic equilibrium, if it exists. Although the deterministic model can be described using a system of differential equations, our results are proved by utilising Markov birth–death processes and Markov chains, via a coupling argument. Similar results have been obtained in [5] for metapopulation models. The method of proof we use is very different to that presented in [5], but Markov processes are again utilised in studying the deterministic model. Furthermore, the results of [5] are not directly applicable to the epidemic model, since [5, condition (H1)] is

violated. In Section 5 we aim to extend the results of Section 3 by establishing a Gaussian limit process for the fluctuations of the stochastic model about the deterministic model. We are only able to do this for exponentially distributed infectious periods, since we require an explicit expression for the deterministic model. However, in Theorem 5.1 we are able to obtain useful bounds for the fluctuations of the stochastic model for more general choices of infectious period. In particular, the bounds are of the same order of magnitude as those obtained from the Gaussian limit process. Finally, in Section 6 a summary of the results and an outline of further work is given.

2. Model set-up

We consider a sequence of epidemic processes $\{E_n\}$ indexed by the total number of households, n, as $n \to \infty$. For $i \geq 1$, let h_i denote the total number of individuals within household i. Note that we assume that, for all $i \leq n$, the ith household in E_n is of size h_i. (This assumption can easily be relaxed but is retained for clarity of exposition.) For $i \geq 1$, label the individuals in household i as $(i, 1), (i, 2), \ldots, (i, h_i)$. For a fixed $n \geq 1$, the epidemic process is constructed as follows. An individual, (i, j) say, the jth individual in household i, becomes infected for the kth time at time t, say, and has infectious period Q_{ijk}, which is distributed according to an arbitrary (but specified) continuous, nonnegative distribution Q. The infectious period Q_{ijk} is independent of all other infectious periods and individual i is infectious in the time interval $[t, t + Q_{ijk})$, returning to the susceptible state at time $t + Q_{ijk}$. During its infectious period, individual (i, j) makes global infectious contact at the points of a homogeneous Poisson point process with rate $\beta_G\{(1/n) \sum_{i=1}^n h_i\}$, and the individual thus contacted is chosen uniformly at random from the entire population, including individual (i, j) itself. Also, for $1 \leq k \leq h_i$ ($k \neq j$), individual (i, j), whilst infectious, makes infectious contact with individual (i, k) at the points of a homogeneous Poisson point process with rate β_L. Those individuals initially infectious at time $t = 0$ are assumed to have independent infectious periods identically distributed according to an arbitrary (but specified) continuous, nonnegative distribution $\tilde{Q}$. Note that $\tilde{Q}$ and Q can be distinct.

We consider the epidemic within individual households when each individual is exposed to a known global infectious pressure. For $i \geq 1$, $t \geq 0$, and $\mathbf{z} = \{z(s) \colon s \geq 0\}$, let $\theta_i(t; \mathbf{z})$ denote the total number of infectives within household i at time t given that each individual within household i is contacted by global infectives at the points of an inhomogeneous Poisson point process with rate $\beta_G z(s)$. The individuals within household i then have infectious periods whose lengths are independently distributed according to Q (with initial infectious periods distributed according to $\tilde{Q}$). An individual, while infectious, makes local infectious contact with a given individual within household i at the points of a homogeneous Poisson point process with rate β_L. The most important fact to note is that, for $i \neq j$ and $s, t \geq 0$, $\theta_i(t; \mathbf{z})$ and $\theta_j(s; \mathbf{z})$ are independent.

Therefore, if we let $\tilde{X}_n(t) = nX_n(t)$ denote the total number of infectious individuals in E_n at time t, then $X_n(t) = (1/n) \sum_{i=1}^n \theta_i(t; \mathbf{X}_n)$. The key point is that with this construction the epidemics within distinct households are conditionally independent, given $\mathbf{X}_n = \{X_n(s) \colon s \geq 0\}$. Clearly this introduces an explicit dependence upon the entire past history of the epidemic when considering $X_n(t)$; however, it transpires that this will not be problematic.

For $k \geq 1$ and $0 \leq l \leq k$, let a_{kl}^n denote the total number of households of size k within E_n which contain l initial infectives. For $k \geq 1$, let $\omega_k^n = (1/n) \sum_{l=0}^k a_{kl}^n$ denote the proportion of households of size k and, for $0 \leq l \leq k$, let $\zeta_{kl}^n = a_{kl}^n / n\omega_k^n$. Suppose that, for $k \geq 1$ and $0 \leq l \leq k$, $\omega_k^n \to \omega_k$ and $\zeta_{kl}^n \to \zeta_{kl}$ as $n \to \infty$, with $\sum_{k=1}^\infty \omega_k = 1$ and $\sum_{l=0}^k \zeta_{kl} = 1$.

Finally, let H be a positive discrete random variable with $P(H = k) = \omega_k$ $(k \geq 1)$. Thus, H denotes the limiting probability distribution for household size, and throughout we will specify conditions on the household size distribution in terms of H.

For $k \geq 1$, $0 \leq l \leq k$, $t \geq 0$, and $\mathbf{z} = \{z(s) : s \geq 0\}$, let $\chi_{kl}(t; \mathbf{z})$ denote the total number of infectives at time t within a household of size k which has l initial infectives and is such that each individual within it is contacted by global infectives at the points of an inhomogeneous Poisson point process with rate $\beta_G z(s)$. Thus, for $i \geq 1$, if $h_i = k$ and $\theta_i(0; \mathbf{z}) = l$, then $\theta_i(t; \mathbf{z}) \stackrel{\mathrm{D}}{=} \chi_{kl}(t; \mathbf{z})$ for all $t \geq 0$. Here, '$\stackrel{\mathrm{D}}{=}$' denotes equality in distribution.

Let $x(0) = \sum_{k=1}^{\infty} \omega_k \sum_{l=0}^{k} l \zeta_{kl}$ and, for $t > 0$, let

$$x(t) = \sum_{k=1}^{\infty} \omega_k \sum_{l=0}^{k} \zeta_{kl} \, \mathrm{E}[\chi_{kl}(t; \mathbf{x})]. \tag{2.1}$$

Thus, $\{x(s) : s \geq 0\}$ describes the total proportion of infectious individuals in the deterministic equivalent of the limiting stochastic model described above. In Section 4 we shall analyse (2.1) in detail for the case $Q \sim \mathrm{Exp}(\gamma)$.

3. Law of large numbers analysis

In this section we show that if $\mathrm{E}[H^2] < \infty$ then, for any $T > 0$,

$$\sup_{0 \leq s \leq T} |X_n(s) - x(s)| \stackrel{\mathrm{P}}{\to} 0 \quad \text{as } n \to \infty, \tag{3.1}$$

where '$\stackrel{\mathrm{P}}{\to}$' denotes convergence in probability.

We begin by stating the following useful proposition.

Proposition 3.1. *For any two inhomogeneous Poisson point processes η_1 and η_2 with respective rates $\alpha_1(s)$ and $\alpha_2(s)$, there exists a coupling such that, for any t $(0 \leq t < Y)$,*

$$\eta_1[0, t] = \eta_2[0, t],$$

where Y is a nonnegative random variable with cumulative distribution function

$$P(Y \leq t) = 1 - \exp\left(-\int_0^t |\alpha_1(s) - \alpha_2(s)| \, \mathrm{d}s\right).$$

Let $x_n(0) = \sum_{k=1}^{\infty} \omega_k^n \sum_{l=0}^{k} l \zeta_{kl}^n$ and, for $t > 0$, let

$$x_n(t) = \sum_{k=1}^{\infty} \omega_k^n \sum_{l=0}^{k} \zeta_{kl}^n \, \mathrm{E}[\chi_{kl}(t; \mathbf{x}_n)] =: \frac{1}{n} \sum_{i=1}^{n} \mathrm{E}[\theta_i^n(t; \mathbf{x}_n)].$$

Thus, $\{x_n(s) : s \geq 0\}$ is the deterministic equivalent of $\{X_n(s) : s \geq 0\}$. Furthermore, we have the following lemma linking $x_n(\cdot)$ and $x(\cdot)$.

Lemma 3.1. *Suppose that $\sum_{k=1}^{\infty} k \sum_{l=0}^{k} |\omega_k^n \zeta_{kl}^n - \omega_k \zeta_{kl}| \to 0$ as $n \to \infty$. Then, for any $T > 0$,*

$$\sup_{0 \leq s \leq T} |x_n(s) - x(s)| \to 0 \quad \text{as } n \to \infty.$$

Proof. For $k \leq 1$ and $0 \leq l \leq k$,

$$\sup_{0 \leq s \leq T} \mathrm{E}[|\chi_{kl}(s; \mathbf{x}) - \chi_{kl}(s; \mathbf{x}_n)|] \leq k \, \mathrm{P}\Big(\sup_{0 \leq s \leq T} |\chi_{kl}(s; \mathbf{x}) - \chi_{kl}(s; \mathbf{x}_n)| \neq 0\Big).$$

By Proposition 3.1, there exists a random variable Y_n^k with

$$\mathrm{P}(Y_n^k \leq T) = 1 - \exp\Big(-k\beta_{\mathrm{G}} \int_0^T |x(s) - x_n(s)| \, \mathrm{d}s\Big),$$

such that the inhomogeneous Poisson point processes η_k and η_k^n with respective rates $k\beta_{\mathrm{G}} x(s)$ and $k\beta_{\mathrm{G}} x_n(s)$ can be coupled as follows, for any t ($0 \leq t < Y_n^k$):

$$\eta_k[0, t] = \eta_k^n[0, t].$$

Therefore, we have

$$\mathrm{P}\Big(\sup_{0 \leq s \leq T} |\chi_{kl}(t; \mathbf{x}) - \chi_{kl}(t; \mathbf{x}_n)| \neq 0\Big) \leq \mathrm{P}(Y_n^k \leq T)$$

$$\leq k\beta_{\mathrm{G}} \int_0^T |x(s) - x_n(s)| \, \mathrm{d}s. \qquad (3.2)$$

By (3.2),

$$\sup_{0 \leq s \leq T} |x(s) - x_n(s)|$$

$$\leq \sum_{k=1}^{\infty} \sum_{l=0}^{k} \sup_{0 \leq s \leq T} |\omega_k \zeta_{kl} \, \mathrm{E}[\chi_{kl}(s; \mathbf{x})] - \omega_k^n \zeta_{kl}^n \, \mathrm{E}[\chi_{kl}(s; \mathbf{x}_n)]|$$

$$\leq \sum_{k=1}^{\infty} k \sum_{l=0}^{k} |\omega_k \zeta_{kl} - \omega_k^n \zeta_{kl}^n| + \sum_{k=1}^{\infty} \omega_k \sum_{l=0}^{k} \zeta_{kl} \, \mathrm{E}\Big[\sup_{0 \leq s \leq T} |\chi_{kl}(s; \mathbf{x}) - \chi_{kl}(s; \mathbf{x}_n)|\Big]$$

$$\leq \sum_{k=1}^{\infty} k \sum_{l=0}^{k} |\omega_k \zeta_{kl} - \omega_k^n \zeta_{kl}^n| + \sum_{k=1}^{\infty} \omega_k k^2 \beta_{\mathrm{G}} \int_0^T |x(s) - x_n(s)| \, \mathrm{d}s$$

$$\leq \sum_{k=1}^{\infty} k \sum_{l=0}^{k} |\omega_k \zeta_{kl} - \omega_k^n \zeta_{kl}^n| + \beta_{\mathrm{G}} \, \mathrm{E}[H^2] \int_0^T \sup_{0 \leq u \leq s} |x(u) - x_n(u)| \, \mathrm{d}s.$$

Therefore, it follows by Gronwall's inequality that

$$\sup_{0 \leq s \leq T} |x(s) - x_n(s)| \leq \sum_{k=1}^{\infty} k \sum_{l=0}^{k} |\omega_k^n \zeta_{kl}^n - \omega_k \zeta_{kl}| \exp(\beta_{\mathrm{G}} T \, \mathrm{E}[H^2]), \qquad (3.3)$$

and the lemma follows since the right-hand side of (3.3) converges to 0 as $n \to \infty$.

