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Risk factors for the evolutionary emergence of pathogens

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Recent outbreaks of novel infectious diseases (e.g. SARS, influenza H1N1) have highlighted the threat of cross-species pathogen transmission. When first introduced to a population, a pathogen is often poorly adapted to its new host and must evolve in order to escape extinction. Theoretical arguments and empirical studies have suggested various factors to explain why some pathogens emerge and others do not, including host contact structure, pathogen adaptive pathways and mutation rates. Using a multi-type branching process, we model the spread of an introduced pathogen evolving through several strains. Extending previous models, we use a network-based approach to separate host contact patterns from pathogen transmissibility. We also allow for arbitrary adaptive pathways. These generalizations lead to novel predictions regarding the impact of hypothesized risk factors. Pathogen fitness depends on the host population in which it circulates, and the ‘riskiest’ contact distribution and adaptive pathway depend on initial transmissibility. Emergence probability is sensitive to mutation probabilities and number of adaptive steps required, with the possibility of large adaptive steps (e.g. simultaneous point mutations or recombination) having a dramatic effect. In most situations, increasing overall mutation probability increases the risk of emergence; however, notable exceptions arise when deleterious mutations are available.

Keywords: evolutionary epidemiology; emerging infectious diseases; multi-type branching process; mutation; contact network; mathematical model

1. INTRODUCTION

The recent outbreaks of SARS coronavirus and avian and swine influenza strains have highlighted the importance of pathogen cross-species transmission, and subsequent evolutionary adaption, in the emergence of new diseases (Woolhouse et al. 2005; Dennehy 2009). Such ‘species jumps’ have been proposed as a major source of novel pathogen introductions (Woolhouse et al. 2005; Day et al. 2006; Kuiken et al. 2006), and indeed many emerging human diseases are zoonotic (Cleaveland et al. 2001; Taylor et al. 2001). Typically, these pathogens are initially poorly adapted to humans because of physiological differences between species (Kuiken et al. 2006). Thus, significant spread of these pathogens within the human population often requires evolutionary adaptation (Dennehy 2009).

A number of risk factors have been proposed to explain why some pathogens emerge and others do not. These include the breadth of the pathogen’s host range (Cleaveland et al. 2001; Taylor et al. 2001; Woolhouse & Gaunt 2007), susceptibility of the host (Woolhouse et al. 2005; Woolhouse & Gaunt 2007), contact patterns in the host population (Woolhouse et al. 2005; Kuiken et al. 2006; Woolhouse & Gaunt 2007; Dennehy 2009), the mechanism(s) of pathogen adaptation (e.g. whether recombination is possible; Woolhouse et al. 2005), pathogen taxonomic classification (Cleaveland et al. 2001; Taylor et al. 2001), pathogen generation time (Cleaveland et al. 2001; Taylor et al. 2001) or growth rate (Dennehy 2009) and pathogen mutability (Cleaveland et al. 2001; Taylor et al. 2001; Woolhouse et al. 2005; Dennehy 2009). Indeed, empirical studies have revealed that some of these factors are often associated with emerging diseases (Cleaveland et al. 2001; Taylor et al. 2001; Woolhouse & Gaunt 2007). In particular, viruses and protozoa display a relatively high propensity for being involved in newly emerging human diseases (Cleaveland et al. 2001; Taylor et al. 2001), and the degree of transmissibility between members of the new host species also appears to be a risk factor where data are available (Taylor et al. 2001).

The association between transmissibility and likelihood of emergence is, perhaps, not surprising. Any factor that increases the expected number of transmitted infections, such as higher initial transmissibility between members of the new host species, means that the pathogen can circulate for longer after the cross-species jump, and thus has greater potential for ultimate evolutionary adaptation (Antia et al. 2003). For the same reason, patterns of contact among hosts should also play an important role in disease emergence, because some contact structures ought to lead to greater scope for transmission than others. To date, however, the most ‘risky’ patterns of host contact are not known.
The association between pathogen taxonomic classification and likelihood of emergence is less easy to explain. It has been suggested that the high incidence of emergence among viruses may be attributed, at least partially, to their high mutation rates (particularly in RNA viruses). A high mutation rate might lead to a greater likelihood of the appropriate adaptive mutations occurring, implying greater evolutionary potential (Cleaveland et al. 2001; Woolhouse et al. 2005). On the other hand, most mutations are deleterious, and a high mutation rate could thereby increase the chance of pathogen extinction (Dennely 2009). Indeed, this propensity for extinction might be exploited clinically by drug-induced ‘lethal mutagenesis’ (Anderson et al. 2004; Clementi 2008). Thus, it remains unclear whether higher mutation rates do indeed lead to a higher likelihood of evolutionary emergence, or whether other processes are required to explain the empirical patterns.

