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Pairwise approximation for *SIR*-type network epidemics with non-Markovian recovery

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We present the generalized mean-field and pairwise models for non-Markovian epidemics on networks with arbitrary recovery time distributions. First we consider a hyperbolic partial differential equation (PDE) system, where the population of infective nodes and links are structured by age since infection. We show that the PDE system can be reduced to a system of integro-differential equations, which is analysed analytically and numerically. We investigate the asymptotic behaviour of the generalized model and provide an implicit analytical expression involving the final epidemic size and pairwise reproduction number. As an illustration of the applicability of the general model, we recover known results for the exponentially distributed and fixed recovery time cases. For gamma- and uniformly distributed infectious periods, new pairwise models are derived. Theoretical findings are confirmed by comparing results from the new pairwise model and explicit stochastic network simulation. A major benefit of the generalized pairwise model lies in approximating the time evolution of the epidemic.

1. Introduction

It has long been acknowledged that the connectivity pattern between individuals in a population is an important factor in determining how diseases invade, spread or how to design or deploy optimal control measures [1–5]. Using networks to model disease transmission, individuals can be represented by nodes

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in a network and the connectivity between individuals can be represented by links between the nodes. This allows modellers to capture a high level of detail of many realistic contact processes. In this framework, we can develop more accurate models, especially when compared to classical compartmental models which usually operate on the assumption of homogeneous random mixing. The most popular node-level models are perhaps the degree-based or heterogeneous mean-field models. The pairwise models offer an explicit treatment of the epidemic process both at the node and link level [6,7]. Such and other models of epidemic dynamics of networks (see [8] for a review) have led to a much better understanding of the role of contact heterogeneity, assortativity and clustering of contacts. While networks deal with the complexity of the contact structure, epidemic models on networks often only consider Markovian transmission and recovery processes. However, empirical observations show that assuming Markovian infectiousness is a strong simplifying assumption [9,10]. Unfortunately, the analysis of non-Markovian systems is significantly more challenging and requires deeper theoretical and numerical tools. This paper is motivated by the renewed interest in non-Markovian processes [11–14] and aims to extend the pairwise model from Markovian to non-Markovian epidemics, where the infection process is Markovian but the infectious period is taken from an arbitrary distribution.

Research in this area is based on different mathematical techniques depending on how the exact stochastic process is approximated. If the main focus is on the early (i.e. epidemic threshold) and asymptotic behaviour (i.e. final epidemic size) of the epidemic, then probabilistic models based on branching process approximations and susceptibility sets as well as percolation models can provide analytical results. In these cases, the impact of the network structure on the epidemic threshold and final epidemic size is clear. For example, in [15] the final epidemic size is given implicitly by an equation connecting it to moments of the network degree and other factors. The percolation theory-based approach [16,17] applies even more widely for general transmission and recovery processes. It provides implicit analytical equations which determine the final epidemic size and links it to average characteristics of the epidemic process (e.g. transmissibility) and network properties (e.g. first and second moment of the degree distribution). However, both approaches fail to characterize the time evolution of the epidemic.

The message passing approach [18,19] is also an effective way to model an epidemic with arbitrary transmission and recovery processes, but at the expense of a system consisting of a large number of integro-differential equations. By using the concept of average message, one can further simplify the equations and gain insight into both the time evolution of the epidemic and final epidemic size. Edge-based compartmental models [20] have also been successful in capturing SIR dynamics on configuration-like networks and for Markovian models, giving perhaps the most compact ODE models that provide an excellent approximation of the exact stochastic network epidemic. They become exact in some appropriate limits and conditions on the underlying network [21–23]. The overwhelming view is that such models complement each other and offer a different or complementary perspective of the exact stochastic process. Often it turns out that such models are in fact equivalent in some well-defined sense or limit [24,25], and they all contribute to a better or more complete understanding of exact stochastic processes on networks.

For the Markovian case, the pairwise model is amenable to extensions to either networks with more exotic properties, such as directed [26] and weighted [27] networks. Here we focus on generalizing this approach to the case of non-Markovian epidemics and test the flexibility of this modelling framework. This paper is structured as follows: in §2, we present the derivation of pairwise and mean-field models for arbitrary infectious periods, with the most technical part of the calculations presented in appendix A. Section 3 includes the mathematical analysis of the resulting systems, with focus on the positivity of solutions, associated reproduction numbers and the implicit relation concerning the final epidemic size. In §4, we illustrate that in special cases the resulting system can be reduced to the well-known and previously studied models. In appendix A, we collect the most technical parts of proofs, namely the calculations involved in the model derivation and the algebraic manipulations of the resulting multiple integrals.

2. Model derivation

We consider an undirected and unweighted regular network with N nodes where each node has n link/edges. For our purposes such networks would be created using the configuration model with clustering going to zero as the network size increases. However, we note that our results will remain valid also for Erdős–Rényi random networks. Each node has a state at any time t, which can be susceptible (S), infected (I) or recovered (R). If an infection occurs along an $S - I$ link, then the state of the susceptible node S changes to I. Each infected node has an infectious period chosen from some given distribution and after it elapses, the node recovers and changes its state to R permanently, which means that the infectious period is the same as the recovery time and recovered nodes remain immune.

We want to build mean-field and pairwise models for the SIR epidemic process with Markovian transmission (i.e. time to infection is exponentially distributed) and general recovery time distribution. We use the notations $[X](t)$, $[XY](t)$ and $[XYZ](t)$ to denote the expected number of nodes in state X, links in state $X - Y$ and triples in state $X - Y - Z$, respectively, where $X, Y, Z \in \{S, I, R\}$. For the derivation of a model at the level of nodes (i.e. for mean-field model), we obtain equations for $[\dot{S}](t)$ and $[\dot{I}](t)$, and these depend on the expected number of pairs. For the pairwise model (at the level of links/pairs), equations for $[\dot{SS}](t)$ and $[\dot{SI}](t)$ are needed, which in turn depend on triples.

First, let $i(t, a)$ represent the density of infected nodes with respect to the age of infection a at the current time t; then $[I](t) = \int_0^\infty i(t, a)\, \mathrm{d}a$. Similarly, $Si(t, a)$ and $ISi(t, a)$ describe the density of $S - i$ links and $I - S - i$ triplets, respectively, where the infected node i has age a at time t and $[SI](t) = \int_0^\infty Si(t, a)\, \mathrm{d}a$, $[ISI](t) = \int_0^\infty ISi(t, a)\, \mathrm{d}a$. We assume that the infection process along $S - I$ links is Markovian with transmission rate $\tau > 0$. The recovery part is considered to be non-Markovian, with a cumulative distribution function $F(a)$ and probability density function $f(a)$. We use the associated survival function $\xi(a) = 1 - F(a)$ and hazard function $h(a) = -\xi'(a)/\xi(a) = f(a)/\xi(a)$.

Using the notations above, we arrive at the following model:

$$[\dot{S}](t) = -\tau[SI](t), \tag{2.1a}$$

$$\left(\frac{\partial}{\partial t} + \frac{\partial}{\partial a}\right) i(t, a) = -h(a)i(t, a), \tag{2.1b}$$

$$[\dot{SS}](t) = -2\tau[SSI](t) \tag{2.1c}$$

and

$$\left(\frac{\partial}{\partial t} + \frac{\partial}{\partial a}\right) Si(t, a) = -\tau ISi(t, a) - (\tau + h(a))Si(t, a), \tag{2.1d}$$

subject to the boundary conditions

$$i(t, 0) = \tau[SI](t) \tag{2.2a}$$

and

$$Si(t, 0) = \tau[SSI](t), \tag{2.2b}$$

and initial conditions

$$[S](0) = [S]_0, \quad [SS](0) = [SS]_0, \quad i(0, a) = \varphi(a) \tag{2.3a}$$

and

$$Si(0, a) = \chi(a) \approx \frac{n}{N}[S]_0 i(0, a) = \frac{n}{N}[S]_0 \varphi(a). \tag{2.3b}$$

We shall use the biologically feasible assumption $\lim_{a \to \infty} \varphi(a) = 0$. To break the dependence on higher-order moments, we apply the closure approximation formula, as given in [28] (see §2(a)

for further details),

$$[XSY](t) = \frac{n-1}{n} \frac{[XS](t)[SY](t)}{[S](t)}, \tag{2.4}$$

which can be also applied for $XSi(t,a)$ in the form

$$XSi(t,a) = \frac{n-1}{n} \frac{[XS](t)Si(t,a)}{[S](t)}, \quad X \in \{S, I\}. \tag{2.5}$$

To obtain a self-consistent system in terms of network-level averaged quantities such as $[S]$, $[SS]$, $[I]$ and $[SI]$, further calculations are needed, which are presented in appendix Aa. The resulting pairwise system is the following integro-differential equation:

$$[\dot{S}](t) = -\tau[SI](t), \tag{2.6a}$$

$$[\dot{SS}](t) = -2\tau \frac{n-1}{n} \frac{[SS](t)[SI](t)}{[S](t)}, \tag{2.6b}$$

$$[\dot{I}](t) = \tau[SI](t) - \int_0^t \tau[SI](t-a)f(a)\,\mathrm{d}a - \int_t^\infty \varphi(a-t)\frac{f(a)}{\xi(a-t)}\,\mathrm{d}a \tag{2.6c}$$

and $\quad [\dot{SI}](t) = \tau \frac{n-1}{n} \frac{[SS](t)[SI](t)}{[S](t)} - \tau \frac{n-1}{n} \frac{[SI](t)}{[S](t)}[SI](t) - \tau[SI](t)$

$$- \int_0^t \tau \frac{n-1}{n} \frac{[SS](t-a)[SI](t-a)}{[S](t-a)} \, \mathrm{e}^{-\int_{t-a}^t \tau((n-1)/n)([SI](s)/[S](s))+\tau\,\mathrm{d}s} f(a)\,\mathrm{d}a$$

$$- \int_t^\infty \frac{n}{N}[S]_0\varphi(a-t)\,\mathrm{e}^{-\int_0^t \tau((n-1)/n)([SI](s)/[S](s))+\tau\,\mathrm{d}s} \frac{f(a)}{\xi(a-t)}\,\mathrm{d}a. \tag{2.6d}$$

From equation (2.6), the associated mean-field model can be easily deduced by using the closure approximation formula for homogeneous networks (i.e. n-regular graphs)

$$[XY](t) = \frac{n}{N}[X](t)[Y](t), \tag{2.7}$$

thus the node-level system becomes

$$\dot{S}(t) = -\tau \frac{n}{N} S(t)I(t) \tag{2.8a}$$

and

$$\dot{I}(t) = \tau \frac{n}{N} S(t)I(t) - \int_0^t \tau \frac{n}{N} S(t-a)I(t-a)f(a)\,\mathrm{d}a - \int_t^\infty \varphi(a-t)\frac{f(a)}{\xi(a-t)}\,\mathrm{d}a. \tag{2.8b}$$

In the following, we investigate these systems from a mathematical and numerical point of view, focusing on the epidemiologically meaningful properties of the models.