For all $t \geq 0$,

$$X_n(t) - x_n(t) = \frac{1}{n} \sum_{i=1}^{n} \{\theta_i(t; \mathbf{X}_n) - \mathrm{E}[\theta_i(t; \mathbf{X}_n) \mid \mathbf{X}_n]\}$$

$$+ \frac{1}{n} \sum_{i=1}^{n} \{\mathrm{E}[\theta_i(t; \mathbf{X}_n) \mid \mathbf{X}_n] - \mathrm{E}[\theta_i(t; \mathbf{x}_n)]\}.$$

We shall make use of a sequence of immigration–death processes $\{I_n\}_{n \geq 1}$ to assist in proving that

$$\sup_{0 \leq s \leq T} \left| \frac{1}{n} \sum_{i=1}^{n} \{\theta_i(s; \mathbf{X}_n) - \mathrm{E}[\theta_i(s; \mathbf{X}_n) \mid \mathbf{X}_n]\} \right| \xrightarrow{\mathrm{P}} 0 \quad \text{as } n \to \infty.$$

For $n \geq 1$, suppose that immigrations occur at the points of a homogeneous Poisson point process with rate

$$nK_n = \frac{1}{4} \frac{\beta_{\mathrm{G}}}{n} \left\{ \sum_{i=1}^{n} h_i \right\}^2 + \beta_{\mathrm{L}} \sum_{i=1}^{n} \frac{h_i^2}{4} = n \frac{1}{4} \left\{ \beta_{\mathrm{G}} \left(\frac{1}{n} \sum_{i=1}^{n} h_i \right)^2 + \beta_{\mathrm{L}} \frac{1}{n} \sum_{i=1}^{n} h_i^2 \right\}.$$

Then

$$K_n \to K = \tfrac{1}{4} \{ \beta_{\mathrm{G}} \, \mathrm{E}[H]^2 + \beta_{\mathrm{L}} \, \mathrm{E}[H^2] \} \quad \text{as } n \to \infty.$$

Upon immigrating into the population, the immigrants have independent lifetimes identically distributed according to Q. That is, if individual i, say, with lifetime Q_i, immigrates into the population at time t, say, then individual i dies at time $t + Q_i$.

Further suppose that, for $n \geq 1$, the process I_n starts at time $t = 0$ with r_n initial individuals in the population. Suppose both that there exists an $r \geq 0$ such that $r_n/n \to r$ as $n \to \infty$ and that the initial individuals have independent and identically distributed death times $\tilde{Q}_1, \tilde{Q}_2, \ldots, \tilde{Q}_{r_n}$, respectively. For $k \geq 1$, let the first two entries of (t_k^n, Q_k, U_k) denote the immigration time and the lifetime, respectively, of the kth immigrant in I_n, and let U_k denote a uniform random variable on $[0, 1]$ which plays no part in the immigration–death process but is instrumental in coupling the epidemic process to the immigration–death process. It is assumed that the random variables (Q_k, U_k) are independent and identically distributed with Q_k and U_k independent.

For $n \geq 1$ and $t \geq 0$, let

$$A_n^{\mathrm{I}}(t) = \{(t_k^n, Q_k, U_k) \colon t_k^n \leq t\},$$
$$A_n^{\mathrm{D}}(t) = \{(t_k^n, Q_k, U_k) \colon t_k^n + Q_k \leq t\} \cup \{\tilde{Q}_k \colon \tilde{Q}_k \leq t\}.$$

Therefore, the sets $A_n^{\mathrm{I}}(t)$ and $A_n^{\mathrm{D}}(t)$ respectively consist of those individuals who have immigrated into I_n and died in I_n, up to and including time t. For $n \geq 1$ and $t \geq 0$, let $\tilde{Z}_n^{\mathrm{I}}(t) = nZ_n^{\mathrm{I}}(t)$ and $\tilde{Z}_n^{\mathrm{D}}(t) = nZ_n^{\mathrm{D}}(t)$ denote the cardinalities of $A_n^{\mathrm{I}}(t)$ and $A_n^{\mathrm{D}}(t)$, respectively. Hence, $\tilde{Z}_n^{\mathrm{I}}(t)$ and $\tilde{Z}_n^{\mathrm{D}}(t)$ respectively denote the total number of immigrations and deaths in I_n up to time t.

The key point in utilising I_n is that, in the epidemic E_n, infections occur at the points of an inhomogeneous Poisson point process with rate $n\lambda_n(t)$, given by

$$\frac{\beta_{\mathrm{G}}}{n} \left\{ \sum_{i=1}^{n} \theta_i(t; \mathbf{X}_n) \right\} \left\{ \sum_{i=1}^{n} (h_i - \theta_i(t; \mathbf{X}_n)) \right\} + \beta_{\mathrm{L}} \sum_{i=1}^{n} \theta_i(t; \mathbf{X}_n)(h_i - \theta_i(t; \mathbf{X}_n)).$$

Hence, $\lambda_n(t) \leq K_n$ for all $t \geq 0$. Thus, for $n \geq 1$, the epidemic E_n can be coupled to the immigration process I_n as follows. Suppose that $r_n = nX_n(0)(= nx_n(0))$, and let the initial infectives in E_n have (remaining) infectious periods $\tilde{Q}_1, \tilde{Q}_2, \ldots, \tilde{Q}_{r_n}$, respectively. Thus, for every removal of an initial infective in E_n there will be a corresponding death of an initial individual in I_n. Now, for $k \geq 1$, consider the kth immigration in I_n. If $U_k \leq \lambda_n(t_k^n)/K_n$ then an infection occurs in E_n and the infectious period of the infective is Q_k. The individual

infected can then be chosen from among the susceptibles according to the correct conditional distribution. Thus, we have a coupling such that, for all $n \geq 1$, s, and t $(0 \leq s \leq t)$,

$$|X_n(t) - X_n(s)| \leq \{Z_n^I(t) - Z_n^I(s)\} + \{Z_n^D(t) - Z_n^D(s)\}, \tag{3.4}$$

where $Z_n^I(\cdot)$ and $Z_n^D(\cdot)$ are more convenient to analyse than $X_n(\cdot)$.

For all $t \geq 0$,

$$Z_n^I(t) \sim \frac{1}{n} \text{Po}(n K_n t),$$

$$Z_n^D(t) \sim \frac{1}{n} \left\{ \text{Bin}(r_n, \tilde{F}(t)) + \text{Po}\left(n K_n \int_0^t F(s) \, ds \right) \right\}, \tag{3.5}$$

where, for $s \geq 0$, $\tilde{F}(s)$ and $F(s)$ denote the cumulative distribution functions of $\tilde{Q}$ and Q, respectively.

Lemma 3.2. *For all $T > 0$,*

$$\sup_{0 \leq s \leq T} \left| \frac{1}{n} \sum_{i=1}^{n} \{\theta_i(s; \mathbf{X}_n) - E[\theta_i(s; \mathbf{X}_n) \mid \mathbf{X}_n]\} \right| \xrightarrow{P} 0 \quad \text{as } n \to \infty.$$

Proof. Firstly note that, using (3.5) and Chebyshev's inequality, it is trivial to show that, for all $s \geq 0$, $|Z_n^I(s) - E[Z_n^I(s)]| \xrightarrow{P} 0$ and $|Z_n^D(s) - E[Z_n^D(s)]| \xrightarrow{P} 0$ as $n \to \infty$. Furthermore, since the $\{\theta_i(s; \mathbf{X}_n)\}$ are conditionally independent given $\mathbf{X}_n$, it follows by Chebyshev's inequality (cf. [14, Lemma 5.4]) that, for any $s \geq 0$ and $\varepsilon > 0$,

$$P\left(\left| \frac{1}{n} \sum_{i=1}^{n} \{\theta_i(s; \mathbf{X}_n) - E[\theta_i(s; \mathbf{X}_n) \mid \mathbf{X}_n]\} \right| > \varepsilon \right) \leq \frac{1}{\varepsilon^2} \frac{1}{n^2} E\left[\text{var}\left(\sum_{i=1}^{n} \theta_i(s; \mathbf{X}_n) \,\Big|\, \mathbf{X}_n \right) \right]$$

$$\leq \frac{1}{\varepsilon^2} \frac{1}{n^2} \sum_{i=1}^{n} h_i^2 = \frac{1}{\varepsilon^2 n} \sum_{k=1}^{\infty} k^2 \omega_k^n$$

$$\to 0 \quad \text{as } n \to \infty.$$

Fix a $T \geq 0$ and an $\varepsilon > 0$. For $0 \leq s \leq T$, let $z^I(s) = Ks$ and $z^D(s) = x(0)\tilde{F}(s) + K \int_0^s F(u) \, du$. Note that $z^I(T), z^D(T) < \infty$ and that $z^I(s)$ and $z^D(s)$ are nondecreasing in s. Therefore, there exist $r \in \mathbb{N}$ and $u_0, \ldots, u_r$ $(0 = u_0 < u_1 < \cdots < u_r = T)$ such that, with $B_k = \{s : u_k \leq s \leq u_{k+1}\}$ $(0 \leq k \leq r-1)$, we have $\max_{s,s' \in B_k} |z^I(s) - z^I(s')| < \varepsilon/10$ and $\max_{s,s' \in B_k} |z^D(s) - z^D(s')| < \varepsilon/10$. Since, for all s $(0 \leq s \leq T)$, $E[Z_n^I(s)] \to z^I(s)$ and $E[Z_n^D(s)] \to z^D(s)$ as $n \to \infty$, it follows that

$$\lim_{n \to \infty} P\left(|Z_n^I(s) - z^I(s)| < \frac{\varepsilon}{10}, \, s \in H_r \right) = 1, \tag{3.6}$$

$$\lim_{n \to \infty} P\left(|Z_n^D(s) - z^D(s)| < \frac{\varepsilon}{10}, \, s \in H_r \right) = 1, \tag{3.7}$$

$$\lim_{n \to \infty} P\left(\left| \frac{1}{n} \sum_{i=1}^{n} \{\theta_i(s; \mathbf{X}_n) - E[\theta_i(s; \mathbf{X}_n) \mid \mathbf{X}_n]\} \right| < \frac{\varepsilon}{10}, \, s \in H_r \right) = 1, \tag{3.8}$$

where $H_r = \{u_0, u_1, \ldots, u_r\}$.

By the triangle inequality, for all k ($0 \leq k \leq r - 1$) and s ($u_k \leq s \leq u_{k+1}$) we have

$$\left| \frac{1}{n} \sum_{i=1}^{n} \{\theta_i(s; \mathbf{X}_n) - \mathrm{E}[\theta_i(s; \mathbf{X}_n) \mid \mathbf{X}_n]\} \right|$$

$$\leq \left| \frac{1}{n} \sum_{i=1}^{n} \{\theta_i(s; \mathbf{X}_n) - \theta_i(u_k; \mathbf{X}_n)\} \right|$$

$$+ \left| \frac{1}{n} \sum_{i=1}^{n} \{\theta_i(u_k; \mathbf{X}_n) - \mathrm{E}[\theta_i(u_k; \mathbf{X}_n) \mid \mathbf{X}_n]\} \right|$$

$$+ \left| \frac{1}{n} \sum_{i=1}^{n} \{\mathrm{E}[\theta_i(s; \mathbf{X}_n) \mid \mathbf{X}_n] - \mathrm{E}[\theta_i(u_k; \mathbf{X}_n) \mid \mathbf{X}_n]\} \right|. \tag{3.9}$$

By (3.4), the first and third terms on the right-hand side of (3.9) are less than

$$Z_n^{\mathrm{I}}(u_{k+1}) - Z_n^{\mathrm{I}}(u_k) + Z_n^{\mathrm{D}}(u_{k+1}) - Z_n^{\mathrm{D}}(u_k) \tag{3.10}$$

and

$$\mathrm{E}[Z_n^{\mathrm{I}}(u_{k+1}) - Z_n^{\mathrm{I}}(u_k)] + \mathrm{E}[Z_n^{\mathrm{D}}(u_{k+1}) - Z_n^{\mathrm{D}}(u_k)], \tag{3.11}$$

respectively. Therefore, letting $W_n(u) = |Z_n^{\mathrm{I}}(u) - z^{\mathrm{I}}(u)| + |Z_n^{\mathrm{D}}(u) - z^{\mathrm{D}}(u)|$ ($u \geq 0$), we have, from (3.9), (3.10), and (3.11),

$$\left| \frac{1}{n} \sum_{i=1}^{n} \{\theta_i(s; \mathbf{X}_n) - \mathrm{E}[\theta_i(s; \mathbf{X}_n) \mid \mathbf{X}_n]\} \right| \leq W_n(u_{k+1}) + W_n(u_k) + \mathrm{E}[W_n(u_{k+1})] + \mathrm{E}[W_n(u_k)]$$

$$+ 2(z^{\mathrm{I}}(u_{k+1}) - z^{\mathrm{I}}(u_k)) + 2(z^{\mathrm{D}}(u_{k+1}) - z^{\mathrm{D}}(u_k))$$

$$+ \left| \frac{1}{n} \sum_{i=1}^{n} \{\theta_i(u_k; \mathbf{X}_n) - \mathrm{E}[\theta_i(u_k; \mathbf{X}_n) \mid \mathbf{X}_n]\} \right|.$$

For all l ($0 \leq l \leq r$), $\mathrm{E}[W_n(u_l)] \to 0$ as $n \to \infty$, so, for all sufficiently large n,

$$\mathrm{E}[W_n(u_{k+1})] + \mathrm{E}[W_n(u_k)] < \frac{\varepsilon}{10}.$$

Thus, by considering each B_k separately it follows that if, for all $u \in H_r$, we have

$$W_n(u) = |Z_n^{\mathrm{I}}(u) - z^{\mathrm{I}}(u)| + |Z_n^{\mathrm{D}}(u) - z^{\mathrm{D}}(u)| < \frac{2\varepsilon}{10},$$

$$\left| \frac{1}{n} \sum_{i=1}^{n} \{\theta_i(u; \mathbf{X}_n) - \mathrm{E}[\theta_i(u; \mathbf{X}_n) \mid \mathbf{X}_n]\} \right| < \frac{\varepsilon}{10},$$

then

$$\sup_{0 \leq s \leq T} \left| \frac{1}{n} \sum_{i=1}^{n} \{\theta_i(s; \mathbf{X}_n) - \mathrm{E}[\theta_i(s; \mathbf{X}_n) \mid \mathbf{X}_n]\} \right| < \varepsilon,$$

and the lemma follows using (3.6), (3.7), and (3.8).