In this paper, we investigate the above factors through mathematical modelling. We ask two main questions: (i) what types of host contact structure lead to the greatest risk of evolutionary emergence? and (ii) how do patterns of mutation affect the risk of evolutionary emergence? We address these questions using a branching process model that tracks the number of infected hosts as a newly introduced pathogen spreads and evolves. There have been two main approaches to using such models in the epidemiological literature, a network-based approach and a phenomenological approach. The former explicitly considers the patterns of contact among individuals in the population and the probability of transmission through any given contact (e.g. Brauer 2008), but has not, to date, allowed for evolutionary adaptation. The latter assumes that the population is well mixed and in some cases allows for evolution, but has not explicitly modelled the contact patterns among individuals (e.g. Antia et al. 2003; Lloyd-Smith et al. 2005; Day et al. 2006; Yates et al. 2006; Reluga et al. 2007). In order to address the above questions, we place these two approaches within a common framework, generalizing to allow for arbitrary contact patterns and arbitrary pathways of evolutionary adaptation.

2. A UNIFIED MODELLING FRAMEWORK

In order to develop a unified modelling framework that encompasses both the network-based and phenomenological approaches, it is useful first to focus on single-strain models that ignore evolution.

2.1. Single-strain models

We model in discrete time, using a Galton–Watson process. To define the branching process, we require a distribution for the number of ‘offspring’ produced by each individual. In the present context, infected hosts are the individuals of interest, and an ‘offspring’ is viewed as a contact to whom the infection is transmitted. The network-based approach and the phenomenological approach arrive at this offspring distribution in different ways. The network-based approach builds up the offspring distribution from underlying assumptions about the processes of host–host contact and pathogen transmission. The phenomenological approach, on the other hand, simply specifies this offspring distribution directly, without explicit consideration of the underlying contact and transmission processes through which it might arise.

The network-based approach represents the host population by a graph: each vertex or node corresponds to an individual, and an edge between two nodes signifies that the two individuals are acquaintances, i.e. can contact and potentially transmit disease to one another. We assume that this network is static, and restrict attention to random graphs in the limit of infinite population size. In this situation, the network becomes a tree graph, with the number of ‘branches’ from each node drawn independently from the arbitrary degree, or contact, distribution (Trapman 2007 and references therein). This restriction is applied for mathematical tractability, but neglects certain realistic network properties such as loops and clustering; we return to this issue in §4.3. We refer to the individual(s) initially infected by a source outside the population as ‘generation 0’ infectives. All individuals infected by a generation $n$ infective ($n = 0, 1, \ldots$) are considered generation $n + 1$ infectives, and ‘later-generation’ infectives (i.e. generation $\geq 1$) receive their infections from other individuals within the population.

Following the derivation presented by Brauer (2008), we suppose that each node has a degree distribution $\{p_d\}$, described by the probability generating function (PGF)

$$g(z) = \sum_{d=0}^{\infty} p_d z^d.$$  

Furthermore, if we randomly choose an edge and follow it to a node, the excess degree of that node (number of other edges emanating out) has distribution $\{\tilde{p}_d\}$ given by the PGF

$$G(z) = \sum_{d=0}^{\infty} \tilde{p}_d z^d = \sum_{d=1}^{\infty} \frac{dz}{d^2} z^{d-1} = \frac{g(z)}{g(1)},$$

where $\langle d \rangle = g(1)$ denotes the expected value of degree $d$.

An infective is assumed to transmit infection to each still-susceptible contact independently with probability $T$, called the transmissibility, taken to be a constant. That is, if $d$ is the number of still-susceptible contacts, then the number of infections transmitted is distributed as Binomial($d, T$). For the initial infective, who has been infected by a source outside the population, all contacts (given by the degree) remain susceptible. Thus, the PGF $\gamma(s)$ for the number of infections transmitted by a randomly chosen initial infective is (Brauer 2008)

$$\gamma(s) = g(1 - T + Ts).$$

A later-generation infective has received the infection from one of its contacts, i.e. it has been arrived at by following a randomly chosen edge from another node. Hence, the number of still-susceptible contacts
is determined from the excess degree distribution. (We implicitly assume that an individual can only be infected once, as in an SI- or SIR-type disease.) Thus, the PGF $\Gamma(s)$ for the number of infections transmitted by a later-generation infective is

$$\Gamma(s) = G(1 - T + Ts).$$

The basic reproductive number, $R_0$, can then be defined as the mean number of infections transmitted by one typical (later-generation) infective:

$$R_0 = \Gamma'(1) = G'(1)T.$$

In this way, we can see how the disease’s reproductive number in the network-based approach is composed of the underlying processes of host–host contact (represented by $G'(1)$) and pathogen transmission (represented by $T$). $R_0$ is an appropriate measure of the fitness of a single strain of pathogen.