(a) The relation of the stochastic and mean-field epidemic model

The underlying epidemic model is a stochastic model unfolding on a network of N nodes with three possible states (S, I, R). When the transmission and the recovery processes are Markovian, the corresponding 3^N forward Kolmogorov equations make the analysis of the model extremely difficult. Starting at the microscopic level and seeking to derive a meaningful mean-field model relies on considering the expected values of some appropriately chosen random variables. In the case of the pairwise model, these are the expected number of singles, pairs and triples of appropriate types. However, developing limiting mean-field models (be these ordinary or integro-differential equations) for these usually depends on higher-order moments or correlations between these random variables. In kinetic theory, the propagation of chaos or mean-field particle methods essentially relies on assuming independence, e.g. the expected value of a product of random variables is equal to the product of the expectations [29], this in our case translates to assuming that the expected number of triples can be approximated in terms of the expected number of pairs and singles. This was shown in [28] by assuming a regular network and that the states of nodes around a given susceptible node are multinomially distributed with probabilities
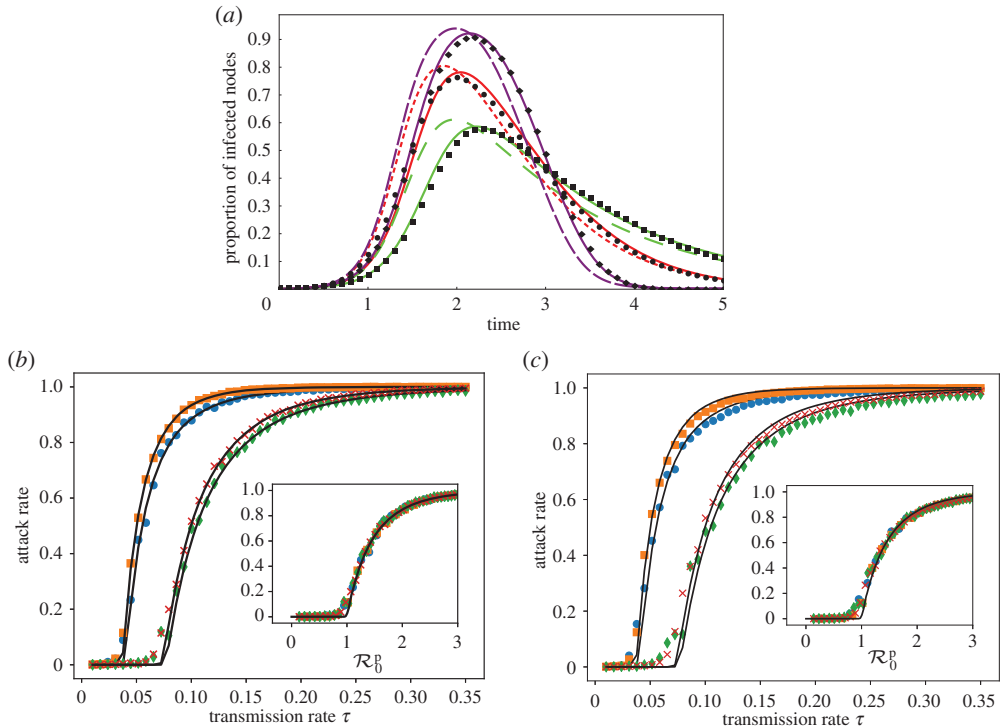
Figure 1. (*a*) Stochastic and numerical experiments for non-Markovian epidemic with various recovery time distributions on regular networks with $N = 1000$ nodes and infection rate $\tau = 0.35$. Squares, circles and diamonds show the mean of 100 simulations on regular graphs with $k = 15$ for exponential distribution with rate $2/3$ (mean $= 3/2$, variance $= 9/4$), gamma distribution with shape $\alpha = 3$ and rate $\beta = 2$ (mean $= 3/2$, variance $= 3/4$) and uniform distribution on interval $[a, b] = [1, 2]$ (mean $= 3/2$, variance $= 1/2$), respectively. Simulations started with a single newly infected node and a matching initial condition was considered for the integro-differential system. Dashed and solid lines correspond to the numerical solution of the mean-field (2.7) and pairwise (2.6) models, respectively. Attack rate based on explicit stochastic network simulations is plotted against τ and $\mathcal{R}_0^p$ (in the inset) for regular (*b*) and Erdős–Rényi networks (*c*) with $\langle k \rangle = 15$; the theoretical curves (continuous black lines) are based on (3.24). The circle, diamond, square and cross stand for gamma (shape $\alpha = 0.5$, $\beta = 0.25$ with mean $= 2$, variance $= 8$), uniform (on $[a, b] = [1, 3]$ with mean $= 2$, variance $= 1/3$), exponential (with rate 1 and mean $= 1$, variance $= 1$) and Dirac delta distributions (fixed at 1 with mean $= 1$, variance $= 0$), respectively. For (*b*) and (*c*), $N = 10\,000$ and results are based on averaging over 1000 simulations where each epidemic starts with exactly one infectious node. The error bars are smaller than the markers and thus not plotted. (Online version in colour.)

depending on the expected number of pairs and singles alone. While here we do not provide a rigorous proof that our model is a large-scale limiting model of the stochastic process, numerical tests confirm the validity of our model (figure 1).

Perhaps related but more widely used in the mathematical–biology community are the formal proofs by Decreusefond *et al.* [22], Barbour & Reinert [21] and Janson *et al.* [23] which are all concerned with the limiting mean-field equations of the SIR stochastic epidemic on configuration networks. Decreusefond *et al.* [22] study a measure-valued process capturing the degrees of susceptible individuals and the number of edges between different types of nodes. They prove that, as $N \to \infty$, the measure-valued process converges to a deterministic limit, from which the Volz [30] equations may be derived as a corollary.

Barbour & Reinert [21] use multitype branching process approximations to prove results approximating the entire course of an SIR epidemic within a more general non-Markovian framework, allowing degree-dependent infection and recovery time distributions. Janson *et al.* [23] relaxes some of the conditions on the degree distribution.

These are strong theoretical results which cement many empirical observations and numerical validations, and such a type of proof in our case is beyond the scope of our paper. In our paper, the derivation of the model is intuitive and its validation is done numerically. However, pairwise models before a closure and for Markovian epidemics have been proved to be exact [31]. Moreover, it is possible that the validity of our model could be established more rigorously using the results in [21] augmented by the argument that the Volz-type and pairwise equations are equivalent [5,24].

3. General results

In this section, we explore the most important features of systems (2.6) and (2.8). First, we find a first integral of the pairwise model (2.6), which allows us to reduce the dimensionality. We show that the solutions of the models are biologically meaningful, i.e. solutions with non-negative data remain non-negative for $t \geq 0$. The central result of this part is the implicit relationship between the reproduction number and the final epidemic size. We summarize the definitions of the associated reproduction numbers referring to [7], where the basic ($\mathcal{R}_0$) and pairwise ($\mathcal{R}_0^{\mathrm{P}}$) reproduction numbers are precisely introduced for mean-field and pairwise models, respectively.

(a) First integral

We use (2.6*a,b*) to find an invariant quantity of the system.

Proposition 3.1. *The function* $U(t) = [SS](t)/[S]^{2((n-1)/n)}(t)$ *is a first integral of system* (2.6).

Proof. To see this, let us divide equation (2.6*b*) by equation (2.6*a*), which gives

$$\frac{\mathrm{d}[SS]}{\mathrm{d}[S]} = \frac{-2\tau((n-1)/n)([SS][SI]/[S])}{-\tau[SI]} = 2\frac{n-1}{n}\frac{[SS]}{[S]}.$$

Solving this equation, we find $[SS] = K[S]^{2((n-1)/n)}$, where K is a constant, thus $U(t) = [SS](t)/[S]^{2((n-1)/n)}(t)$ is an invariant quantity in the system and its value is

$$U(0) = K = \frac{[SS](0)}{[S]^{2((n-1)/n)}(0)} = \frac{[SS]_0}{[S]_0^{2((n-1)/n)}} = \frac{n[S]_0([S]_0/N)}{[S]_0^{2((n-1)/n)}} = \frac{n}{N}[S]_0^{2/n}. \qquad \blacksquare$$

Consequently, using this first integral, we obtain

$$[SS](t) = \frac{n}{N}[S]_0^{2/n}[S]^{2((n-1)/n)}(t). \tag{3.1}$$

Applying equation (3.1), we can reduce our pairwise model to a two-dimensional system:

$$[\dot{S}](t) = -\tau[SI](t)$$

and

$$\left.\begin{aligned}
[\dot{SI}](t) &= \tau\kappa[S]^{(n-2)/n}(t)[SI](t) - \tau[SI](t) - \tau\frac{n-1}{n}\frac{[SI](t)}{[S](t)}[SI](t) \\
&\quad - \int_0^t \tau\kappa[S]^{(n-2)/n}(t-a)[SI](t-a)\,\mathrm{e}^{-\int_{t-a}^t \tau((n-1)/n)([SI](s)/[S](s))+\tau\,\mathrm{d}s} f(a)\,\mathrm{d}a \\
&\quad - \int_t^\infty \frac{n}{N}[S]_0\varphi(a-t)\,\mathrm{e}^{-\int_0^t \tau((n-1)/n)([SI](s)/[S](s))+\tau\,\mathrm{d}s}\frac{f(a)}{\xi(a-t)}\,\mathrm{d}a,
\end{aligned}\right\} \tag{3.2}$$

where

$$\kappa = \frac{n-1}{N}[S]_0^{2/n}.$$

(b) Positivity

We are interested only in non-negative solutions of system (2.6). The following proposition shows that the solutions remain non-negative provided that the initial conditions are non-negative.