We are now in a position to prove (3.1).

Theorem 3.1. *For all $T > 0$,*

$$\sup_{0 \le s \le T} |X_n(s) - x(s)| \xrightarrow{\text{P}} 0 \quad \text{as } n \to \infty.$$

Proof. By Lemma 3.1 and the triangle inequality, it is sufficient to show that

$$\sup_{0 \le s \le T} |X_n(s) - x_n(s)| \xrightarrow{\text{P}} 0 \quad \text{as } n \to \infty.$$

Note that, by the triangle inequality,

$$\sup_{0 \le s \le T} |X_n(s) - x_n(s)| \le A_n(T) + B_n(T), \tag{3.12}$$

where, for $t \ge 0$,

$$A_n(t) = \sup_{0 \le s \le t} \left| \frac{1}{n} \sum_{i=1}^{n} \{\theta_i(s; \mathbf{X}_n) - \text{E}[\theta_i(s; \mathbf{X}_n) \mid \mathbf{X}_n]\} \right|,$$

$$B_n(t) = \sup_{0 \le s \le t} \left| \frac{1}{n} \sum_{i=1}^{n} \{\text{E}[\theta_i(s; \mathbf{X}_n) \mid \mathbf{X}_n] - \text{E}[\theta_i(s; \mathbf{x}_n)]\} \right|$$

$$= \sup_{0 \le s \le t} \left| \sum_{k=1}^{\infty} \omega_k^n \sum_{l=0}^{k} \zeta_{kl}^n \{\text{E}[\chi_{kl}(s; \mathbf{X}_n) \mid \mathbf{X}_n] - \text{E}[\chi_{kl}(s; \mathbf{x}_n)]\} \right|.$$

Therefore, by arguments similar to those used in Lemma 3.1, for $t \ge 0$ we have

$$B_n(t) \le \left\{ \sum_{k=1}^{\infty} k^2 \omega_k^n \right\} \beta_\text{G} \int_0^t \sup_{0 \le u \le s} |X_n(u) - x_n(u)| \, ds. \tag{3.13}$$

Thus, by using (3.13) and applying Gronwall's inequality to (3.12) we find that, for $T \ge 0$,

$$\sup_{0 \le s \le T} |X_n(s) - x_n(s)| \le A_n(T) \exp\left(\left\{ \sum_{k=1}^{\infty} k^2 \omega_k^n \right\} \beta_\text{G} T \right). \tag{3.14}$$

By Lemma 3.2, the right-hand side of (3.14) converges in probability to 0 as $n \to \infty$, and the theorem follows.

4. Deterministic model

In order to study the deterministic model $x(\cdot)$, we restrict attention to the case $Q \sim \text{Exp}(\gamma)$ where $\gamma > 0$; we can then use Markov chains to analyse $x(\cdot)$. In particular, we prove a generalisation of [1, Theorem 3.1] and, hence, prove a related conjecture (see [1, p. 64]) under the weak condition that $\text{E}[H] < \infty$.

We begin by considering a household of size m, for some $m \ge 1$. For $u \ge 0$, let $\mathbf{G}_m(u)$ denote an $(m + 1) \times (m + 1)$ matrix with typical entries $g_{ij}^m(u)$ $(0 \le i, j \le m)$, where

$$g_{i(i+1)}^m(u) = (m - i)\beta_\text{G} u + (m - i)i\beta_\text{L} \qquad (0 \le i \le m - 1),$$

$$g_{i(i-1)}^m(u) = i\gamma \qquad (1 \le i \le m),$$

$$g_{ij}^m(u) = 0 \qquad (|i - j| \ge 2, \ 0 \le i, j \le m),$$

$$g_{ii}^m(u) = -\sum_{j \ne i} g_{ij}^m(u) \qquad (0 \le i \le m).$$

Hence, $g_{ij}^m(u)$ is the infinitesimal transition rate from there being i infectives to there being j infectives, given that there are u units of global infectious pressure. We shall use $\boldsymbol{G}_m(u)$ to construct a time-inhomogeneous Markov chain to study the total number of infectives within the household at any given point in time. Note that $\boldsymbol{G}_m(\cdot)$ does not satisfy the birth condition (H1) of [5].

Suppose that each individual within the household is contacted by global infectives at the points of an inhomogeneous Poisson point process with rate $\beta_G z(t)$, for some nonnegative function $z(\cdot)$. For $0 \le a \le b$, let $\boldsymbol{S}_m(a, b; \mathbf{z}) = \exp(\int_a^b \boldsymbol{G}_m(z(s))\, ds)$ with typical entries $s_{ij}^m(a, b; \mathbf{z})$ $(0 \le i, j \le m)$. Thus, for $0 \le i, j \le m$, $s_{ij}^m(a, b; \mathbf{z})$ denotes the probability that there are j infectives within the household at time b given that there were i infectives at time a.

Therefore, turning our attention to $x(\cdot)$, we note that, for $t \ge 0$, $x(t)$ solves the equation

$$x(t) = \sum_{k=1}^{\infty} \omega_k \boldsymbol{k} \{\boldsymbol{\zeta}_k \boldsymbol{S}_k(0, t; \mathbf{x})\}^{\top} \tag{4.1}$$

with $x(0) = \sum_{k=1}^{\infty} \omega_k \boldsymbol{k} \boldsymbol{\zeta}_k^{\top}$, where $\boldsymbol{k} = (0, 1, \ldots, k)$ and $\boldsymbol{\zeta}_k = (\zeta_{k0}, \zeta_{k1}, \ldots \zeta_{kk})$ for $k \ge 1$.

In order to analyse $x(\cdot)$ and, in particular, $\lim_{t \to \infty} x(t)$, we need to introduce some basic notation and results. For $k \ge 1$, let

$$R_*^{(k)} = \frac{\beta_G}{\gamma} \, \mathrm{E}[H] \frac{(k-1)!}{\rho^{k-1}} \sum_{i=0}^{k-1} \frac{\rho^i}{i!}$$

and

$$R_* = \sum_{k=1}^{\infty} \frac{k \omega_k R_*^{(k)}}{\mathrm{E}[H]} = \sum_{k=1}^{\infty} \omega_k \frac{\beta_G}{\gamma} \frac{k!}{\rho^{k-1}} \sum_{i=0}^{k-1} \frac{\rho^i}{i!},$$

where $\rho = \gamma/\beta_L$. The quantity R_* plays a vital role in both the stochastic and deterministic analyses of the epidemic model. In this situation, $R_*^{(k)}$ denotes the mean number of global infectious contacts (births) emanating from the epidemic within a household of size k (individual in the branching process) where initially there is one infective within the household and there are no global infections into the household. Then, for the stochastic model, it was shown in [1] that if $R_* \le 1$ then the approximating branching process goes extinct, almost surely, and the epidemic also dies out. However, if $R_* > 1$ then there is a nonzero probability that the branching process does not go extinct, corresponding to the epidemic taking off. The deterministic model is analysed below. We show that if $R_* \le 1$ then there exists only one equilibrium point, $x^* = 0$, and this point is an attractor, that is, for all $x(0) \ge 0$, $x(t) \to x^*(= 0)$ as $t \to \infty$. For $R_* > 1$, there are two equilibrium points, $x^* = 0$ and $s^* > 0$. Then x^* is an unstable equilibrium point while s^* is an attractor, in that, for any configuration of initial infectives such that $x(0) > 0$, $x(t) \to s^*$ as $t \to \infty$. An analysis of the distribution of the total number of infectives within the differently sized households, in equilibrium, is also given.

The first step is to consider, for $m \ge 1$ and $s \ge 0$, time-homogeneous Markov birth–death processes with transition matrices, $\boldsymbol{G}_m(s)$, corresponding to epidemics within households of size m subjected to a constant global infectious pressure s. Let $\boldsymbol{\pi}_m(s)$ denote the stationary distribution of the birth–death process. Then

$$\boldsymbol{0} = \boldsymbol{\pi}_m(s) \boldsymbol{G}_m(s),$$

and if we define $\tilde{\boldsymbol{S}}_m(t; s) = \exp(t \boldsymbol{G}_m(s))$ for $t \ge 0$, then

$$\boldsymbol{\pi}_m(s) = \boldsymbol{\pi}_m(s) \tilde{\boldsymbol{S}}_m(t; s)$$

for all $t \geq 0$. For all $m \geq 1$, let

$$\mathcal{F}_m = \left\{ \boldsymbol{a} = (a_0, a_1, \dots, a_m) \in \mathbb{R}^{m+1} : 0 \leq a_i \ (0 \leq i \leq m), \sum_{i=0}^{m} a_i = 1 \right\}.$$

For any $m \geq 1$, and $\boldsymbol{a}, \boldsymbol{b} \in \mathcal{F}_m$, let $\boldsymbol{a} \leq \boldsymbol{b}$ if $\sum_{i=k}^{m} a_i \leq \sum_{i=k}^{m} b_i$ for all k ($1 \leq k \leq m$), and let $\boldsymbol{a} < \boldsymbol{b}$ if the same conditions hold with strict inequality for at least one value of k. It is trivial to prove that, for $s < s'$, $\boldsymbol{\pi}_m(s) < \boldsymbol{\pi}_m(s')$, since for $s > 0$ we have

$$\pi_m^0(s) = \left\{ 1 + \sum_{k=1}^{m} \prod_{i=1}^{k} \frac{(m+1-i)(\beta_{\mathrm{G}} s + (i-1)\beta_{\mathrm{L}})}{i\gamma} \right\}^{-1}$$

and for $1 \leq k \leq m$ we have

$$\pi_m^k(s) = \frac{(m+1-k)(\beta_{\mathrm{G}} s + (k-1)\beta_{\mathrm{L}})}{k\gamma} \pi_m^{k-1}(s).$$

For $s \geq 0$, let $\mu_m(s) = \sum_{i=1}^{m} i \pi_m^i(s)$ denote the mean number of infectives, in stationarity, within a household of size m given that the household is subjected to a constant global infectious pressure s, and let $\mu(s) = \sum_{k=1}^{\infty} \omega_k \mu_k(s)$.

We shall consider the solutions to $\mu(s) = s$ after the following preliminary lemma.

Lemma 4.1. *For $m \geq 1$ and $a_i, b_i \geq 0$ ($0 \leq i \leq m$), suppose that $f_m(x) = \sum_{i=0}^{m} a_i x^i$ and $g_m(x) = \sum_{i=0}^{m} b_i x^i$. Suppose that, for $0 \leq j < k \leq m$, $a_j/b_j < a_k/b_k$. Then, for all $x \geq 0$,*

$$\frac{\mathrm{d}}{\mathrm{d}x}\left(\frac{f_m(x)}{g_m(x)}\right) > 0 \quad and \quad \frac{\mathrm{d}^2}{\mathrm{d}x^2}\left(\frac{f_m(x)}{g_m(x)}\right) < 0.$$

Proof. The lemma trivially holds for $m = 1$ and can then be proved using induction on m by considering

$$\frac{\mathrm{d}}{\mathrm{d}x}\left(\frac{a_m x^m + f_{m-1}(x)}{b_m x^m + g_{m-1}(x)}\right) \quad and \quad \frac{\mathrm{d}^2}{\mathrm{d}x^2}\left(\frac{a_m x^m + f_{m-1}(x)}{b_m x^m + g_{m-1}(x)}\right).$$

An immediate consequence of Lemma 4.1 is the following corollary.