Proposition 3.2. *If initial conditions* $[S]_0$, $[SS]_0$ *are non-negative and* $\varphi(a) \geq 0$ *for* $a \geq 0$, *then* $[S](t) \geq 0$, $[SS](t) \geq 0$, $[I](t) \geq 0$ *and* $[SI](t) \geq 0$ *hold for* $t \geq 0$.

Proof. It is clear that $[SS](t)$ remains non-negative if the initial condition $[SS](0)$ is non-negative, because $[SS](t)$ can be expressed from equation (2.6b) in the form

$$[SS](t) = [SS]_0 \, e^{-2\tau((n-1)/n)\int_0^t ([SI](s)/[S](s))\,ds}.$$

Moreover, if $[SS]_0$ is positive, then $[SS](t) > 0$ for all $t \geq 0$. From equation (3.1), we obtain that $[S](t)$ cannot be zero if $[SS](t)$ is positive for all $t \geq 0$, which implies (from the continuity of solutions) $[S](t) > 0$ for $t \geq 0$. From the derivation of system (2.6) (see appendix A), we have the following formulae for $[I](t)$ and $[SI](t)$:

$$[I](t) = \int_0^t \tau [SI](t-a)\xi(a)\,da + \int_t^\infty \varphi(a-t)\frac{\xi(a)}{\xi(a-t)}\,da \tag{3.3}$$

and

$$[SI](t) = \int_0^t \tau \frac{n-1}{n}\frac{[SS](t-a)[SI](t-a)}{[S](t-a)} \, e^{-\int_{t-a}^t \tau((n-1)/n)([SI](s)/[S](s))+\tau\,ds}\xi(a)\,da$$

$$+ \int_t^\infty \frac{n}{N}[S]_0\varphi(a-t)\, e^{-\int_0^t \tau((n-1)/n)([SI](s)/[S](s))+\tau\,ds}\frac{\xi(a)}{\xi(a-t)}\,da. \tag{3.4}$$

It can be seen that $[I](t)$ remains non-negative if $[SI](t)$ is non-negative for $t \geq 0$. On the other hand, $[SI](t_0)$ cannot be zero for some $t_0 \geq 0$, because the right-hand side of (3.4) depends on the $[S](t; t < t_0)$, $[SS](t; t < t_0)$ and $[S](t; t < t_0)$, which are positive, hence $[SI](t) > 0$. ∎

In the case of the mean-field model (2.8), the positivity of $S(t)$ is clear. To see the positivity of $I(t)$, we substitute (2.7) into (3.3), which gives

$$I(t) = \int_0^t \tau \frac{n}{N}S(t-a)I(t-a)\xi(a)\,da + \int_t^\infty \varphi(a-t)\frac{\xi(a)}{\xi(a-t)}\,da. \tag{3.5}$$

Note that $I(t)$ remains non-negative if $S(t)$ is non-negative for $t \geq 0$.

(c) Reproduction numbers $\mathcal{R}_0$ and $\mathcal{R}_0^{\mathrm{p}}$

To determine the reproduction numbers for our models, we start with the usual interpretation, which specifies $\mathcal{R}_0$ as the number of secondary infections generated by a 'typical' infected individual introduced into a fully susceptible population during its infectious period. In [7], the reproduction numbers are precisely described in both cases: in the context of a mean-field model, we use the *basic* reproduction number $\mathcal{R}_0$, which is the expected lifetime of an I node multiplied by the number of newly generated I nodes per unit time. On the other hand, the *pairwise* reproduction number $\mathcal{R}_0^{\mathrm{p}}$ is the expected lifetime of an $S-I$ link multiplied by the number of newly generated $S-I$ links per unit time. These definitions above give

$$\mathcal{R}_0 = \tau[SI]_0 \mathbb{E}(\mathcal{I}), \tag{3.6}$$

where $\mathbb{E}(\mathcal{I})$ denotes the expected value of the random variable $\mathcal{I}$ defined by the infectious period of an infected node, and

$$\mathcal{R}_0^{\mathrm{p}} = \tau[SSI]_0 \mathbb{E}(\mathcal{Z}) = \tau[SSI]_0 \frac{(1 - \mathcal{L}[f](\tau))}{\tau}, \tag{3.7}$$

where $\mathbb{E}(\mathcal{Z})$ denotes the expected value of the random variable $\mathcal{Z}$, defined by the lifetime of an $S-I$ link, and $\mathcal{L}[f](\tau)$ denotes the Laplace transform of f, the density of the recovery process at

τ. Applying the mean-field closure assumption (2.7) for (3.7), we get

$$\mathcal{R}_0 = \tau \frac{n}{N} S_0 \mathbb{E}(\mathcal{I}), \tag{3.8}$$

and using the pairwise closure approximation (2.4) and first integral (3.1) in (3.7), we find

$$\mathcal{R}_0^{\mathrm{p}} = \frac{n-1}{N}[S]_0(1 - \mathcal{L}[f](\tau)). \tag{3.9}$$

We omit the detailed calculations here [7]. Note that while in compartmental models $\mathcal{R}_0$ can be interpreted as the growth factor of subsequent generations of infected individuals in the initial phase of the epidemic, $\mathcal{R}_0^{\mathrm{p}}$ in the pairwise model can intuitively be understood as the growth factor of subsequent generations of infected links. The well-known form of the basic reproduction number for stochastic epidemics on networks is [32]

$$\mathcal{R}_0^{\mathrm{s}} = T\left(\frac{\langle k^2 \rangle - \langle k \rangle}{\langle k \rangle}\right), \tag{3.10}$$

where T is the average transmissibility, and $\langle k \rangle$ and $\langle k^2 \rangle$ are the first and second moment of the network's degree distribution, respectively. In our case $\langle k \rangle = n$, $\langle k^2 \rangle = n^2$ and $T = 1 - \mathcal{L}[f](\tau)$. The latter equality can be seen as follows: consider an isolated $S - I$ link, and let $\mathcal{E}$ be the exponentially distributed random variable of the time of infection along this link, with parameter τ. Then the probability of transmission is the same as the probability that infection occurs before recovery, that is

$$T = P(\mathcal{E} < \mathcal{I}) = \int_0^\infty F_{\mathcal{E}}(y)f(y)\,\mathrm{d}y = \int_0^\infty (1 - \mathrm{e}^{-\tau y})f(y)\,\mathrm{d}y = 1 - \mathcal{L}[f](\tau). \tag{3.11}$$

Hence,

$$\mathcal{R}_0^{\mathrm{p}} = \frac{n-1}{N}[S]_0(1 - \mathcal{L}[f](\tau)) \underset{[S]_0 \to N}{=} (1 - \mathcal{L}[f](\tau))\left(\frac{n^2 - n}{n}\right) = \mathcal{R}_0^{\mathrm{s}}, \tag{3.12}$$

and thus the two approaches are equivalent. The intuitive derivation for $\mathcal{R}_0^{\mathrm{p}}$ follows from considering the rate at which new $S - I$ links are created. From (2.6d), and focusing on the single positive term on the right-hand side, it follows that $S - I$ links are created at rate $(\tau(n-1)/n)([SS]/[S])$, which at time $t = 0$ and with a vanishingly small initial number of infected nodes reduces to $\tau(n-1)$. Now, multiplying this by the average lifetime of an $S - I$ link, which is $\mathbb{E}(\mathcal{Z}) = 1 - \mathcal{L}[f](\tau)/\tau$, gives the desired threshold value in the limit of $[S] \to N$ at $t = 0$.

(d) Final size relation

In this part, we derive final size relations that allow us to calculate the total number of infected nodes during an epidemic outbreak on the network. We use the notation $s_\infty = [S]_\infty/[S]_0$, where $[S]_\infty = \lim_{t \to \infty}[S](t)$ and $1 - s_\infty$ is called the attack rate (the fraction of infected nodes).

Theorem 3.3. *The final size relation associated with the mean-field model (2.8) is*

$$\ln(s_\infty) = \mathcal{R}_0(s_\infty - 1), \tag{3.13}$$

where the basic reproduction number $\mathcal{R}_0$ is defined in (3.8).

Proof. From (2.8a), we obtain

$$S_\infty - S_0 = -\tau \frac{n}{N} \int_0^\infty S(u)I(u)\,\mathrm{d}u \tag{3.14}$$

and

$$\ln\left(\frac{S_\infty}{S_0}\right) = -\tau \frac{n}{N} \int_0^\infty I(u)\,\mathrm{d}u. \tag{3.15}$$

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Substituting (3.5) into (3.15), we get

$$
\ln\left(\frac{S_\infty}{S_0}\right) = -\tau\frac{n}{N}\int_0^\infty\int_0^u \tau\frac{n}{N}S(u-a)I(u-a)\xi(a)\,\mathrm{d}a\,\mathrm{d}u
$$
$$
-\tau\frac{n}{N}\int_0^\infty\int_u^\infty \varphi(a-u)\frac{\xi(a)}{\xi(a-u)}\,\mathrm{d}a\,\mathrm{d}u.
$$

Neglecting the small number of initial infecteds ($\varphi(a)\approx 0$), we obtain

$$
\ln\left(\frac{S_\infty}{S_0}\right) = -\left(\tau\frac{n}{N}\right)^2\int_0^\infty\int_0^u S(u-a)I(u-a)\xi(a)\,\mathrm{d}a\,\mathrm{d}u. \tag{3.16}
$$

After some algebraic manipulation (for details, see appendix Ab), we obtain

$$
\ln\left(\frac{S(\infty)}{S(0)}\right) = \tau\frac{n}{N}\mathbb{E}(\mathcal{I})(S(\infty)-S(0)), \tag{3.17}
$$

where $\mathcal{I}$ denotes the infectious period of an infected node. Therefore, we found (3.13). ∎

We note that in [33] a similar calculation has been performed to derive the final size relation for an age-of-infection model. In the following, we derive our main mathematical result that is the final size relation for the pairwise system (2.6).

Theorem 3.4. *The final size relation associated with the pairwise model (2.6) is*

$$
\frac{s_\infty^{1/n}-1}{1/(n-1)} = \mathcal{R}_0^{\mathrm{P}}(s_\infty^{(n-1)/n}-1), \tag{3.18}
$$

where the pairwise reproduction number $\mathcal{R}_0^{\mathrm{P}}$ is defined in (3.9).