Corollary 4.1. *For all $m \geq 1$, $\mu_m(s)$ is a concave function with*

$$\frac{\mathrm{d}}{\mathrm{d}s}\mu_m(s) > 0 \quad and \quad \frac{\mathrm{d}^2}{\mathrm{d}s^2}\mu_m(s) < 0 \tag{4.2}$$

for all $s \geq 0$. Hence, $\mu(s)$ is a concave function with

$$\frac{\mathrm{d}}{\mathrm{d}s}\mu(s) > 0 \quad and \quad \frac{\mathrm{d}^2}{\mathrm{d}s^2}\mu(s) < 0 \tag{4.3}$$

for all $s \geq 0$.

Proof. For $m \geq 1$ and $k \geq 1$, let

$$\prod_{i=1}^{k}\left\{ \frac{(m+1-i)(\beta_{\mathrm{G}} s + (i-1)\beta_{\mathrm{L}})}{i\gamma} \right\} = \sum_{i=0}^{k} \varphi_{ki}^m s^i, \quad \text{say.}$$

Therefore,

$$\mu_m(s) = \sum_{i=0}^{m} i\pi_m^i(s) = \frac{f_m(s)}{g_m(s)},$$

where

$$f_m(s) = \sum_{k=1}^{m} k \prod_{i=1}^{k} \left\{ \frac{(m+1-i)(\beta_G s + (i-1)\beta_L)}{i\gamma} \right\} = \sum_{k=1}^{m} k \sum_{i=0}^{k} \varphi_{ki}^m s^i \qquad (4.4)$$

and

$$g_m(s) = 1 + \sum_{k=1}^{m} \prod_{i=1}^{k} \left\{ \frac{(m+1-i)(\beta_G s + (i-1)\beta_L)}{i\gamma} \right\} = 1 + \sum_{k=1}^{m} \sum_{i=0}^{k} \varphi_{ki}^m s^i. \qquad (4.5)$$

Interchanging the order of summations in (4.4) and (4.5) yields

$$f_m(s) = \sum_{i=0}^{m} s^i \sum_{k=i}^{m} k\varphi_{ki}^m, \qquad g_m(s) = 1 + \sum_{i=0}^{m} s^i \sum_{k=i}^{m} \varphi_{ki}^m.$$

Therefore, the conditions of Lemma 4.1 are satisfied and (4.2) follows.

Equation (4.3) follows since $\mu(s)$ is a linear combination of the $\mu_m(s)$.

Note that $\mu(0) = 0$ and $\mu(\infty) = E[H]$. Thus, from Corollary 4.1, there exists at most one $s > 0$ such that $\mu(s) = s$. Furthermore, such a solution will exist if and only if $(d/ds)\mu(s)|_{s=0} > 1$.

Lemma 4.2. *For all $m \geq 1$,*

$$\frac{d}{ds}\mu_m(s)\bigg|_{s=0} = \lim_{\varepsilon \downarrow 0} \varepsilon^{-1}\mu_m(\varepsilon) = \frac{m R_*^{(m)}}{E[H]}$$

and, hence,

$$\frac{d}{ds}\mu(s)\bigg|_{s=0} = \lim_{\varepsilon \downarrow 0} \varepsilon^{-1}\mu(\varepsilon) = R_*.$$

Proof. For $m \geq 1$ and $1 \leq k \leq m$,

$$\pi_m^k(\varepsilon) = \pi_m^0(\varepsilon) \prod_{i=1}^{k} \frac{(m+1-i)(\beta_G \varepsilon + (i-1)\beta_L)}{i\gamma}.$$

Thus, $\pi_m^1(\varepsilon) = (m\beta_G/\gamma)\varepsilon\pi_m^0(\varepsilon)$ and, for $2 \leq k \leq m$,

$$\pi_m^k(\varepsilon) = \frac{m\beta_G}{\gamma}\varepsilon\pi_m^0(\varepsilon) \prod_{i=2}^{k} \frac{(m+1-i)(i-1)\beta_L}{i\gamma} + o(\varepsilon)$$

with $\pi_m^0(\varepsilon) = 1 - O(\varepsilon)$. Therefore, for $1 \leq k \leq m$,

$$\pi_m^k(\varepsilon) = \frac{m\beta_G}{\gamma}\varepsilon\frac{(m-1)!}{k(m-k)!}\rho^{-(k-1)} + o(\varepsilon).$$

Thus,

$$
\begin{aligned}
\mu_m(\varepsilon) &= \sum_{k=0}^{m} k \pi_m^k(\varepsilon) \\
&= \frac{m\beta_{\mathrm{G}}}{\gamma} \varepsilon \sum_{k=1}^{m} k \frac{(m-1)!}{k(m-k)!} \rho^{-(k-1)} + o(\varepsilon) \\
&= \frac{m}{\mathrm{E}[H]} R_*^{(m)} \varepsilon + o(\varepsilon)
\end{aligned}
$$

and, so, $\lim_{\varepsilon \downarrow 0} \varepsilon^{-1} \mu_m(\varepsilon) = m R_*^{(m)} / \mathrm{E}[H]$, as required.

The preceding results are drawn together in Lemma 4.3.

Lemma 4.3. *For $R_* \leq 1$, the only $s \geq 0$ such that $\mu(s) = s$ is $s = 0$. For $R_* > 1$, there exists a unique $s^* > 0$ such that $\mu(s^*) = s^*$. Moreover, for $s_1 < s^* < s_2$, we have $s_1 < \mu(s_1)$ and $\mu(s_2) < s_2$.*

Before returning to $x(\cdot)$, we state a very useful general result for time-inhomogeneous Markov birth–death processes.

Consider any two continuous-time, time-inhomogeneous Markov birth–death processes, labelled one and two, with respective infinitesimal transition rate matrices $\mathbf{H}_1(u)$ and $\mathbf{H}_2(u)$ at time $u \geq 0$. For $u \geq 0$, let $W_1(u)$ and $W_2(u)$ respectively denote the total numbers of individuals alive in processes one and two at time u. Suppose that the maximum population size in both processes is $m \geq 1$, and that, for $j = 1, 2$, the transition matrices $\mathbf{H}_j(u)$ are $(m+1) \times (m+1)$ matrices of the form

$$
\begin{aligned}
h_{i(i+1)}^j(u) &> 0 & (0 \leq i \leq m-1), \\
h_{i(i-1)}^j(u) &= i\gamma & (1 \leq i \leq m), \\
h_{ik}^j(u) &= 0 & (|i-k| \geq 2,\ 0 \leq i, k \leq m), \\
h_{ii}^j(u) &= -\sum_{k \neq i} h_{ik}^j(u) & (0 \leq i \leq m).
\end{aligned}
$$

Proposition 4.1. *Suppose that, for $0 \leq i \leq m-1$,*

$$
h_{i(i+1)}^1(u) \leq h_{i(i+1)}^2(u) < \infty \qquad (u \geq 0) \tag{4.6}
$$

and

$$
W_1(0) \leq W_2(0). \tag{4.7}
$$

Then a coupling exists such that, for all $t \geq 0$,

$$
W_1(t) \leq W_2(t) \quad \text{almost surely.} \tag{4.8}
$$

Furthermore, if either the inequality in (4.7) or the inequalities in (4.6) are strict, then, for all $t > 0$,

$$
\mathrm{P}(W_1(t) < W_2(t)) > 0 \tag{4.9}
$$

and, so,

$$
\mathrm{E}[W_1(t)] < \mathrm{E}[W_2(t)]. \tag{4.10}
$$

Proof. We assume that processes one and two behave independently whenever $W_1(t) \neq W_2(t)$. Note that, for birth–death processes, if $W_1(s) < W_2(s)$ and $W_1(u) > W_2(u)$ ($s < u$) then there exists a t ($s < t < u$) such that $W_1(t) = W_2(t)$. Therefore, it suffices to specify a coupling for $W_1(t) = W_2(t)$.

Suppose that, at time $t \geq 0$, $W_1(t) = W_2(t) = i$ ($0 \leq i \leq m$). The two processes can be coupled as follows. Let η_1^i and η_2^i be inhomogeneous Poisson point processes with rates $h_{i(i+1)}^1(u)$ and $h_{i(i+1)}^2(u) - h_{i(i+1)}^1(u)$, respectively. Let $D_i \sim \text{Exp}(i\gamma)$. If there are no points in either $\eta_1^i(t, t + D_i]$ or $\eta_2^i(t, t + D_i]$, then a death occurs in both processes at time $t + D_i$ and $W_1(t + D_i) = W_2(t + D_i) = i - 1$. Alternatively, if there is at least one point in $(t, t + D_i]$ on the superposition of η_1^i and η_2^i, let B_i ($t < B_i \leq t + D_i$) denote the time of the first such point. If the point corresponds to a point in η_1^i, then a birth occurs in both processes and $W_1(B_i) = W_2(B_i) = i + 1$. Otherwise, a birth only occurs in process two and $W_2(B_i) = i + 1$ with $W_1(B_i) = i$. In this case, the two processes evolve independently until such time, $s > B_i$, that $W_1(s) = W_2(s)$. Therefore, (4.8) holds.

Since the maximum population size is m, for both process one and process two there is always a nonzero probability of no births or deaths occurring in any finite interval. Thus, if $W_1(0) < W_2(0)$ then

$$P(W_1(t) < W_2(t)) \geq P(\text{no births or deaths in either process in } [0, t]) > 0.$$

Now suppose that $W_1(0) = W_2(0) < m$ and that the strict inequalities (4.6) hold. Then $P(W_1(t) < W_2(t))$ is greater than the probability that there is only one birth in process two with no corresponding birth in process one, and no deaths in either process. This probability is positive, since whenever there are the same number of individuals in both processes a birth can occur in process two with no corresponding birth in process one. Thus, (4.9) is proved for $W_1(0) = W_2(0) < m$. A simple adaptation can be applied to prove it in the case $W_1(0) = W_2(0) = m$, and (4.10) is then immediate.

For $j = 1, 2$ and $0 \leq s \leq t$, let $R_j(s, t) = \exp(\int_s^t H_j(u)\, ds)$. The next corollary then follows immediately from (4.10).

Corollary 4.2. *For $m \geq 1$ and $0 \leq i \leq m - 1$, suppose that*

$$h_{i(i+1)}^1(u) \leq h_{i(i+1)}^2(u) \qquad (u \geq 0) \tag{4.11}$$

and that $x, y \in \mathcal{F}_m$ with $x \leq y$. If either $x < y$ or the inequality in (4.11) is strict, then, for all a and b ($0 \leq a < b$),

$$x R_1(a, b) < y R_2(a, b).$$

Applying Corollary 4.2 to the household model yields the following useful results.

Lemma 4.4. *Suppose that, for all $m \geq 1$, $a_m, b_m \in \mathcal{F}_m$ with $a_m \leq b_m$. Let $x_a(0) = \sum_{k=1}^\infty \omega_k k a_k^\top$ and $x_b(0) = \sum_{k=1}^\infty \omega_k k b_k^\top$ with*

$$x_a(t) = \sum_{k=1}^\infty \omega_k k \{a_k S_k(0, t; x_a)\}^\top \quad and \quad x_b(t) = \sum_{k=1}^\infty \omega_k k \{b_k S_k(0, t; x_b)\}^\top.$$

Suppose that there exists a $k \geq 1$ such that $\omega_k > 0$ and $a_k < b_k$. Then, for all $t > 0$, $x_a(t) < x_b(t)$ and, for all $m \geq 1$,

$$a_m S_m(0, t; x_a) < b_m S_m(0, t; x_b).$$

For $i = 1, 2$, let $\mathbf{v}_i = \{v_i(u) \colon u \geq 0\}$. Suppose that $v_1(u) < v_2(u)$ for all $u \geq 0$. Then, for all $m \geq 1$, $\mathbf{c}_m < \mathbf{d}_m$ (where $\mathbf{c}_m, \mathbf{d}_m \in \mathcal{F}_m$), and $t > 0$,

$$\mathbf{c}_m \mathbf{S}_m(0, t; \mathbf{v}_1) < \mathbf{c}_m \mathbf{S}_m(0, t; \mathbf{v}_2) \tag{4.12}$$

and

$$\mathbf{c}_m \mathbf{S}_m(0, t; \mathbf{v}_1) < \mathbf{d}_m \mathbf{S}_m(0, t; \mathbf{v}_1). \tag{4.13}$$

Thus, we have shown that the SIS household epidemic model satisfies a monotonicity condition. That is, two populations with identical household structures and disease dynamics can be coupled household by household such that if, for all $i \geq 1$, there are initially at least as many infectives in household i in population two as there are in population one, then there are at least as many infectives in household i in population two as there are in population one at all times $t \geq 0$.