Proof. The second equation of the two-dimensional system (3.2) has the general form

$$
x'(t) = \alpha(t) - \beta(t)x(t),
$$

where

$$
\alpha(c) = \tau\kappa[S]^{(n-2)/n}(c)[SI](c)
$$
$$
-\int_0^c \tau\kappa[S]^{(n-2)/n}(c-a)[SI](c-a)f(a)\,\mathrm{e}^{-\int_{c-a}^c \tau((n-1)/n)([SI](s)/[S](s))+\tau\,\mathrm{d}s}\,\mathrm{d}a
$$
$$
-\int_c^\infty \frac{n}{N}[S]_0\varphi(a-c)\frac{f(a)}{\xi(a-c)}\,\mathrm{e}^{-\int_0^c \tau((n-1)/n)([SI](s)/[S](s))+\tau\,\mathrm{d}s}\,\mathrm{d}a,
$$
$$
\beta(w) = \tau + \tau\frac{n-1}{n}\frac{[SI](w)}{[S](w)},
$$
$$
x(t) = [SI](t),
$$

and has the solution

$$
x(u) = \mathrm{e}^{-\int_0^u \beta(w)\,\mathrm{d}w}x(0) + \int_0^u \mathrm{e}^{-\int_c^u \beta(w)\,\mathrm{d}w}\alpha(c)\,\mathrm{d}c. \tag{3.19}
$$

Using (2.1a), simple calculations give the relations

$$
\mathrm{e}^{-\int_0^u \tau+\tau((n-1)/n)([SI](s)/[S](s))\,\mathrm{d}s} = \mathrm{e}^{-\tau u}\frac{[S]^{(n-1)/n}(u)}{[S]^{(n-1)/n}(0)},
$$
$$
\mathrm{e}^{-\int_c^u \tau+\tau((n-1)/n)([SI](s)/[S](s))\,\mathrm{d}s} = \mathrm{e}^{-\tau(u-c)}\frac{[S]^{(n-1)/n}(u)}{[S]^{(n-1)/n}(c)}.
$$

Using these relations, from (3.19) we get

$$[SI](u) = \frac{[SI](0)}{[S]^{(n-1)/n}(0)} e^{-\tau u} [S]^{(n-1)/n}(u) + \int_0^u \tau\kappa [S]^{-1/n}(c)[SI](c) e^{\tau c} e^{-\tau u} [S]^{(n-1)/n}(u) \, dc$$
$$- \int_0^u \int_0^c \tau\kappa [S]^{-1/n}(c-a)[SI](c-a)f(a) e^{-\tau a} e^{\tau c} e^{-\tau u} [S]^{(n-1)/n}(u) \, da \, dc$$
$$- \int_0^u \int_c^\infty \frac{n}{N}[S]_0^{1/n}\varphi(a-c)\frac{f(a)}{\xi(a-c)} e^{-\tau u} [S]^{(n-1)/n}(u) \, da \, dc.$$

Then, substituting this formula into the first equation of (3.2), we find an equation in general form

$$[S]'(t) = -\tau A(t)[S]^{(n-1)/n}(t), \tag{3.20}$$

where

$$A(u) = \frac{[SI](0)}{[S]^{(n-1)/n}(0)} e^{-\tau u} + \int_0^u \tau\kappa [S]^{-1/n}(c)[SI](c) e^{\tau c} e^{-\tau u} \, dc$$
$$- \int_0^u \int_0^c \tau\kappa [S]^{-1/n}(c-a)[SI](c-a)f(a) e^{-\tau a} e^{\tau c} e^{-\tau u} \, da \, dc$$
$$- \int_0^u \int_c^\infty \frac{n}{N}[S]_0^{1/n}\varphi(a-c)\frac{f(a)}{\xi(a-c)} e^{-\tau u} \, da \, dc. \tag{3.21}$$

Solving this scalar equation, we have

$$[S]^{1/n}(t) = [S]_0^{1/n} - \frac{\tau}{n} \int_0^t A(u) \, du.$$

For the final size relation, we consider the following equation:

$$[S]_\infty^{1/n} = [S]_0^{1/n} - \frac{\tau}{n} \int_0^\infty A(u) \, du. \tag{3.22}$$

Using the linearity of integration, we have to calculate the following four integrals on the right-hand side:

$$I_1 = \int_0^\infty \frac{[SI](0)}{[S]^{(n-1)/n}(0)} e^{-\tau u} \, du,$$

$$I_2 = \int_0^\infty \int_0^u \tau\kappa [S]^{-1/n}(c)[SI](c) e^{\tau c} e^{-\tau u} \, dc \, du,$$

$$I_3 = \int_0^\infty \int_0^u \int_0^c \tau\kappa [S]^{-1/n}(c-a)[SI](c-a)f(a) e^{-\tau a} e^{\tau c} e^{-\tau u} \, da \, dc \, du,$$

$$I_4 = \int_0^\infty \int_0^u \int_c^\infty \frac{n}{N}[S]_0^{1/n}\varphi(a-c)\frac{f(a)}{\xi(a-c)} e^{-\tau u} \, da \, dc \, du.$$

After lengthy calculations (see appendix Ac), we arrive at the relation

$$[S]_\infty^{1/n} = [S]_0^{1/n} + \kappa \frac{1}{n-1}\left(1 - \int_0^\infty f(a) e^{-\tau a} \, da\right)([S]_\infty^{(n-1)/n} - [S]_0^{(n-1)/n}). \tag{3.23}$$

After some algebraic manipulation and substituting back the formula of κ, we have

$$\frac{s_\infty^{1/n} - 1}{1/(n-1)} = \frac{n-1}{N}(1 - \mathcal{L}[f](\tau))[S]_0(s_\infty^{(n-1)/n} - 1), \tag{3.24}$$

where $\mathcal{L}[f](\tau)$ denotes the Laplace transform of f, the PDF of recovery time at τ. ■

Note that, for $n \to \infty$, the relation (3.18) takes the form $\ln(s_\infty) = \mathcal{R}_0^p(s_\infty - 1)$, which is exactly the classical form of final size relations. Furthermore, simple algebraic manipulations show that our final size relation (3.24) agrees with that derived in [34].

4. Special cases

In this section, we investigate some common choices for the recovery time. As we expect, if $\mathcal{I} \sim \exp(\gamma)$ (i.e. the infectious period $\mathcal{I}$ is exponentially distributed), we get back the classical Markovian models. In the case of fixed recovery time, the models reduce to the systems studied in detail in [7]. We can also recover the multistage infection model of [35] with gamma-distributed recovery time. Finally, we consider $\mathcal{I} \sim \text{Uniform}(A, B)$ and write down the associated equations in a compact form. In this section, we assume that the initial infecteds are 'newborn', i.e. the initial distribution of infected nodes $\varphi(a) = [I]_0 \delta(a)$, where $\delta(a)$ is the Dirac delta function. Then,

$$\int_t^\infty \varphi(a-t) \frac{f(a)}{\xi(a-t)} \, da = [I]_0 f(t) \tag{4.1}$$

and

$$\int_t^\infty \frac{n}{N} [S]_0 \varphi(a-t) \, e^{-\int_0^t \tau((n-1)/n)([SI](s)/[S](s))+\tau \, ds} \frac{f(a)}{\xi(a-t)} \, da$$
$$= \frac{n}{N} [S]_0 \, e^{-\int_0^t \tau((n-1)/n)([SI](s)/[S](s))+\tau \, ds} f(t). \tag{4.2}$$

(a) Exponential distribution with parameter γ

The most widely used distribution in disease modelling is the exponential distribution. Both the stochastic and deterministic approaches exploit the memorylessness property to build tractable models. The resulting deterministic systems are ordinary differential equations, which are favoured due to their simpler structure and numerical solvability. In the exponential case, $\xi(t) = e^{-\gamma t}$ and $f(t) = \gamma \, e^{-\gamma t}$. Using the assumption $\varphi(a) = [I]_0 \delta(a)$, (3.3) and $f(t) = \gamma \, \xi(t)$, from (2.6c) we obtain

$$[\dot{I}](t) = \tau [SI](t) - \gamma [I](t),$$

which gives the classical Markovian-type pairwise equation for $[I](t)$. With similar arguments, from (2.6d) we obtain

$$[\dot{SI}](t) = \tau \frac{n-1}{n} \frac{[SS](t)[SI](t)}{[S](t)} - \tau \frac{n-1}{n} \frac{[SI](t)}{[S](t)} [SI](t) - \tau [SI](t) - \gamma [SI](t).$$

For the mean-field model (2.8), the same calculation gives the classical Markovian mean-field equation for $\dot{I}(t)$:

$$[\dot{I}](t) = \tau S(t) I(t) - \gamma I(t).$$

(b) Fixed recovery time σ

In several models, it is a reasonable assumption for the infectious period to have a fixed, constant duration, e.g. for measles [36]. In the case of fixed recovery time σ, we have

$$\xi(t) = \begin{cases} 1 & \text{if } 0 \le t < \sigma, \\ 0 & \text{if } t \ge \sigma, \end{cases}$$

and

$$f(t) = \delta(t - \sigma),$$

where $\delta(t)$ denotes the Dirac delta function. Applying the fundamental property of $\delta(t)$, from (2.6c) and $\varphi(a) = [I]_0 \delta(a)$ we have

$$[\dot{I}](t) = \tau [SI](t) - \begin{cases} 0 & \text{if } 0 \le t < \sigma, \\ \tau [SI](t-\sigma) & \text{if } t \ge \sigma, \end{cases}$$

and from (2.6d), if $0 \le t < \sigma$, we obtain

$$[\dot{SI}](t) = \tau \frac{n-1}{n} \frac{[SS](t)[SI](t)}{[S](t)} - \tau \frac{n-1}{n} \frac{[SI](t)}{[S](t)} [SI](t) - \tau [SI](t).$$

If $t > \sigma$, we get

$$[\dot{SI}](t) = \tau \frac{n-1}{n} \frac{[SS](t)[SI](t)}{[S](t)} - \tau \frac{n-1}{n} \frac{[SI](t)}{[S](t)}[SI](t) - \tau[SI](t)$$

$$- \tau \frac{n-1}{n} \frac{[SS](t-\sigma)[SI](t-\sigma)}{[S](t-\sigma)} e^{-\int_{t-\sigma}^{t} \tau((n-1)/n)([SI](s)/[S](s)) + \tau \, ds}.$$

which is exactly the same system that was studied in detail in [7]. The mean-field model for fixed recovery time [7] can also be derived from (2.8b) using the same arguments.