We now consider the stationary distributions $\boldsymbol{\pi}_m(s)$ ($m \geq 1$, $s \geq 0$).

Lemma 4.5. *For $m \geq 1$, $0 \leq r < s$, and all $t > 0$,*

$$\boldsymbol{\pi}_m(r) < \boldsymbol{\pi}_m(r)\tilde{\mathbf{S}}_m(t; s) < \boldsymbol{\pi}_m(s) \tag{4.14}$$

and, similarly,

$$\boldsymbol{\pi}_m(r) < \boldsymbol{\pi}_m(s)\tilde{\mathbf{S}}_m(t; r) < \boldsymbol{\pi}_m(s). \tag{4.15}$$

Proof. We prove (4.14); (4.15) follows similarly.

Fix r and s ($r < s$). For all $u \geq 0$, let $v_1(u) = r$ and $v_2(u) = s$ in Lemma 4.4. Then, by stationarity, (4.12), and (4.13), we have

$$\boldsymbol{\pi}_m(r) = \boldsymbol{\pi}_m(r)\tilde{\mathbf{S}}_m(t; r) < \boldsymbol{\pi}_m(r)\tilde{\mathbf{S}}_m(t; s) < \boldsymbol{\pi}_m(s)\tilde{\mathbf{S}}_m(t; s) = \boldsymbol{\pi}_m(s),$$

as required.

Lemmas 4.3, 4.4, and 4.5 lead to the following key result.

Lemma 4.6. *Let $R_* > 1$, and let $s^* > 0$ be a solution to $\mu(s^*) = s^*$.*

(i) *For $s > s^*$, let $\mu(s) = s_0$. Then $s^* < s_0 < s$ and, for any s_1 ($s_0 < s_1 < s$), there exists a $t_1 > 0$ such that, for all $m \geq 1$,*

$$\boldsymbol{\pi}_m(s)\mathbf{S}_m(0, t_1; \mathbf{y}^s) < \boldsymbol{\pi}_m(s_1),$$

where, for $t, u \geq 0$, $\mathbf{y}^u(t) = \sum_{k=1}^{\infty} \omega_k \mathbf{k}\{\boldsymbol{\pi}_k(u)\mathbf{S}_k(0, t; \mathbf{y}^u)\}^{\top}$.

(ii) *For $0 < r < s^*$, let $\mu(r) = r_0$. Then $r < r_0 < s^*$ and, for any r_1 ($r < r_1 < r_0$), there exists a $t_1 > 0$ such that, for all $m \geq 1$,*

$$\boldsymbol{\pi}_m(r)\mathbf{S}_m(0, t_1; \mathbf{y}^r) > \boldsymbol{\pi}_m(r_1).$$

Proof. We shall prove statement (i); statement (ii) follows similarly.

Fix s and s^* ($s > s^*$) and $\mu(s) = s_0 < s_1 < s$. Firstly, note that $y^s(0) = s_0$. Now suppose that there exists a $t_2 > 0$ such that $y^s(t_2) > s_0$ and, for all t ($0 \leq t < t_2$), $y^s(t) \leq s_0$. This is a

contradiction since, by Lemma 4.4,

$$y^s(t_2) = \sum_{k=1}^{\infty} \omega_k \mathbf{k} \{ \boldsymbol{\pi}_k(s) \mathbf{S}_k(0, t_2; \mathbf{y}^s) \}^{\top}$$

$$\leq \sum_{k=1}^{\infty} \omega_k \mathbf{k} \{ \boldsymbol{\pi}_k(s) \tilde{\mathbf{S}}_k(t_2; s_0) \}^{\top}$$

$$\leq \sum_{k=1}^{\infty} \omega_k \mathbf{k} \boldsymbol{\pi}_k(s)^{\top}$$

$$= s_0.$$

Thus, for any $t_2 > 0$ and for $y^s(t_2) > s_0$, we require that there exist a t_3 $(0 < t_3 < t_2)$ such that $y^s(t_3) > s_0$, or, equivalently, that there exist a $t_2 > 0$ such that $y^s(t_2) > s_0$ only if

$$\frac{\mathrm{d}}{\mathrm{d}t} y^s(t) \Big|_{t=0} \geq 0.$$

However,

$$\frac{\mathrm{d}}{\mathrm{d}t} y^s(t) \Big|_{t=0} = \sum_{k=1}^{\infty} \omega_k \mathbf{k} \{ \boldsymbol{\pi}_k(s) \mathbf{G}_k(s_0) \}^{\top} < \sum_{k=1}^{\infty} \omega_k \mathbf{k} \{ \boldsymbol{\pi}_k(s) \mathbf{G}_k(s) \}^{\top} = \sum_{k=1}^{\infty} \omega_k \mathbf{k} \mathbf{0}^{\top} = 0.$$

Therefore, for all $t \geq 0$, $y^s(t) \leq s_0$ and, hence, by Lemma 4.4, for all $m \geq 1$ we have

$$\boldsymbol{\pi}_m(s) \mathbf{S}_m(0, t; \mathbf{y}^s) \leq \boldsymbol{\pi}_m(s) \tilde{\mathbf{S}}_m(t; s_0). \tag{4.16}$$

Then, since

$$\boldsymbol{\pi}_m(s) \tilde{\mathbf{S}}_m(t; s_0) \to \boldsymbol{\pi}_m(s_0) \quad \text{as } t \to \infty,$$

it follows that there exists a $t_1 > 0$ such that

$$\boldsymbol{\pi}_m(s) \tilde{\mathbf{S}}_m(t_1; s_0) < \boldsymbol{\pi}_m(s_1). \tag{4.17}$$

Hence, statement (i) follows by (4.16) and (4.17).

Lemma 4.7. *Let $R_* > 1$, and let $s^* > 0$ be a solution to $\mu(s^*) = s^*$. Suppose that there exists an $\varepsilon > 0$ such that, for all $m \geq 1$ with $\omega_m > 0$, $\boldsymbol{\zeta}_m \geq \boldsymbol{\pi}_m(\varepsilon)$. Then*

$$x(t) \to s^* \quad \text{as } t \to \infty.$$

Proof. Fix an ε $(0 < \varepsilon < s^*)$ such that, for all $m \geq 1$,

$$a_m = \boldsymbol{\pi}_m(\varepsilon) \leq \boldsymbol{\zeta}_m \leq \boldsymbol{\pi}_m(\infty) = b_m.$$

For $t \geq 0$, let

$$x_a(t) = \sum_{k=1}^{\infty} \omega_k \mathbf{k} \{ a_k \mathbf{S}_k(0, t; \mathbf{x}_a) \}^{\top},$$

$$x_b(t) = \sum_{k=1}^{\infty} \omega_k \mathbf{k} \{ b_k \mathbf{S}_k(0, t; \mathbf{x}_b) \}^{\top}.$$

By successive applications of Lemma 4.6, for any r_1 and r_2 $(r_1 < s^* < r_2)$, there exists a $t_1 > 0$ such that, for all $m \geq 1$,

$$\boldsymbol{\pi}_m(r_1) < \boldsymbol{a}_m \boldsymbol{S}_m(0, t_1; \mathbf{x}_a),$$
$$\boldsymbol{\pi}_m(r_2) > \boldsymbol{b}_m \boldsymbol{S}_m(0, t_1; \mathbf{x}_b).$$

Moreover, Lemmas 4.5 and 4.6 can then be utilised to show that, for all $t \geq 0$,
$$\boldsymbol{\pi}_m(r_1) < \boldsymbol{\pi}_m(r_1)\tilde{\boldsymbol{S}}_m(t; \mu(r_1)) < \boldsymbol{a}_m \boldsymbol{S}_m(0, t_1 + t; \mathbf{x}_a),$$
$$\boldsymbol{\pi}_m(r_2) > \boldsymbol{\pi}_m(r_2)\tilde{\boldsymbol{S}}_m(t; \mu(r_2)) > \boldsymbol{b}_m \boldsymbol{S}_m(0, t_1 + t; \mathbf{x}_b).$$

Thus, for all $t \geq t_1$,

$$x_a(t) > \sum_{k=1}^{\infty} \omega_k k \boldsymbol{\pi}_k(r_1)^\top = \mu(r_1),$$

$$x_b(t) < \sum_{k=1}^{\infty} \omega_k k \boldsymbol{\pi}_k(r_2)^\top = \mu(r_2).$$

By Lemma 4.4, $x_a(t) < x(t) < x_b(t)$ for all $t \geq 0$. Hence, for all $t > t_1$,

$$\mu(r_1) < x(t) < \mu(r_2).$$

Since the above result holds for all r_1 and r_2 $(r_1 < s^* < r_2)$ and $\mu(s^*) = s^*$, the lemma follows.

The equivalent result for the case where $R_* \leq 1$ is as follows.

Lemma 4.8. *Suppose that $R_* \leq 1$. Then*

$$x(t) \to 0 \quad as \ t \to \infty.$$

Proof. The proof is similar to that in the case $R_* > 1$; hence, the details are omitted.

Lemma 4.7 shows that if $R_* > 1$ then, for most initial configurations of infectives, the mean number of infectives per household converges to $s^* > 0$ as $t \to \infty$, i.e. an endemic equilibrium exists. Moreover, in equilibrium the proportion of households of size m with i infectives is given by $\pi_m^i(s^*)$. However, there is still some work to be done to achieve our goal of showing that $x(t) \to s^*$ as $t \to \infty$ if $x(0) > 0$ and $R_* > 1$. Suppose that, for any $x(0) > 0$, there exist $t_1 > 0$ and $\varepsilon > 0$ such that, for all $m \geq 1$, with $\omega_m > 0$,

$$\boldsymbol{\pi}_m(\varepsilon) < \boldsymbol{\zeta}_m \boldsymbol{S}_m(0, t_1; \mathbf{x}).$$

We can then apply Lemma 4.7 to prove the required result. Thus, we proceed by showing that $t_1 > 0$ and $\varepsilon > 0$ exist.

Lemma 4.9. *Suppose that $x(0) > 0$. Then, for all $m \geq 1$ and $t > 0$,*

$$\boldsymbol{\zeta}_m \boldsymbol{S}_m(0, t; \mathbf{x}) > \boldsymbol{\pi}_m(0) = (1, 0, \ldots, 0).$$

Proof. Note that, for any $m \geq 1$ and $t > 0$, if $\boldsymbol{\zeta}_m > (1, 0, \ldots, 0)$ then

$$\boldsymbol{\zeta}_m \tilde{\boldsymbol{S}}_m(t; 0) > \boldsymbol{\pi}_m(0)\tilde{\boldsymbol{S}}_m(t; 0) = \boldsymbol{\pi}_m(0).$$

Therefore, by Lemma 4.4, for all $t > 0$,

$$x(t) = \sum_{k=1}^{\infty} \omega_k \boldsymbol{k} \{ \boldsymbol{\zeta}_k \boldsymbol{S}_k(0, t; \mathbf{x}) \}^{\top} \geq \sum_{k=1}^{\infty} \omega_k \boldsymbol{k} \{ \boldsymbol{\zeta}_k \tilde{\boldsymbol{S}}_k(t; 0) \}^{\top} > 0.$$

Thus, $\int_0^t x(s) \, ds > 0$ for any $t > 0$, corresponding to all individuals being subjected to total global infectious pressure $\beta_G \int_0^t x(s) \, ds > 0$ up to time t. Hence, for all $t > 0$, each individual has a positive probability of being infectious at time t, and, so, the lemma follows.

Lemma 4.10. *Suppose that $x(0) > 0$. Then, for all $m \geq 1$ and $t > 0$, there exists an $\varepsilon_m > 0$ such that*

$$\boldsymbol{\zeta}_m \boldsymbol{S}_m(0, t; \mathbf{x}) > \boldsymbol{\pi}_m(\varepsilon_m).$$

Proof. Fix $m \geq 1$ and $t_1, t_2 > 0$ with $t = t_1 + t_2$ and note that, by construction, for all $i \geq 1$ and $t_2 > 0$, $\tilde{s}_{im}^m(t_2; 0) > 0$, where $\tilde{s}_{jk}^m(t_2; s)$ $(0 \leq j, k \leq m)$ denotes a typical element of $\tilde{\boldsymbol{S}}_m(t_2; s)$. Thus, by Lemma 4.9, for all $m \geq 1$ there exists a $\delta_m > 0$ such that

$$\boldsymbol{\zeta}_m \boldsymbol{S}_m(0, t_1 + t_2; \mathbf{x}) \geq \boldsymbol{\zeta}_m \boldsymbol{S}_m(0, t_1; \mathbf{x}) \tilde{\boldsymbol{S}}_m(t_2; 0) > (1 - \delta_m, 0, \ldots, 0, \delta_m).$$

Hence, by choosing an $\varepsilon_m > 0$ such that $\pi_m^0(\varepsilon_m) = 1 - \delta_m$, the lemma is proved.

Theorem 4.1. *Let $R_* > 1$, and let $s^* > 0$ be a solution to $\mu(s^*) = s^*$. Suppose that $x(0) = \sum_{k=1}^{\infty} \omega_k \boldsymbol{k} \boldsymbol{\zeta}_k^{\top} > 0$. Then*

$$x(t) \to s^* \quad as \ t \to \infty.$$

Proof. Suppose that there exists an $M \geq 1$ such that, for all $k > M$, $\omega_k = 0$. Then it follows immediately from Lemmas 4.7 and 4.10 that, for $x(0) > 0$,

$$x(t) \to s^* \quad \text{as } t \to \infty.$$

For $M \geq 1$, we can construct lower bound and upper bound approximations to the epidemic process in which, for all $t \geq 0$, all individuals in households of size $k > M$ are respectively susceptible and infectious. Since we can take M to be arbitrarily large and $\sum_{k=M+1}^{\infty} k \omega_k \to 0$ as $M \to \infty$, we can make the lower bound and upper bound approximations to the epidemic process arbitrarily close to the actual epidemic process. The theorem then follows.

5. Fluctuations and Gaussian limit processes

In this section we aim to extend the results of Section 3 to obtain a Gaussian limit process for the fluctuations in the mean number of infectives per household, $X_n(\cdot)$, about the deterministic limit, $x(\cdot)$. In other words, for any $T > 0$, we wish to show that $V_n(\cdot) = \sqrt{n}(X_n(\cdot) - x(\cdot))$ converges to a Gaussian process $V(\cdot)$ on $[0, T]$. This is possible for $Q \sim \text{Exp}(\gamma)$ since we have an explicit expression for $x(\cdot)$; see Section 4. For more general Q, we are unable to obtain a Gaussian limit but are able to show that, for any $T \geq 0$, $\{\sup_{0 \leq s \leq T} |V_n(s)| : n \geq 1\}$ is stochastically bounded.

Firstly, for $n \geq 1$, $t \geq 0$, and $\mathbf{y} = \{y(s) : s \geq 0\}$, let

$$Y_n(t; \mathbf{y}) = \frac{1}{\sqrt{n}} \sum_{i=1}^{n} \{\theta_i(t; \mathbf{y}) - \text{E}[\theta_i(t; \mathbf{y})]\}.$$

Note that, for $s \geq 0$,

$$V_n(s) = Y_n(s; \mathbf{X}_n) + \frac{1}{\sqrt{n}} \sum_{i=1}^{n} \{E[\theta_i(s; \mathbf{X}_n) \mid \mathbf{X}_n] - E[\theta_i(s; \mathbf{x})]\}.$$

Thus, we begin by analysing $Y_n(\cdot; \mathbf{X}_n)$, and we shall assume that $E[H^4] < \infty$.

For $m \in \mathbb{N}$ and $\boldsymbol{t} = (t_1, t_2, \ldots, t_m)$, $\boldsymbol{\gamma} = (\gamma_1, \gamma_2, \ldots, \gamma_m) \in \mathbb{R}^m$, let

$$Z_n^{\boldsymbol{\gamma}}(\boldsymbol{t}; \mathbf{y}) = \sum_{k=1}^{m} \gamma_k Y_n(t_k; \mathbf{y})$$

$$= \frac{1}{\sqrt{n}} \sum_{i=1}^{n} \sum_{k=1}^{m} \gamma_k (\theta_i(t_k; \mathbf{y}) - E[\theta_i(t_k; \mathbf{y})])$$

and

$$z_n^{\boldsymbol{\gamma}}(\boldsymbol{t}; \mathbf{y}) = \frac{1}{n} \sum_{i=1}^{n} \sum_{j=1}^{m} \sum_{k=1}^{m} \gamma_j \gamma_k \operatorname{cov}(\theta_i(t_j; \mathbf{y}), \theta_i(t_k; \mathbf{y})).$$

Lemma 5.1. *For any $m \in \mathbb{N}$ and $\boldsymbol{t} \in \mathbb{R}^m$ with $\boldsymbol{t} \geq \mathbf{0}$,*

$$(Y_n(t_1; \mathbf{x}), Y_n(t_2; \mathbf{x}), \ldots, Y_n(t_m; \mathbf{x})) \xrightarrow{\mathrm{D}} (Y(t_1; \mathbf{x}), Y(t_2; \mathbf{x}), \ldots, Y(t_m; \mathbf{x})) \quad \text{as } n \to \infty,$$

where $\mathbf{Y}$ is a multivariate normal distribution with mean $\mathbf{0}$ and covariance matrix $\boldsymbol{\Sigma}(\boldsymbol{t})$, and '$\xrightarrow{\mathrm{D}}$' denotes convergence in distribution. The (j, k)th element of $\boldsymbol{\Sigma}(\boldsymbol{t})$ is

$$\sum_{i=1}^{\infty} \omega_i \sum_{l=0}^{i} \zeta_{il} \operatorname{cov}(\chi_{il}(t_j; \mathbf{x}), \chi_{il}(t_k; \mathbf{x})).$$

Proof. Fix a $\boldsymbol{\gamma} \in \mathbb{R}^m$. Then, since $E[H^2] < \infty$, it follows by Lindeberg's central limit theorem (see, for example, [7, Theorem 7.2]) that

$$\frac{Z_n^{\boldsymbol{\gamma}}(\boldsymbol{t}; \mathbf{x})}{z_n^{\boldsymbol{\gamma}}(\boldsymbol{t}; \mathbf{x})} \xrightarrow{\mathrm{D}} \mathrm{N}(0, 1) \quad \text{as } n \to \infty.$$

Note that

$$z_n^{\boldsymbol{\gamma}}(\boldsymbol{t}; \mathbf{x}) = \sum_{i=1}^{\infty} \omega_i^n \sum_{l=0}^{i} \zeta_{il}^n \sum_{j=1}^{m} \sum_{k=1}^{m} \gamma_j \gamma_k \operatorname{cov}(\chi_{il}(t_j; \mathbf{x}), \chi_{il}(t_k; \mathbf{x}))$$

$$\to \sum_{j=1}^{m} \sum_{k=1}^{m} \gamma_j \gamma_k \sum_{i=1}^{\infty} \omega_i \sum_{l=0}^{i} \zeta_{il} \operatorname{cov}(\chi_{il}(t_j; \mathbf{x}), \chi_{il}(t_k; \mathbf{x}))$$

$$= z^{\boldsymbol{\gamma}}(\boldsymbol{t}; \mathbf{x}), \quad \text{say, as } n \to \infty.$$

Therefore $Z_n^{\boldsymbol{\gamma}}(\boldsymbol{t}; \mathbf{x}) \xrightarrow{\mathrm{D}} \mathrm{N}(0, z^{\boldsymbol{\gamma}}(\boldsymbol{t}; \mathbf{x}))$ as $n \to \infty$ and the lemma follows by the Cramér–Wold device (see, for example, [7, pp. 48–49]).

In order to make use of Lemma 5.1, we need to show that $\{Y_n(t; \mathbf{X}_n)\}$ has the same asymptotic limiting distribution as $\{Y_n(t; \mathbf{x})\}$ as $n \to \infty$.

Lemma 5.2. *For any $t \geq 0$ and $\varepsilon > 0$,*

$$P(|Y_n(t; \mathbf{X}_n) - Y_n(t; \mathbf{x})| > \varepsilon) \to 0 \quad as \ n \to \infty.$$

Proof. As noted in [14, Lemma 5.4], by Chebyshev's inequality, for any $\varepsilon > 0$,

$$P(|Y_n(t; \mathbf{X}_n) - Y_n(t; \mathbf{x})| > \varepsilon) \leq \frac{1}{\varepsilon^2} E[\mathrm{var}(Y_n(t; \mathbf{X}_n) - Y_n(t; \mathbf{x}) \mid \mathbf{X}_n)]$$

$$= \frac{1}{\varepsilon^2} \frac{1}{n} \sum_{i=1}^{n} E[\mathrm{var}(\theta_i(t; \mathbf{X}_n) - \theta_i(t; \mathbf{x}) \mid \mathbf{X}_n)]$$

$$\leq \frac{1}{\varepsilon^2} \frac{1}{n} \sum_{i=1}^{n} h_i^2 E[P(\theta_i(t; \mathbf{X}_n) \neq \theta_i(t; \mathbf{x}) \mid \mathbf{X}_n)]. \tag{5.1}$$

The right-hand side of (5.1) is equal to

$$\frac{1}{\varepsilon^2} \sum_{k=1}^{\infty} k^2 \omega_k^n \sum_{l=0}^{k} \zeta_{kl}^n E[P(\chi_{kl}(t; \mathbf{X}_n) \neq \chi_{kl}(t; \mathbf{x}) \mid \mathbf{X}_n)].$$

By arguments similar to those employed in Lemma 3.1, for $k \geq 1$ and $0 \leq l \leq k$ we have

$$P(\chi_{kl}(t; \mathbf{X}_n) \neq \chi_{kl}(t; \mathbf{x}) \mid \mathbf{X}_n) \leq k\beta_G \int_0^t |X_n(s) - x(s)| \, ds$$

$$\leq k\beta_G t \sup_{0 \leq s \leq t} |X_n(s) - x(s)|.$$

Thus, it follows from (5.1) that

$$P(|Y_n(t; \mathbf{X}_n) - Y_n(t; \mathbf{x})| > \varepsilon) \leq \frac{1}{\varepsilon^2} \beta_G t \, E\left[\sup_{0 \leq s \leq t} |X_n(s) - x(s)|\right] \sum_{k=1}^{\infty} k^3 \omega_k^n. \tag{5.2}$$

Note that, by Lemma 3.2, $\sup_{0 \leq s \leq t} |X_n(s) - x(s)| \xrightarrow{P} 0$ as $n \to \infty$, for all $t \geq 0$. Therefore, since $X_n(s) \leq \sum_{k=1}^{\infty} k\omega_k^n \ (s \geq 0)$, it follows that

$$E\left[\sup_{0 \leq s \leq t} |X_n(s) - x(s)|\right] \to 0 \quad as \ n \to \infty.$$

Thus, the right-hand side of (5.2) converges to 0 as $n \to \infty$, and the lemma is proved.

Corollary 5.1. *For any $m \in \mathbb{N}$ and $\mathbf{t} \in \mathbb{R}^m$ with $\mathbf{t} \geq \mathbf{0}$,*

$$(Y_n(t_1; \mathbf{X}_n), Y_n(t_2; \mathbf{X}_n), \ldots, Y_n(t_m; \mathbf{X}_n)) \xrightarrow{D} (Y(t_1; \mathbf{x}), Y(t_2; \mathbf{x}), \ldots, Y(t_m; \mathbf{x})) \quad as \ n \to \infty,$$

where $Y(\cdot; \mathbf{x})$ is as defined in Lemma 5.1.

Proof. The Corollary follows immediately from Lemmas 5.1 and 5.2 by [7, Theorem 4.1].

We have thus established that the finite-dimensional distributions of $Y_n(\cdot; \mathbf{X}_n)$ converge to the finite-dimensional distributions of $Y(\cdot; \mathbf{x})$. The next step is to show that $\{Y_n(\cdot; \mathbf{X}_n)\}$ is tight. Then, for $T > 0$, by defining $Y(\cdot; \mathbf{x})$ and $Y_n(\cdot; \mathbf{X}_n)$ $(n \geq 1)$ on $D[0, T]$ endowed with the Skorokhod topology, we will be able to show that $Y_n(\cdot; \mathbf{X}_n) \Rightarrow Y(\cdot; \mathbf{x})$ on $D[0, T]$, where '$\Rightarrow$' denotes convergence of the stochastic process.

Lemma 5.3. *For any* $\mathbf{y} = \{y(s)\colon s \geq 0\}$ *and* $L > 0$ *such that* $\sup_{s \geq 0} |y(s)| \leq L$, *and any* s, t, *and* u *with* $0 \leq s \leq t \leq u$, *there exists a finite constant* D_L, *independent of* s, t, *and* u, *such that*

$$\mathrm{E}[(Y_n(t; \mathbf{y}) - Y_n(s; \mathbf{y}))^2 (Y_n(u; \mathbf{y}) - Y_n(t; \mathbf{y}))^2] \leq D_L (u - s)^2$$

for all $n \geq 1$.