(c) Gamma distribution with shape $K \in \mathbb{Z}^+$ and rate $K\gamma$

The case of gamma-distributed recovery time was studied in [35].

Using pairwise approximation with a standard closure, the authors have been able to analytically derive a number of important characteristics of disease dynamics. These included the final size of an epidemic and the epidemic threshold. Their results have shown that a higher number of disease stages, but with the same average duration of the infectious period, results in faster epidemic outbreaks with a higher peak prevalence and a larger final size of the epidemic. The pairwise model in [35] has the following equations for nodes:

$$[\dot{S}] = -\tau \sum_{i=1}^{K} [SI_i],$$

$$[\dot{I_1}] = \tau \sum_{i=1}^{K} [SI_i] - K\gamma[I_1] \tag{4.3}$$

and
$$[\dot{I_j}] = K\gamma[I_{j-1}] - K\gamma[I_j], \quad j = 2,3,\ldots,K,$$

where I_i, $i = 1, 2, \ldots, K$ are the infectious stages, where nodes spend an exponentially distributed time with parameter $K\gamma$. The distribution of the total infectious period is the sum of K exponential distributions with parameter $K\gamma$, which gives the gamma distribution with shape K and rate $K\gamma$ (thus the expected infectious period is $K \times 1/K\gamma = 1/\gamma$). Clearly, $[I](t) = \sum_{j=1}^{K}[I_i](t)$ and $[SI](t) = \sum_{i=1}^{K}[SI_i](t)$, and the sum of equations for infectious stages gives

$$[\dot{I}](t) = \tau[SI](t) - K\gamma[I_K](t).$$

On the other hand, using (4.1), the PDF and survival function of gamma distribution

$$f(a) = \frac{(K\gamma)^K}{(K-1)!} a^{K-1} e^{-K\gamma a}$$

and
$$\xi(a) = e^{-K\gamma a} \sum_{k=0}^{K-1} \frac{(K\gamma)^k}{k!} a^k,$$

and inserting into (2.6c) and (3.3), we have

$$[\dot{I}](t) = \tau[SI](t) - K\gamma \left(\int_0^t \tau[SI](t-a) \frac{(K\gamma)^{K-1}}{(K-1)!} a^{K-1} e^{-K\gamma a} \, da - [I]_0 \frac{(K\gamma)^{K-1}}{(K-1)!} t^{K-1} e^{-K\gamma t} \right) \tag{4.4}$$

and

$$[I](t) = \sum_{k=0}^{K-1} \left(\int_0^t \tau[SI](t-a) \frac{(K\gamma)^k}{k!} a^k e^{-K\gamma a} \, da - [I]_0 \frac{(K\gamma)^k}{k!} t^k e^{-K\gamma t} \right). \tag{4.5}$$

These equations suggest the relations

$$[I_j](t) = \int_0^t \tau[SI](t-a) \frac{(K\gamma)^{j-1}}{(j-1)!} a^{j-1} e^{-K\gamma a} \, da + [I]_0 \frac{(K\gamma)^{j-1}}{(j-1)!} t^{j-1} e^{-K\gamma t}, \quad j = 1,2,\ldots,K. \tag{4.6}$$

To show this, we consider the equations for infectious stages in (4.3) as first-order, linear differential equation with variation of constants formulae:

$$[I_1](t) = [I_1](0)\, e^{-K\gamma t} + \int_0^t e^{-K\gamma(t-s)} \tau[SI](s)\, ds \tag{4.7}$$

and

$$[I_j](t) = [I_j](0)\, e^{-K\gamma t} + \int_0^t e^{-K\gamma(t-s)} K\gamma[I_{j-1}](s)\, ds, \quad j = 2, 3, \ldots, K. \tag{4.8}$$

If all infecteds are newborn, we have $[I_1](0) = [I]_0$ and $[I_2](0) = [I_3](0) = \cdots = [I_K](0) = 0$. Proceeding by induction yields that (4.6) satisfies (4.7) for $j = 1$ and (4.8) for $j = 2, 3, \ldots, K$ (for details, see appendix Ad). It is analogous to derive the equations for $[SI_j](t)$.

(d) Uniform distribution on interval $[A, B]$

The uniform distribution is one of the most natural probability distributions and preferred in agent-based modelling [37], and was applied also for avian influenza [38]. Let the recovery time be distributed uniformly on interval $[A, B]$ (we assume $0 < A < B$), i.e.

$$f(t) = \begin{cases} \dfrac{1}{B-A} & \text{if } t \in (A, B), \\ 0 & \text{otherwise} \end{cases}$$

and

$$\xi(t) = \begin{cases} 1 & \text{if } t \le A, \\ \dfrac{B-t}{B-A} & \text{if } t \in (A, B), \\ 0 & \text{if } t \ge B. \end{cases}$$

We have to study the three cases $t < A$, $A < t < B$ and $t > B$. Writing the equation for $[\dot{I}](t)$, we have (after changing the variable)

$$[\dot{I}](t = \tau[SI](t) - \begin{cases} 0 & \text{if } t < A, \\ \displaystyle\int_0^{t-A} \dfrac{\tau[SI](u)}{B-A}\, du + \dfrac{[I]_0}{B-A} & \text{if } t \in [A, B], \\ \displaystyle\int_{t-B}^{t-A} \dfrac{\tau[SI](u)}{B-A}\, du & \text{if } t > B. \end{cases}$$

With a more compact notation,

$$[\dot{I}](t) = \tau[SI](t) - \int_{\max(0,t-B)}^{\max(0,t-A)} \dfrac{\tau[SI](u)}{B-A}\, du - \dfrac{[I]_0}{B-A}\chi_{[A,B]}(t),$$

where $\chi_{[A,B]}(t)$ is the indicator function of interval $[A, B]$. The same argument gives

$$[\dot{SI}](t) = \tau\dfrac{n-1}{n}\dfrac{[SS](t)[SI](t)}{[S](t)} - \tau\dfrac{n-1}{n}\dfrac{[SI](t)}{[S](t)}[SI](t) - \tau[SI](t)$$

$$- \int_{\max(0,t-B)}^{\max(0,t-A)} \dfrac{\tau}{B-A}\dfrac{n-1}{n}\dfrac{[SS](u)[SI](u)}{[S](u)}\, e^{-\int_u^t \tau((n-1)/n)([SI](s)/[S](s)) + \tau\, ds}\, du$$

$$- \dfrac{n}{N}[S]_0\, e^{-\int_0^t \tau((n-1)/n)([SI](s)/[S](s)) + \tau\, ds}\dfrac{[I]_0}{B-A}\chi_{[A,B]}(t).$$

For $t > B$, the model becomes a system of differential equations with distributed delays.

5. Discussion

While the main focus of this paper is on the derivation and rigorous analysis of the model, we have performed a number of numerical tests where the results of explicit stochastic network

simulations on networks are compared to the output from the generalized pairwise model. In figure 1a, regular random networks were considered and the average of 100 simulations is compared to the numerical solutions of mean-field (2.7) and pairwise (2.6) models. Several observations can be made: (i) the agreement of the simulation results with the numerical solution of the pairwise model is excellent and (ii) the mean-field model, which largely ignores the network structure, performs poorly. We note that distributions with the same mean but smaller variance lead to epidemics that grow faster initially (see also [15,39]). We emphasize that a key strength of our model is to approximate the whole time course of the epidemic. Furthermore, in figure 1b,c we test if the analytical threshold (3.9) and final epidemic size formula (3.24) are accurate when compared to simulations. These clearly demonstrate that our analytical results agree with simulations, and this gives us great confidence that the generalized pairwise model can and will be used in different contexts as dictated by empirical or other theoretical studies.

The generalized model is more challenging to analyse due to its complexity, but it largely relies on tools from the theory of integro-differential equations. Further extensions of the model could focus on relaxing the assumption of regular networks and extend the model to networks with heterogeneous degree distribution (e.g. [40,41]) or to consider modelling the situation where both the infectious and recovery processes are non-Markovian.

Our pairwise model is developed for regular networks where each node has the same number of links. It is well known that such ODE-based models will also provide good approximations if epidemics are considered on Erdős–Rényi networks with the same mean, due to the efficient mixing within the network. It will, however, fail to provide good agreement for networks with highly heterogeneous degrees even if the mean is the same. Our proposed model, as most pairwise models and models based on the message-passing approach and edge-based compartmental models, are primarily designed for Configuration Model networks, and thus with clustering going to zero in the limit of large networks. Extending any of these to clustered networks is still a major challenge and has so far been only done when clustering is introduced in a very specific way, e.g. non-overlapping triangles or other clustering inducing subgraphs or motifs [42,43]. Pairwise models for Markovian epidemics and for infectious periods of a fixed length can be extended to heterogeneous networks, at the cost of a much larger number of equations. Thus, our general model may require us to start with a system of PDEs with many equations to capture degree heterogeneity. We foresee that while this may be possible, it would probably involve highly complex and technical calculations. Potentially, a more natural extension of our model would be to relax the assumption of Markovian transmission, and this is indeed a more promising future research direction. We note that Wilkinson et al. [44] have independently derived a similar pairwise model by starting from the message-passing system [18], assuming that the initial distribution of infected nodes is $\xi(a) = [I]_0 \delta(a)$. However, our model can handle arbitrary initial conditions.

Several different approaches exist to model non-Markovian epidemics on networks. These are largely guided by the choice of model and variables to be tracked. Notable examples include the message-passing approach, often referred to as the cavity model [18,19], the edge-based compartmental model [45], which has recently been generalized to arbitrary infection and recovery processes, and the percolation-based approach [1,16,17,46]. While the latter only offers information about the final state of the epidemic, the former two describes the temporal evolution of the epidemic. Generalizations of the pairwise model to gamma-distributed infectious periods have also been proposed and this has been developed for both homogeneous and heterogeneous networks [35,40]. As for Markovian epidemics, we expect that many of the models mentioned above are complementary and offer different perspectives on the time evolution or final state of the epidemic. We expect that many of the non-Markovian models will in fact be equivalent under appropriately chosen initial conditions and appropriate averaging. With the model we proposed in this paper, we wanted to emphasize opportunities to frame models of epidemics on networks in more rigorous mathematical terms and use existing mathematical theory to enhance our understanding of stochastic processes on networks and their average behaviour as captured by mean-field models.

Appendix A

(a) Calculations for model derivation

Repeating equation (2.1a) and applying the moment-closure formula (2.4) to equation (2.1c), we have

$$[\dot{S}](t) = -\tau[SI](t)$$

and

$$[\dot{SS}](t) = -2\tau \frac{n-1}{n} \frac{[SS](t)[SI](t)}{[S](t)}.$$

Using $[I](t) = \int_0^\infty i(t, a)\, da$, from equation (2.1b) we obtain

$$[\dot{I}](t) = \int_0^\infty \frac{\partial}{\partial t} i(t, b)\, db = \int_0^\infty \left(-h(b)i(t, b) - \frac{\partial}{\partial b} i(t, b) \right) db$$

$$= -\int_0^\infty h(b)i(t, b)\, db - (i(t, \infty) - i(t, 0)) = -\int_0^\infty h(b)i(t, b)\, db - i(t, \infty) + i(t, 0). \quad \text{(A 1)}$$

Solving the first-order linear PDE (2.1b) along characteristic lines, we obtain

$$i(t, a) = \begin{cases} i(t - a, 0)\, e^{-\int_0^a h(b)\, db}, & \text{if } t > a; \\ i(0, a - t)\, e^{-\int_{a-t}^a h(b)\, db}, & \text{if } t \leq a. \end{cases}$$

Plugging (2.2a) and (2.3a) into the solution above, we have

$$i(t, a) = \begin{cases} \tau[SI](t - a)\, e^{-\int_0^a h(b)\, db}, & \text{if } t > a; \\ \varphi(a - t)\, e^{-\int_{a-t}^a h(b)\, db}, & \text{if } t \leq a. \end{cases} \quad \text{(A 2)}$$

Applying this formula for $[I](t) = \int_0^\infty i(t, a)\, da$, we find

$$[I](t) = \int_0^t \tau[SI](t - a)\, e^{-\int_0^a h(b)\, db}\, da + \int_t^\infty \varphi(a - t)\, e^{-\int_{a-t}^a h(b)\, db}\, da. \quad \text{(A 3)}$$

Finally, using that along the characteristic lines, $i(t, \infty) = i(0, \infty) = \varphi(\infty) = 0$ from the assumption, substituting (A 2) and the boundary condition (2.2a) into (A 1), we get

$$[\dot{I}](t) = \tau[SI](t) - \int_0^t \tau[SI](t - a)h(a)\, e^{-\int_0^a h(b)\, db}\, da - \int_t^\infty \varphi(a - t)h(a)\, e^{-\int_{a-t}^a h(b)\, db}\, da. \quad \text{(A 4)}$$

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Using the definition and properties of the hazard function, we can deduce the following formulae:

$$e^{-\int_0^a h(b)\,db} = \frac{\xi(a)}{\xi(0)} = \xi(a), \tag{A 5a}$$

$$e^{-\int_{a-t}^a h(b)\,db} = \frac{\xi(a)}{\xi(a-t)}, \tag{A 5b}$$

$$h(a)\,e^{-\int_0^a h(b)\,db} = f(a) \tag{A 5c}$$

and

$$h(a)\,e^{-\int_{a-t}^a h(b)\,db} = \frac{f(a)}{\xi(a-t)}. \tag{A 5d}$$

Applying these formulae to equations (A 3) and (A 4), we have

$$[I](t) = \int_0^t \tau[SI](t-a)\xi(a)\,da + \int_t^\infty \varphi(a-t)\frac{\xi(a)}{\xi(a-t)}\,da \tag{A 6}$$

and

$$[\dot{I}](t) = \tau[SI](t) - \int_0^t \tau[SI](t-a)f(a)\,da - \int_t^\infty \varphi(a-t)\frac{f(a)}{\xi(a-t)}\,da. $$

To compute the equation for $[SI](t)$, we follow the calculation process above. First, applying (2.5) to equation (2.1d), we get

$$\left(\frac{\partial}{\partial t} + \frac{\partial}{\partial a}\right) Si(t,a) = -\frac{\tau(n-1)}{n}\frac{[SI](t)}{[S](t)}Si(t,a) - (\tau + h(a))Si(t,a). \tag{A 7}$$

Using $[SI](t) = \int_0^\infty Si(t,a)\,da$, from equation (A 7) we find

$$[\dot{SI}](t) = \int_0^\infty \frac{\partial}{\partial t}Si(t,a)\,da$$

$$= \int_0^\infty \left(-\frac{\tau(n-1)}{n}\frac{[SI](t)}{[S](t)}Si(t,a)\right)da - \int_0^\infty (\tau + h(a))Si(t,a)\,da - \int_0^\infty \frac{\partial}{\partial a}Si(t,a)\,da$$

$$= -\tau\frac{n-1}{n}\frac{[SI](t)}{[S](t)}[SI](t) - \tau[SI](t) - \int_0^\infty h(a)Si(t,a)\,da - Si(t,\infty) + Si(t,0). \tag{A 8}$$

We want to express the variable $Si(t,a)$ as a function of classical network variables. To achieve this, let us consider the following first-order PDE:

$$\left(\frac{\partial}{\partial t} + \frac{\partial}{\partial a}\right) x(t,a) = -f(t)x(t,a) - g(a)x(t,a)$$

with boundary conditions

$$x(t,0) = \phi(t), \quad x(0,a) = \psi(a).$$

Solving along the characteristic lines $t - a = c$, we find that

$$x(t,a) = \begin{cases} \phi(t-a)\,e^{-\int_{t-a}^t f(s)\,ds}\,e^{-\int_0^a g(b)\,db}, & \text{if } t > a; \\ \psi(a-t)\,e^{-\int_0^t f(s)\,ds}\,e^{-\int_{a-t}^a g(b)\,db}, & \text{if } t \le a. \end{cases} \tag{A 9}$$

In our case, $x(t,a) = Si(t,a)$, $f(t) = \tau((n-1)/n)([SI](t)/[S](t))$, $g(a) = \tau + h(a)$, $\phi(t) = \tau((n-1)/n)$ $([SS](t)[SI](t)/[S](t))$ (from closure approximation (2.5)) and $\psi(a) = (n/N)[S]_0\varphi(a)$, hence from (A 9) we get

$$Si(t,a) = \begin{cases} \tau\dfrac{n-1}{n}\dfrac{[SS](t-a)[SI](t-a)}{[S](t-a)}\,e^{-\int_{t-a}^t \tau((n-1)/n)([SI](s)/[S](s))\,ds}\,e^{-\int_0^a \tau+h(b)\,db}, & \text{if } t > a; \\[4mm] \dfrac{n}{N}[S]_0\varphi(a-t)\,e^{-\int_0^t \tau(n-1)/n)([SI](s)/[S](s))\,ds}\,e^{-\int_{a-t}^a \tau+h(b)\,db}, & \text{if } t \le a. \end{cases} \tag{A 10}$$

Again, along the characteristic lines $Si(t, \infty) = Si(0, \infty) = \chi(\infty) = 0$. Putting (A 10) into $[SI](t) = \int_0^\infty Si(t, a)\,da$, we obtain

$$[SI](t) = \int_0^t \tau \frac{n-1}{n} \frac{[SS](t-a)[SI](t-a)}{[S](t-a)} e^{-\int_{t-a}^t \tau((n-1)/n)([SI](s)/[S](s))\,ds} e^{-\int_0^a \tau + h(b)\,db}\,da$$
$$+ \int_t^\infty \frac{n}{N}[S]_0 \varphi(a-t) e^{-\int_0^t \tau((n-1)/n)([SI](s)/[S](s))\,ds} e^{-\int_{a-t}^a \tau + h(b)\,db}\,da. \qquad (A\ 11)$$

If we substitute (A 10) back into equation (A 8), we obtain

$$[\dot{SI}](t) = \tau \frac{n-1}{n} \frac{[SS](t)[SI](t)}{[S](t)} - \frac{\tau(n-1)}{n} \frac{[SI](t)}{[S](t)}[SI](t) - \tau[SI](t)$$
$$- \int_0^t \tau \frac{n-1}{n} \frac{[SS](t-a)[SI](t-a)}{[S](t-a)} e^{-\int_{t-a}^t \tau((n-1)/n)([SI](s)/[S](s))\,ds} e^{-\int_0^a \tau + h(b)\,db} h(a)\,da$$
$$- \int_t^\infty \frac{n}{N}[S]_0 \varphi(a-t) e^{-\int_0^t \tau((n-1)/n)([SI](s)/[S](s))\,ds} e^{-\int_{a-t}^a \tau + h(b)\,db} h(a)\,da. \qquad (A\ 12)$$

Applying the formulae (A 5a–d) in equations (A 11) and (A 12), we have

$$[SI](t) = \int_0^t \tau \frac{n-1}{n} \frac{[SS](t-a)[SI](t-a)}{[S](t-a)} e^{-\int_{t-a}^t \tau((n-1)/n)([SI](s)/[S](s)) + \tau\,ds} \xi(a)\,da$$
$$+ \int_t^\infty \frac{n}{N}[S]_0 \varphi(a-t) e^{-\int_0^t \tau((n-1)/n)([SI](s)/[S](s)) + \tau\,ds} \frac{\xi(a)}{\xi(a-t)}\,da \qquad (A\ 13)$$

and

$$[\dot{SI}](t) = \tau \frac{n-1}{n} \frac{[SS](t)[SI](t)}{[S](t)} - \tau \frac{n-1}{n} \frac{[SI](t)}{[S](t)}[SI](t) - \tau[SI](t)$$
$$- \int_0^t \tau \frac{n-1}{n} \frac{[SS](t-a)[SI](t-a)}{[S](t-a)} e^{-\int_{t-a}^t \tau((n-1)/n)([SI](s)/[S](s)) + \tau\,ds} f(a)\,da$$
$$- \int_t^\infty \frac{n}{N}[S]_0 \varphi(a-t) e^{-\int_0^t \tau((n-1/n)([SI](s)/[S](s)) + \tau\,ds} \frac{f(a)}{\xi(a-t)}\,da.$$

(b) Calculation for final size relation (3.13)