Proof. For $n \geq 1$ and $1 \leq i \leq n$, let $\tilde{\theta}_i(t; \mathbf{y}) = \theta_i(t; \mathbf{y}) - \mathrm{E}[\theta_i(t; \mathbf{y})]$. Since $\mathrm{E}[\tilde{\theta}_i(t; \mathbf{y})] = 0$ and the distinct households are conditionally independent given $\mathbf{y}$, we have

$$\mathrm{E}[(Y_n(t; \mathbf{y}) - Y_n(s; \mathbf{y}))^2 (Y_n(u; \mathbf{y}) - Y_n(t; \mathbf{y}))^2]$$

$$\leq \frac{1}{n^2} \sum_{i=1}^{n} \sum_{j=1}^{n} \sum_{k=1}^{n} \sum_{l=1}^{n} \mathrm{E}[\{\tilde{\theta}_i(t; \mathbf{y}) - \tilde{\theta}_i(s; \mathbf{y})\}\{\tilde{\theta}_j(t; \mathbf{y}) - \tilde{\theta}_j(s; \mathbf{y})\}$$

$$\times \{\tilde{\theta}_k(u; \mathbf{y}) - \tilde{\theta}_k(t; \mathbf{y})\}\{\tilde{\theta}_l(u; \mathbf{y}) - \tilde{\theta}_l(u; \mathbf{y})\}]$$

$$\leq \frac{1}{n^2} \sum_{i=1}^{n} \mathrm{E}[(\tilde{\theta}_i(t; \mathbf{y}) - \tilde{\theta}_i(s; \mathbf{y}))^2] \sum_{j=1}^{n} \mathrm{E}[(\tilde{\theta}_j(u; \mathbf{y}) - \tilde{\theta}_j(t; \mathbf{y}))^2]$$

$$+ \frac{2}{n^2} \left\{ \sum_{i=1}^{n} \mathrm{E}[(\tilde{\theta}_i(t; \mathbf{y}) - \tilde{\theta}_i(s; \mathbf{y}))(\tilde{\theta}_i(u; \mathbf{y}) - \tilde{\theta}_i(t; \mathbf{y}))] \right\}^2$$

$$+ \frac{1}{n^2} \sum_{i=1}^{n} \mathrm{E}[(\tilde{\theta}_i(t; \mathbf{y}) - \tilde{\theta}_i(s; \mathbf{y}))^2 (\tilde{\theta}_i(u; \mathbf{y}) - \tilde{\theta}_i(t; \mathbf{y}))^2]. \tag{5.3}$$

Note that

$$\mathrm{E}[(\tilde{\theta}_i(t; \mathbf{y}) - \tilde{\theta}_i(s; \mathbf{y}))^2] = \mathrm{var}(\theta_i(t; \mathbf{y}) - \theta_i(s; \mathbf{y}))$$

$$\leq \mathrm{E}[(\theta_i(t; \mathbf{y}) - \theta_i(s; \mathbf{y}))^2]$$

$$\leq h_i^2 \, \mathrm{P}(\theta_i(t; \mathbf{y}) \neq \theta_i(s; \mathbf{y})). \tag{5.4}$$

Now, $\mathrm{P}(\theta_i(t; \mathbf{y}) \neq \theta_i(s; \mathbf{y}))$ is less than the probability that there are no infections or removals within household i in the time interval $(s, t]$. Infections take place within household i at the points of an inhomogeneous Poisson point process with rate $(h_i - \theta_i(s; \mathbf{y}))\{\beta_{\mathrm{G}} y(s) + \beta_{\mathrm{L}} \theta_i(s; \mathbf{y})\}$. Therefore, the probability that there are no infections in household i in the interval $(s, t]$ is greater than or equal to $\exp(-\frac{1}{4}\{4\beta_{\mathrm{G}} h_i L + \beta_{\mathrm{L}} h_i^2\}(t - s))$ since $\sup_{r \geq 0} |y(r)| \leq L$. A similar argument shows that the probability that there are no removals within household i in the interval $(s, t]$ is greater than or equal to $\{1 - \alpha(t - s)\}^{h_i}$, where $\alpha = \sup_{x \geq 0} f_Q(x)$ and $f_Q(\cdot)$ denotes the probability density function of Q.

Thus, it follows from (5.4) that

$$\mathrm{E}[(\tilde{\theta}_i(t; \mathbf{y}) - \tilde{\theta}_i(s; \mathbf{y}))^2] \leq h_i^2 \left\{ 1 - \exp\left(-\tfrac{1}{4}\{4\beta_{\mathrm{G}} h_i L + \beta_{\mathrm{L}} h_i^2\}(t - s)\right) \right\}$$

$$+ h_i^2 \{1 - (1 - \alpha(t - s))^{h_i}\}$$

$$\leq h_i^2 \left(\tfrac{1}{4}\{4\beta_{\mathrm{G}} h_i L + \beta_{\mathrm{L}} h_i^2\}(t - s)\right) + h_i^2 (h_i \alpha(t - s)).$$

Therefore, there exists a constant $C_L < \infty$, independent of t, s, and h_i, such that

$$\mathrm{E}[(\tilde{\theta}_i(t; \mathbf{y}) - \tilde{\theta}_i(s; \mathbf{y}))^2] \leq C_L h_i^4 (t - s). \tag{5.5}$$

Similarly, we can show that

$$|E[\{\tilde{\theta}_i(t; \mathbf{y}) - \tilde{\theta}_i(s; \mathbf{y})\}\{\tilde{\theta}_i(u; \mathbf{y}) - \tilde{\theta}_i(t; \mathbf{y})\}]| \leq 2h_i^4 C_L(u - s) \tag{5.6}$$

and

$$E[\{\tilde{\theta}_i(t; \mathbf{y}) - \tilde{\theta}_i(s; \mathbf{y})\}^2\{\tilde{\theta}_i(u; \mathbf{y}) - \tilde{\theta}_i(t; \mathbf{y})\}^2] \leq 6C_L^2 h_i^8 (u - s)^2. \tag{5.7}$$

Therefore, it follows from (5.3)–(5.7) that

$$E[(Y_n(t; \mathbf{y}) - Y_n(s; \mathbf{y}))^2 (Y_n(u; \mathbf{y}) - Y_n(t; \mathbf{y}))^2]$$

$$\leq \left\{\frac{1}{n} \sum_{i=1}^n C_L h_i^4 (u - s)\right\}^2 + 2\left\{\frac{1}{n} \sum_{i=1}^n 2C_L h_i^4 (u - s)\right\}^2 + \frac{1}{n^2} \sum_{i=1}^n 6C_L^2 h_i^8 (u - s)^2$$

$$\leq 11 C_L^2 (u - s)^2 \sum_{k=1}^\infty k^4 \omega_k^n.$$

Thus, if $D_L = 11C_L^2 (E[H^4] + 1)$ then $0 < D_L < \infty$ and there exists an $n_0 \in \mathbb{N}$ such that, for all $n \geq n_0$,

$$E[(Y_n(t; \mathbf{y}) - Y_n(s; \mathbf{y}))^2 (Y_n(u; \mathbf{y}) - Y_n(t; \mathbf{y}))^2] \leq D_L(u - s)^2,$$

as required.

The following corollary is an immediate consequence of Lemma 5.3.

Corollary 5.2. *Let* $A = E[H]$. *Then, for any* s, t, *and* u $(0 \leq s \leq t \leq u)$, *there exists an* $n_0 \in \mathbb{N}$ *such that, for all* $n \geq n_0$,

$$E[(Y_n(t; \mathbf{X}_n) - Y_n(s; \mathbf{X}_n))^2 (Y_n(u; \mathbf{X}_n) - Y_n(t; \mathbf{X}_n))^2] \leq D_A(u - s)^2. \tag{5.8}$$

Hence, for any $T > 0$,

$$Y_n(\cdot; \mathbf{X}_n) \Rightarrow Y(\cdot; \mathbf{x})$$

on $D[0, T]$ *as* $n \to \infty$.

Proof. For $r > 0$, let $\mathcal{G}_r = \{\mathbf{y} = \{|y(s)|: s \geq 0\}: \sup_{s \geq 0} y(s) \leq r\}$ and note that $\mathbf{X}_n \in \mathcal{G}_A$ almost surely. Therefore, by Lemma 5.3,

$$E[(Y_n(t; \mathbf{X}_n) - Y_n(s; \mathbf{X}_n))^2 (Y_n(u; \mathbf{X}_n) - Y_n(t; \mathbf{X}_n))^2]$$

$$= E[E[(Y_n(t; \mathbf{X}_n) - Y_n(s; \mathbf{X}_n))^2 (Y_n(u; \mathbf{X}_n) - Y_n(t; \mathbf{X}_n))^2 \mid \mathbf{X}_n]]$$

$$\leq \sup_{\mathbf{y} \in \mathcal{G}_A} E[(Y_n(t; \mathbf{y}) - Y_n(s; \mathbf{y}))^2 (Y_n(u; \mathbf{y}) - Y_n(t; \mathbf{y}))^2]$$

$$\leq D_A(u - s)^2.$$

Thus (5.8) is proved and, by [7, Theorem 15.6], the result follows immediately from Corollary 5.1 and (5.8).

The final step in the analysis of $\{Y_n(\cdot; \mathbf{X}_n)\}$ before returning to $\{V_n(\cdot)\}$ is to show that the limiting Gaussian process $Y(\cdot; \mathbf{x})$ has almost surely continuous sample paths.

Lemma 5.4. *The Gaussian process* $Y(\cdot; \mathbf{x})$ *has a continuous version (see [15, p. 59]) and, hence, for* $T > 0$, $Y(\cdot; \mathbf{x})$ *has almost surely continuous sample paths on* $D[0, T]$.

Proof. Fix a $T > 0$. By arguments similar to those employed in Lemma 5.3, it is straightforward to show that there exists a constant $C < \infty$ such that, for all s and t ($0 \le s, t \le T$),

$$
\begin{aligned}
& | \mathrm{E}[Y(s; \mathbf{x})Y(t; \mathbf{x})] - \mathrm{E}[Y(t; \mathbf{x})Y(t; \mathbf{x})]| \\
& = \left| \sum_{i=1}^{\infty} \omega_i \sum_{l=0}^{i} \zeta_{il}\{\mathrm{cov}(\chi_{il}(s; \mathbf{x}) - \chi_{il}(t; \mathbf{x}), \chi_{il}(t; \mathbf{x}))\} \right| \\
& \le C|s - t|.
\end{aligned}
$$

The lemma then follows by [15, Chapter 1, Corollary 25.6]. ∎

The following theorem utilises Corollary 5.2 and Lemma 5.4 to show that, for all $T > 0$, V_n is stochastically bounded on $[0, T]$. We shall then focus on the case $Q \sim \mathrm{Exp}(\gamma)$, where an explicit Gaussian limit for V_n can be obtained.