In this section, we show the steps of going from (3.16) to (3.17):

$$\ln\left(\frac{S(\infty)}{S(0)}\right) = -\left(\tau \frac{n}{N}\right)^2 \int_0^\infty \int_0^u S(u-a)I(u-a)\xi(a)\,da\,du$$
$$= -\left(\tau \frac{n}{N}\right)^2 \int_0^\infty \int_0^u S(v)I(v)\xi(u-v)\,dv\,du = -\left(\tau \frac{n}{N}\right)^2 \int_0^\infty \int_v^\infty S(v)I(v)\xi(u-v)\,du\,dv$$
$$= -\left(\tau \frac{n}{N}\right)^2 \int_0^\infty S(v)I(v)\left[\int_v^\infty \xi(u-v)\,du\right]dv = -\left(\tau \frac{n}{N}\right)^2 \int_0^\infty S(v)I(v)\left[\int_0^\infty \xi(p)\,dp\right]dv$$
$$= \tau \frac{n}{N}\left[\int_0^\infty \xi(p)\,dp\right](S(\infty) - S(0)) = \tau \frac{n}{N}\left[\int_0^\infty \int_p^\infty f(q)\,dq\,dp\right](S(\infty) - S(0))$$
$$= \tau \frac{n}{N}\left[\int_0^\infty \int_0^q f(q)\,dp\,dq\right](S(\infty) - S(0)) = \tau \frac{n}{N}\left[\int_0^\infty qf(q)\,dq\right](S(\infty) - S(0))$$
$$= \tau \frac{n}{N}\mathbb{E}(\mathcal{I})(S(\infty) - S(0)).$$

(c) Calculation for final size relation (3.18)

We compute the integrals that appear on the right-hand side of equation (3.22). For the first one, we have

$$I_1 = \int_0^\infty \frac{[SI](0)}{[S]^{(n-1)/n}(0)} e^{-\tau u}\, du = \frac{[SI](0)}{[S]^{(n-1)/n}(0)} \left[\frac{e^{-\tau u}}{-\tau}\right]_0^\infty = \frac{[SI](0)}{[S]^{(n-1)/n}(0)} \frac{1}{\tau}.$$

After some algebraic manipulation, we obtain the following expression for the second integral I_2:

$$I_2 = \int_0^\infty \int_0^u \tau\kappa[S]^{-1/n}(c)[SI](c)\, e^{\tau c}\, e^{-\tau u}\, dc\, du = \int_0^\infty \int_c^\infty \tau\kappa[S]^{-1/n}(c)[SI](c)\, e^{\tau c}\, e^{-\tau u}\, du\, dc$$

$$= \int_0^\infty \tau\kappa[S]^{-1/n}(c)[SI](c)\, e^{\tau c} \left[\frac{e^{-\tau u}}{-\tau}\right]_c^\infty dc = \int_0^\infty \tau\kappa[S]^{-1/n}(c)[SI](c)\, e^{\tau c}\frac{e^{-\tau c}}{\tau}\, dc$$

$$= -\frac{1}{\tau}\kappa \int_0^\infty [S]^{-\frac{1}{n}}(c)[\dot{S}](c)\, dc = -\frac{1}{\tau}\kappa\frac{n}{n-1}\left([S]_\infty^{(n-1)/n} - [S]_0^{(n-1)/n}\right).$$

The most challenging one is the third integral I_3:

$$I_3 = \int_0^\infty \int_0^u \int_0^c \tau\kappa[S]^{-1/n}(c-a)[SI](c-a)f(a)\, e^{-\tau a}\, e^{\tau c}\, e^{-\tau u}\, da\, dc\, du$$

$$= \int_0^\infty \int_c^\infty \int_0^c \tau\kappa[S]^{-1/n}(c-a)[SI](c-a)f(a)\, e^{-\tau a}\, e^{\tau c}\, e^{-\tau u}\, da\, du\, dc$$

$$= \int_0^\infty \int_0^c \int_c^\infty \tau\kappa[S]^{-1/n}(c-a)[SI](c-a)f(a)\, e^{-\tau a}\, e^{\tau c}\, e^{-\tau u}\, du\, da\, dc$$

$$= \int_0^\infty \int_0^c \tau\kappa[S]^{-1/n}(c-a)[SI](c-a)f(a)\, e^{-\tau a}\, e^{\tau c} \left[\frac{e^{-\tau u}}{-\tau}\right]_c^\infty da\, dc$$

$$= \frac{1}{\tau} \int_0^\infty \int_0^c \tau\kappa[S]^{-1/n}(c-a)[SI](c-a)f(a)\, e^{-\tau a}\, da\, dc$$

$$= -\frac{1}{\tau}\kappa \int_0^\infty f(a)\, e^{-\tau a} \left[\frac{[S]^{(n-1)/n}(c-a)}{(n-1)/n}\right]_a^\infty da$$

$$= -\frac{1}{\tau}\kappa\frac{n}{n-1}([S]_\infty^{(n-1)/n} - [S]_0^{(n-1)/n}) \int_0^\infty f(a)\, e^{-\tau a}\, da.$$

For the fourth integral, we get

$$I_4 = \int_0^\infty \int_0^u \int_c^\infty \frac{n}{N}[S]_0^{1/n}\varphi(a-c)\frac{f(a)}{\xi(a-c)}\, e^{-\tau u}\, da\, dc\, du$$

$$= \int_0^\infty \int_c^\infty \int_c^\infty \frac{n}{N}[S]_0^{1/n}\varphi(a-c)\frac{f(a)}{\xi(a-c)}\, e^{-\tau u}\, da\, du\, dc$$

$$= \int_0^\infty \int_c^\infty \int_c^\infty \frac{n}{N}[S]_0^{1/n}\varphi(a-c)\frac{f(a)}{\xi(a-c)}\, e^{-\tau u}\, du\, da\, dc$$

$$= \int_0^\infty \int_c^\infty \frac{n}{N}[S]_0^{1/n}\varphi(a-c)\frac{f(a)}{\xi(a-c)}\left[\frac{e^{-\tau u}}{-\tau}\right]_c^\infty da\, dc$$

$$= \frac{1}{\tau} \int_0^\infty \int_c^\infty \frac{n}{N}[S]_0^{1/n}\varphi(a-c)\frac{f(a)}{\xi(a-c)}\, e^{-\tau c}\, da\, dc.$$

Having a small amount of initial infecteds (i.e. $[I](0) = \int_0^\infty \varphi(a)\, da \ll 1$), the integrals I_1 and I_4 are approximately zero.

(d) Calculations for proof of equivalence in the case of gamma distribution

Here, we obtain the formula (4.6) by induction from variation of constants formulae (4.7) and (4.8). Letting $j = 1$ in (4.6), we have

$$[I_1](t) = \int_0^t \tau[SI](t-a) \, e^{-K\gamma a} \, da + [I]_0 \, e^{-K\gamma t},$$

which comes directly from (4.7). Assuming that (4.6) holds for $1 < j$, we prove that it holds for $j + 1$. Indeed, we can do the following elaboration:

$$[I_{j+1}](t) = [I_{j+1}](0) \, e^{-K\gamma t} + \int_0^t e^{-K\gamma(t-s)} K\gamma [I_j](s) \, ds$$

$$= \int_0^t e^{-K\gamma(t-s)} K\gamma \left(\int_0^s \tau[SI](s-a) \frac{(K\gamma)^{j-1}}{(j-1)!} a^{j-1} \, e^{-K\gamma a} \, da + [I]_0 \frac{(K\gamma)^{j-1}}{(j-1)!} s^{j-1} \, e^{-K\gamma s} \right) ds$$

$$= \int_0^t \frac{(K\gamma)^j}{(j-1)!} e^{-K\gamma(t-s)} \left(\int_0^s \tau[SI](s-a) a^{j-1} \, e^{-K\gamma a} \, da \, ds \right) + [I]_0 \frac{(K\gamma)^j}{(j-1)!} e^{-K\gamma t} \int_0^t s^{j-1} \, ds$$

$$= \int_0^t \frac{(K\gamma)^j}{(j-1)!} e^{-K\gamma(t-s)} \left(\int_0^s \tau[SI](u)(s-u)^{j-1} \, e^{-K\gamma(s-u)} \, du \right) ds + [I]_0 \frac{(K\gamma)^j}{j!} t^j \, e^{-K\gamma t}$$

$$= \int_0^t \frac{(K\gamma)^j}{(j-1)!} e^{-K\gamma(t-u)} \tau[SI](u) \left(\int_u^t (s-u)^{j-1} \, ds \right) du + [I]_0 \frac{(K\gamma)^j}{j!} t^j \, e^{-K\gamma t}$$

$$= \int_0^t \tau[SI](u) \frac{(K\gamma)^j}{j!} (t-u)^j \, e^{-K\gamma(t-u)} \, du + [I]_0 \frac{(K\gamma)^j}{j!} t^j \, e^{-K\gamma t}$$

$$= \int_0^t \tau[SI](t-a) \frac{(K\gamma)^j}{j!} a^j \, e^{-K\gamma a} \, da + [I]_0 \frac{(K\gamma)^j}{j!} t^j \, e^{-K\gamma t}.$$

(e) Implementation of numerical simulations

As a validation of our models, we implemented an event-based stochastic algorithm for simulating non-Markovian SIR process with arbitrary recovery time. In the code, the waiting times for possible events are generated from appropriate distributions. After selecting the smallest waiting time, the associated event (infection or recovery) happens, and according to the type of event, the necessary updates are executed.

For the numerical solution of integro-differential equations (2.6) and (2.7), we developed a numerical scheme based on collocation method. The numerical methods in [47] were adapted to the reduced, but highly nonlinear pairwise system, having the following general form:

$$x'(t) = f(x(t), y(t))$$

and
$$y'(t) = g(x(t), y(t)) - \int_0^t F(t-a, x(a), y(a)) \, e^{-\int_a^t G(x(s), y(s)) \, ds} \, da$$
$$\qquad\qquad - H\left(t, \int_0^t G(x(s), y(s)) \, ds \right). \tag{A 14}$$

A collocation solution u_h to a functional equation on an interval I is an element from some finite-dimensional function space (the collocation space) which satisfies the equation on an appropriate finite subset of points in I (the set of collocation points), whose cardinality essentially matches the dimension of the collocation space. For integro-differential equations, the collocation equations are not yet in a form amenable to numerical computation, due to the presence of the memory term given by the integral operator, thus another discretization step, based on appropriate quadrature approximations, is necessary to obtain the fully discretized collocation scheme. The presence of the double integral in (A 14) makes our scheme different from standard methods.

References

1. Newman MEJ. 2002 Spread of epidemic disease on networks. *Phys. Rev. E* **66**, 016128. (doi:10.1103/PhysRevE.66.016128)
2. Newman MEJ. 2003 The structure and function of complex networks. *SIAM Rev.* **45**, 167–256. (doi:10.1137/S003614450342480)
3. Keeling MJ, Eames KTD. 2005 Networks and epidemic models. *J. R. Soc. Interface* **2**, 295–307. (doi:10.1098/rsif.2005.0051)
4. Boccaletti S, Latora V, Moreno Y, Chavez M, Hwang D-U. 2006 Complex networks: structure and dynamics. *Phys. Rep.* **424**, 175–308. (doi:10.1016/j.physrep.2005.10.009)
5. Kiss IZ, Miller JC, Simon PL. 2017 *Mathematics of epidemics on networks: from exact to approximate models*, vol. 46. IAM Series. Berlin, Germany: Springer.
6. Keeling MJ. 1999 The effects of local spatial structure on epidemiological invasions. *Proc. R. Soc. Lond. B* **266**, 859–867. (doi:10.1098/rspb.1999.0716)
7. Kiss IZ, Röst G, Vizi Z. 2015 Generalization of pairwise models to non-Markovian epidemics on networks. *Phys. Rev. Lett.* **115**, 078701. (doi:10.1103/PhysRevLett.115.078701)
8. Pastor-Satorras R, Castellano C, Van Mieghem P, Vespignani A. 2015 Epidemic processes in complex networks. *Rev. Mod. Phys.* **87**, 925. (doi:10.1103/RevModPhys.87.925)
9. Keeling MJ, Grenfell BT. 2002 Understanding the persistence of measles: reconciling theory, simulation and observation. *Proc. R. Soc. Lond. B* **269**, 335–343. (doi:10.1098/rspb.2001.1898)
10. Lloyd AL. 2001 Realistic distributions of infectious periods in epidemic models: changing patterns of persistence and dynamics. *Theor. Popul. Biol.* **60**, 59–71. (doi:10.1006/tpbi.2001.1525)
11. Boguná M, Lafuerza LF, Toral R, Serrano MA. 2014 Simulating non-Markovian stochastic processes. *Phys. Rev. E* **90**, 042108. (doi:10.1103/PhysRevE.90.042108)
12. Cooper F. 2013 Non-Markovian network epidemics. MA thesis, University of Warwick, Warwick, UK. See www.dtc.ox.ac.uk/people/13/cooperf/files/MA469ThesisFergusCooper.pdf.
13. Jo H-H, Perotti JI, Kaski K, Kertész J. 2014 Analytically solvable model of spreading dynamics with non-Poissonian processes. *Phys. Rev. X* **4**, 011041. (doi:10.1103/PhysRevX.4.011041)
14. Min B, Goh KI, Kim IM. 2013 Suppression of epidemic outbreaks with heavy-tailed contact dynamics. *Europhys. Lett.* **103**, 50002. (doi:10.1209/0295-5075/103/50002)
15. Ball F, Sirl D, Trapman P. 2010 Analysis of a stochastic SIR epidemic on a random network incorporating household structure. *Math. Biosci.* **224**, 53–73. (doi:10.1016/j.mbs.2009.12.003)
16. Kenah E, Robins JM. 2007 Second look at the spread of epidemics on networks. *Phys. Rev. E* **76**, 036113. (doi:10.1103/PhysRevE.76.036113)
17. Miller JC. 2007 Epidemic size and probability in populations with heterogeneous infectivity and susceptibility. *Phys. Rev. E* **76**, 010101(R). (doi:10.1103/PhysRevE.76.010101)
18. Karrer B, Newman MEJ. 2010 Message passing approach for general epidemic models. *Phys. Rev. E* **82**, 016101. (doi:10.1103/PhysRevE.82.016101)
19. Wilkinson RR, Sharkey KJ. 2014 Message passing and moment closure for susceptible-infected-recovered epidemics on finite networks. *Phys. Rev. E* **89**, 022808. (doi:10.1103/PhysRevE.89.022808)
20. Miller JC, Slim A, Volz EM. 2012 Edge-based compartmental modelling for infectious disease spread. *J. R. Soc. Interface* **9**, 890–906. (doi:10.1098/rsif.2011.0403)
21. Barbour A, Reinert G. 2013 Approximating the epidemic curve. *Electron. J. Probab.* **18**, paper 54. (doi:10.1214/ejp.v18-2557)
22. Decreusefond L, Dhersin J-S, Moyal P, Tran VC. 2012 Large graph limit for an SIR process in random network with heterogeneous connectivity. *Ann. Appl. Probab.* **22**, 541–575. (doi:10.1214/11-AAP773)
23. Janson S, Luczak M, Windridge P. 2014 Law of large numbers for the SIR epidemic on a random graph with given degrees. *Random Struct. Algorithms* **45**, 724–761. (doi:10.1002/rsa.20575)
24. Miller JC, Kiss IZ. 2014 Epidemic spread in networks: existing methods and current challenges. *Math. Model. Nat. Phenom.* **9**, 4–42. (doi:10.1051/mmnp/20149202)
25. Taylor TJ, Kiss IZ. 2014 Interdependency and hierarchy of exact and approximate epidemic models on networks. *J. Math. Biol.* **69**, 182–211. (doi:10.1007/s00285-013-0699-x)
26. Sharkey KJ, Fernandez C, Morgan KL, Peeler E, Thrush M, Turnbull JF, Bowers RG. 2006 Pair-level approximations to the spatio-temporal dynamics of epidemics on asymmetric contact networks. *J. Math. Biol.* **53**, 61–85. (doi:10.1007/s00285-006-0377-3)

27. Rattana P, Miller JC, Kiss IZ. 2014 Pairwise and edge-based models of epidemic dynamics on correlated weighted networks. *Math. Model. Nat. Phenom.* **9**, 58–81. (doi:10.1051/mmnp/20149204)
28. Rand DA. 1999 Correlation equations and pair approximations for spatial ecologies. In *Advanced ecological theory: principles and applications* (ed. J McGlade), ch. 4, pp. 100–142. Oxford, UK: Blackwell Science Ltd.
29. Spohn. H. 2012 *Large scale dynamics of interacting particles*. Berlin, Germany: Springer Science & Business Media.
30. Volz E. 2008 SIR dynamics in random networks with heterogeneous connectivity. *J. Math. Biol* **56**, 293–310. (doi:10.1007/s00285-007-0116-4)
31. Taylor M, Simon PL, Green DM, House T, Kiss IZ. 2012 From Markovian to pairwise epidemic models and the performance of moment closure approximations. *J. Math. Biol* **64**, 1021–1042. (doi:10.1007/s00285-011-0443-3)
32. Meyers L. 2007 Contact network epidemiology: bond percolation applied to infectious disease prediction and control. *Bull. AMS* **44**, 63–86. (doi:10.1090/S0273-0979-06-01148-7)
33. Brauer F. 2008 Age-of-infection and the final size relation. *Math. Biosci. Eng.* **5**, 681–690. (doi:10.3934/mbe.2008.5.681)
34. Diekmann O, DeJong MCM, Metz JAJ. 1998 A deterministic epidemic model taking account of repeated contacts between the same individuals. *J. App. Probab.* **35**, 448–462. (doi:10.1017/S0021900200015072)
35. Sherborne N, Blyuss KB, Kiss IZ. 2015 Dynamics of multi-stage infections on networks. *Bull. Math. Biol.* **77**, 1909–1933. (doi:10.1007/s11538-015-0109-1)
36. Bailey N. 1956 On the latent and infectious period of measles. *Biometrika* **43**, 15–22. (doi:10.1093/biomet/43.1-2.15)
37. Laskowski M, Mostago-Guidolin LC, Greer AL, Wu J, Moghadas SM. 2011 The impact of demographic variables on disease spread: influenza in remote communities. *Sci. Rep.* **1**, 105. (doi:10.1038/srep00105)
38. Yang Y, Halloran ME, Sugimoto JD, Longini Jr. IM. 2007 Detecting human-to-human transmission of avian influenza A (H5N1). *Emerg. Infect. Dis.* **13**, 1348–1353. (doi:10.3201/eid1309.070111)
39. Röst G, Vizi Z, Kiss IZ. 2016 Impact of non-Markovian recovery on network epidemics. In *BIOMAT 2015* (ed. RP Mondaini), pp. 40–53. Singapore: World Scientific.
40. Sherborne N, Blyuss KB, Kiss IZ. 2016 Compact pairwise models for epidemics with multiple infectious stages on degree heterogeneous and clustered networks. *J. Theor. Biol* **407**, 387–400. (doi:10.1016/j.jtbi.2016.07.015)
41. Simon. PL, Kiss IZ. 2016 Super compact pairwise model for SIS epidemic on heterogeneous networks. *J. Complex Netw.* **4**, 187–200. (doi:10.1093/comnet/cnv018)
42. Newman MEJ. 2009 Random graphs with clustering. *Phys. Rev. Lett.* **103**, 058701. (doi:10.1103/PhysRevLett.103.058701)
43. Volz EM, Miller JC, Galvani A, Meyers LA. 2011 Effects of heterogeneous and clustered contact patterns on infectious disease dynamics. *PLoS Comput. Biol.* **7**, e1002042. (doi:10.1371/journal.pcbi.1002042)
44. Wilkinson RR, Ball FG, Sharkey KJ. 2017 The relationship between message passing, pairwise, Kermack-McKendrick and stochastic SIR epidemic models. *J. Math. Biol.* **75**, 1563–1590. (doi:10.1007/s00285-017-1123-8)
45. Sherborne N, Miller JC, Blyuss KB, Kiss IZ. 2017 Mean-field models for non-Markovian epidemics on networks. *J. Math. Biol.* **76**, 755–778. doi:10.1007/s00285-017-1155-0)
46. Miller JC. 2008 Bounding the size and probability of epidemics on networks. *J. Appl. Probab.* **45**, 498–512. (doi:10.1017/S0021900200004381)
47. Brunner H. 2004 *Collocation methods for Volterra integral and related functional differential equations*, vol. 15. Cambridge, UK: Cambridge University Press.