Theorem 5.1. *For any $T > 0$, $\{\sup_{0 \le s \le T} V_n(s) : n \ge 1\}$ is stochastically bounded.*

Proof. Note that, for all $t \ge 0$,

$$
V_n(t) = Y_n(t; \mathbf{X}_n) + \sqrt{n} \left\{ \frac{1}{n} \sum_{i=1}^{n} (\mathrm{E}[\theta_i(t; \mathbf{X}_n) \mid \mathbf{X}_n] - \mathrm{E}[\theta_i(t; \mathbf{x})]) \right\}.
$$

Now using arguments identical to those employed in Lemma 3.1,

$$
\mathrm{E}[\theta_i(t; \mathbf{X}_n) \mid \mathbf{X}_n] - \mathrm{E}[\theta_i(t; \mathbf{x})] \le h_i \int_0^t h_i \beta_{\mathrm{G}} |X_n(s) - x(s)| \, \mathrm{d}s.
$$

Hence,

$$
\begin{aligned}
\sqrt{n} \left\{ \frac{1}{n} \sum_{i=1}^{n} (\mathrm{E}[\theta_i(t; \mathbf{X}_n) \mid \mathbf{X}_n] - \mathrm{E}[\theta_i(t; \mathbf{x})]) \right\} & \le \sqrt{n} \left\{ \frac{1}{n} \sum_{i=1}^{n} h_i^2 \beta_{\mathrm{G}} \int_0^t |X_n(s) - x(s)| \, \mathrm{d}s \right\} \\
& = \beta_{\mathrm{G}} \sum_{k=1}^{\infty} k^2 \omega_k^n \int_0^t |V_n(s)| \, \mathrm{d}s.
\end{aligned}
$$

Thus,

$$
\begin{aligned}
\sup_{0 \le s \le T} |V_n(s)| & \le \sup_{0 \le s \le T} |Y_n(s; \mathbf{X}_n)| + \beta_{\mathrm{G}} \sum_{k=1}^{\infty} k^2 \omega_k^n \sup_{0 \le s \le T} \int_0^s |V_n(u)| \, \mathrm{d}u \\
& \le \sup_{0 \le s \le t} |Y_n(s; \mathbf{X}_n)| + \beta_{\mathrm{G}} \sum_{k=1}^{\infty} k^2 \omega_k^n \int_0^T \sup_{0 \le u \le s} |V_n(u)| \, \mathrm{d}u
\end{aligned}
$$

and, hence, by Gronwall's inequality and Corollary 5.2,

$$
\begin{aligned}
\sup_{0 \le s \le T} |V_n(s)| & \le \sup_{0 \le s \le T} |Y_n(s; \mathbf{X}_n)| \exp\left(T\beta_{\mathrm{G}} \sum_{k=1}^{\infty} k^2 \omega_k^n \right) \\
& \xrightarrow{\mathrm{D}} \sup_{0 \le s \le T} |Y(s; \mathbf{x})| \exp\left(T\beta_{\mathrm{G}} \sum_{k=1}^{\infty} k^2 \omega_k \right) \quad \text{as } n \to \infty.
\end{aligned}
$$

The theorem now follows since $Y(\,\cdot\,; \mathbf{x})$ is continuous (see Lemma 5.4). ∎

5.1. Exponential infectious periods

For $k \geq 1$, let $\boldsymbol{B}_k$ denote a $(k+1) \times (k+1)$ matrix with typical entries b_{ij}^k $(0 \leq i, j \leq k)$, where $b_{i(i+1)}^k = k - i$, $b_{ii}^k = -(k-i)$ $(0 \leq i \leq k-1)$, and $b_{ij}^k = 0$ otherwise. It then follows that

$$\sqrt{n} \int_0^t \{\boldsymbol{G}_k(X_n(s)) - \boldsymbol{G}_k(x(s))\} \, \mathrm{d}s = \beta_{\mathrm{G}} \int_0^t V_n(s) \, \mathrm{d}s \, \boldsymbol{B}_k.$$

We shall require that there exists an $a > 0$ such that $\mathrm{E}[\exp(aH)] < \infty$.

Note that

$$\sqrt{n} \sum_{k=1}^\infty \omega_k \boldsymbol{k}(\{\boldsymbol{\zeta}_k^n \boldsymbol{S}_k(0, t; \mathbf{X}_n)\}^\top - \{\boldsymbol{\zeta}_k \boldsymbol{S}_k(0, t; \mathbf{x})\}^\top)$$

$$= \sqrt{n} \sum_{k=1}^\infty \omega_k \boldsymbol{k}\{(\boldsymbol{\zeta}_k^n - \boldsymbol{\zeta}_k) \boldsymbol{S}_k(0, t; \mathbf{X}_n)\}^\top + \sqrt{n} \sum_{k=1}^\infty \omega_k \boldsymbol{k}\{\boldsymbol{S}_k(0, t; \mathbf{X}_n) - \boldsymbol{S}_k(0, t; \mathbf{x})\}^\top \boldsymbol{\zeta}_k^\top$$

$$= \varepsilon_n^1(t) + \sqrt{n} \sum_{k=1}^\infty \omega_k \boldsymbol{k}\{\boldsymbol{S}_k(0, t; \mathbf{X}_n) - \boldsymbol{S}_k(0, t; \mathbf{x})\}^\top \boldsymbol{\zeta}_k^\top, \quad \text{say.}$$

Therefore, provided that

$$\sqrt{n} \sum_{k=1}^\infty \omega_k k \sum_{l=0}^k |\zeta_{kl}^n - \zeta_{kl}| \to 0 \quad \text{as } n \to \infty,$$

it will follow that $\boldsymbol{\varepsilon}_n^1 \Rightarrow \boldsymbol{0}$ as $n \to \infty$ on $[0, T]$, for all $T \geq 0$.

Lemma 5.5. *Suppose that there exists an $a > 0$ such that $\mathrm{E}[\exp(aH)] < \infty$. For all $n \geq 1$ and $t \geq 0$, let*

$$\sqrt{n} \sum_{k=1}^\infty \omega_k \boldsymbol{k}\{\boldsymbol{S}_k(0, t; \mathbf{X}_n)^\top - \boldsymbol{S}_k(0, t; \mathbf{x})^\top\} \boldsymbol{\zeta}_k^\top$$

$$= \beta_{\mathrm{G}} \int_0^t V_n(s) \, \mathrm{d}s \sum_{k=1}^\infty \omega_k \boldsymbol{k} \boldsymbol{B}_k^\top \boldsymbol{S}_k(0, t; \mathbf{x})^\top \boldsymbol{\zeta}_k^\top + \varepsilon_n^2(t),$$

where

$$\varepsilon_n^2(t) = \sqrt{n} \sum_{k=1}^\infty \omega_k \boldsymbol{k} \boldsymbol{C}_k^n(t) \boldsymbol{S}_k(0, t; \mathbf{x})^\top \boldsymbol{\zeta}_k^\top$$

with

$$\boldsymbol{C}_k^n(t) = \exp\left(\frac{\beta_{\mathrm{G}}}{\sqrt{n}} \int_0^t V_n(s) \, \mathrm{d}s \, \boldsymbol{B}_k\right)^\top - \boldsymbol{I}_{k+1} - \frac{\beta_{\mathrm{G}}}{\sqrt{n}} \int_0^t V_n(s) \, \mathrm{d}s \, \boldsymbol{B}_k^\top$$

for $k \geq 1$, $\boldsymbol{I}_{k+1}$ denoting the $(k+1)$-dimensional identity matrix.

Then, for all $T \geq 0$, $\boldsymbol{\varepsilon}_n^2 \Rightarrow \boldsymbol{0}$ as $n \to \infty$ on $[0, T]$.

Proof. For all $k \geq 1$,

$$|\boldsymbol{k} \boldsymbol{C}_k^n(t) \boldsymbol{S}_k(0, t; \mathbf{x})^\top \boldsymbol{\zeta}_k^\top| \leq \sum_{j=2}^\infty \frac{1}{j!} \left| \boldsymbol{k}\left(\frac{\beta_{\mathrm{G}}}{\sqrt{n}} \int_0^t V_n(s) \, \mathrm{d}s\right)^j (\boldsymbol{B}_k^j)^\top \boldsymbol{S}_k(0, t; \mathbf{x})^\top \boldsymbol{\zeta}_k^\top \right|.$$

For $j \geq 1$, the maximum element of $\mathbf{S}_k(0, t; \mathbf{x}) \mathbf{B}_k^j$ is less than or equal to $(2k)^j$, since $\mathbf{S}_k(0, t; \mathbf{x})$ is a stochastic matrix. Therefore,

$$|\mathbf{k}(\mathbf{B}_k^j)^\top \mathbf{S}_k(0, t; \mathbf{x})^\top \boldsymbol{\zeta}_k^\top| \leq k(2k)^j = 2^j k^{j+1}.$$

Thus, if $A_n(t) = 2\beta_\mathrm{G}| \int_0^t V_n(s) \, \mathrm{d}s|$, by Theorem 5.1 we have $\mathrm{P}(A_n(t) < \infty) = 1$ and, so,

$$\sqrt{n} \sum_{k=1}^\infty \omega_k \sum_{j=2}^\infty \left| \frac{1}{j!} \left(\frac{\beta_\mathrm{G}}{\sqrt{n}} \int_0^t V_n(s) \, \mathrm{d}s \right)^j \right| 2^j k^{j+1}$$

$$\leq \sqrt{n} \sum_{k=1}^\infty k\omega_k \left| \exp\left(k \frac{1}{\sqrt{n}} A_n(t) \right) - 1 - k \frac{1}{\sqrt{n}} A_n(t) \right|. \tag{5.9}$$

Then, since there exists an $a > 0$ such that $\mathrm{E}[\exp(aH)] < \infty$, it is straightforward to show that the right-hand side of (5.9) converges in probability to 0 as $n \to \infty$.

Thus, for all $t \geq 0$, $\varepsilon_n^2(t) \overset{\mathrm{P}}{\to} 0$ as $n \to \infty$, and the lemma follows.

For $t \geq 0$, let

$$r(t; \mathbf{x}) = \sum_{k=1}^\infty \omega_k \mathbf{k} \mathbf{B}_k^\top \mathbf{S}_k(0, t; \mathbf{x})^\top \boldsymbol{\zeta}_k^\top.$$

It follows that $r(t; \mathbf{x}) < \infty$ since $\mathrm{E}[H^2] < \infty$.

Theorem 5.2. *Suppose that there exists an $a > 0$ such that $\mathrm{E}[\exp(aH)] < \infty$. For all $T \geq 0$, $V_n \Rightarrow V$ as $n \to \infty$ on $[0, T]$, where V satisfies*

$$V(t) = Y(t; \mathbf{x}) + \beta_\mathrm{G} r(t; \mathbf{x}) \int_0^t V(s) \, \mathrm{d}s$$

Proof. By Lemma 5.5, for all $t \geq 0$,

$$V_n(t) = Y_n(t; \mathbf{X}_n) + \varepsilon_n^1(t) + \varepsilon_n^2(t) + \beta_\mathrm{G} r(t; \mathbf{x}) \int_0^t V_n(s) \, \mathrm{d}s.$$

For $m \geq 0$ and $0 \leq s \leq t$, define $C_m(s, t; \mathbf{x})$ as follows. Let $C_0(s, t; \mathbf{x}) = 1$ and, for $m \geq 1$, let

$$C_m(s, t; \mathbf{x}) = \int_s^t \beta_\mathrm{G} r(u; \mathbf{x}) C_{m-1}(u, t; \mathbf{x}) \, \mathrm{d}u.$$

Following [17], if we let

$$K(s, t; \mathbf{x}) = \sum_{m=0}^\infty C_m(s, t; \mathbf{x})$$

then, for all s and t ($0 \leq s \leq t$), $K(s, t; \mathbf{x}) < \infty$ and

$$V_n(t) = Y_n(t; \mathbf{X}_n) + \varepsilon_n^1(t) + \varepsilon_n^2(t) + \beta_\mathrm{G} r(t; \mathbf{x}) \int_0^t K(s, t; \mathbf{x})\{Y_n(s; \mathbf{X}_n) + \varepsilon_n^1(s) + \varepsilon_n^2(s)\} \, \mathrm{d}s.$$

Then $J : D \to D$ defined by

$$Jy(t) = y(t) + \beta_\mathrm{G} r(t; \mathbf{x}) \int_0^t K(s, t; \mathbf{x}) y(s) \, \mathrm{d}s$$

is continuous. Also, $V_n(t) = J(Y_n + \varepsilon_n^1 + \varepsilon_n^2)$ and $V(t) = J(Y)$. Therefore, by the continuous mapping theorem [8, Theorem 25.7, Corollary 1], $V_n \Rightarrow V$ as $n \to \infty$ on $[0, T]$.

6. Summary

We here give a brief summary of the main results of this paper and suggest possible avenues for future work. The results are divided into two categories, those for general infectious periods and those for exponentially distributed infectious periods.

For general infectious periods, we have proved a weak law of large numbers for the convergence of the mean number of infectives over time to a suitably defined deterministic trajectory, in Theorem 3.1. Moreover, in Theorem 5.1, bounds for the fluctuations of the stochastic model about the deterministic trajectory were derived. These bounds are of the order of magnitude that one would expect.

For exponentially distributed infectious periods an explicit equation for the deterministic model is easily derived and was given in (4.1). This explicit expression allows us to go further with this model than we can using Theorems 3.1 and 5.1. In particular, it enabled us to derive the asymptotic behaviour as $t \to \infty$, in Theorem 4.1, showing that if $R_* \leq 1$ the epidemic goes extinct, while if $R_* > 1$ then the epidemic settles down to an endemic equilibrium which is easily obtained from the stationary distributions of suitably defined Markov chains. Furthermore, in Theorem 5.2, we derived the limiting stochastic process for the fluctuations of the stochastic model about the deterministic trajectory.

Finally the SIS epidemic model is the simplest epidemic model to exhibit endemic behaviour. It would be interesting to extend the above analysis to other endemic household epidemic models such as SIRS and open-population SIR models.

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