The phenomenological approach (e.g. Antia et al. 2003; Lloyd-Smith et al. 2005; Day et al. 2006; Yates et al. 2006; Reluga et al. 2007) does not build up the process of disease spread from a description of host contacts and pathogen transmission. Rather, it directly specifies a distribution of number of new infections, $X$, produced by an infected individual. The approach typically uses a Poisson distribution of infections, implicitly assuming homogeneous mixing in the population, but sometimes incorporates individual heterogeneity by allowing the mean of the distribution itself to be a random variable. For example, Lloyd-Smith et al. (2005) generally draw the mean, $\nu$, from a Gamma distribution with mean $R_0$ and dispersion parameter $\beta$; then $X$ has a negative binomial distribution with mean $R_0$ and dispersion $\beta$. As special cases, $\beta = 1$ corresponds to $\nu \sim \text{Exp}(R_0)$ and $X \sim \text{Geometric}(R_0)$, while $\beta \to \infty$ corresponds to $\nu \sim R_0$ (no individual variation) and $X \sim \text{Poisson}(R_0)$. In any case, the key difference from the network-based approach is that $\Gamma(s)$ is effectively specified directly. As before, the one then defines the basic reproductive number as $R_0 = \Gamma'(1)$. Notice, however, that unlike the network-based approach, no distinction is made here between generation 0 infectives, strain types, and the intervention from an outside source and later-generation infectives. (In special cases of the network model, all generations are in fact equivalent; see appendix A.2.) If one then considers only later-generation infectives, the phenomenological approach can be obtained via the network-based approach, provided that the contact distribution in the latter is chosen to obtain the same end result for the offspring distribution (appendix A.3).

For example, if the contact distribution is such that the number of still-susceptible contacts has a negative binomial distribution with mean $\lambda$ and dispersion $\beta$ (appendix A.1), i.e. $G(z) = (1 + (\lambda/\beta)(1 - z))^{-\beta}$ (Lloyd-Smith et al. 2005), then the offspring distribution will also be negative binomial with mean $\lambda T$ and dispersion $\beta$. $\Gamma(s) = G(1 - T + Ts) = (1 + (\lambda T/\beta)(1 - s))^{-\beta}$. Since $R_0 = \lambda T$, this gives exact correspondence with the phenomenological approach of Lloyd-Smith et al. (2005) described above. Other examples of contact distributions and the resulting offspring distributions are described in appendix B.1 and illustrated in figure 1.

Regardless of which approach is used to obtain the offspring distribution, the extinction probability of the process—that is, the probability that the disease outbreak eventually ends, infecting only a finite number of people—is the smallest non-negative solution of the equation $\Gamma(s) = s$. The epidemic is guaranteed to go extinct if $R_0 \leq 1$, but persists with non-zero probability if $R_0 > 1$ (Allen 2003). Recall, however, that the network-based approach also distinguishes the generation 0 infective from all others, and if this initial infective is chosen uniformly at random, then the overall extinction probability in that approach is $g(1 - T + Tq) = \gamma(q)$ (Brauer 2008).

### 2.2. Multiple strain model

A phenomenological approach has also been used to explore how pathogen evolution affects disease emergence by accounting for multiple pathogen strains (Antia et al. 2003; André & Day 2005; Day et al. 2006; Yates et al. 2006; Reluga et al. 2007). These models typically assume a Poisson distribution of infectious contacts, which, interestingly, has been found usually to be a poor fit to epidemiological data (Lloyd-Smith et al. 2005). Mathematically similar models have also been used to model evolution and ‘escape’ in a population of replicating individuals (Iwasa et al. 2003, 2004; Serra & Haccou 2007). In the most general of these, Serra & Haccou (2007) outline the model for an arbitrary offspring distribution as well as arbitrary mutation scheme and fitness landscape. However, to date, such generalizations and their implications have not been explored in the context of evolutionary epidemiology, nor have underlying mechanisms contributing to the offspring distribution been considered separately. One can readily extend the network-based framework outlined in §2.1 to investigate these questions.

We account for pathogen evolution using a multi-type branching process. An individual’s type $i$ $(i = 1, \ldots, m)$ denotes which one of the $m$ possible pathogen strains is infecting that host. We allow for arbitrary contact distribution and assume that the contact network is determined by the host, independently of the pathogen strain. Thus, as before, degree is described by the PGF $g(z)$ and the excess degree by $G(z)$ for every individual, regardless of type. We retain the assumption that transmissions occur independently to each contact, and further assume that transmissibility $T$ is strain-specific, denoted $T_i$ for strain $i$. Thus, the probability of making an infectious contact depends only on the current infective’s strain type. However, a different strain may be transmitted as a result of pathogen mutation. Specifically, given that a type $i$ infective makes an infectious contact, strain $j$ is transmitted with probability $\mu_{ij}$ $(\sum_j \mu_{ij} = 1, \forall i)$. We call the $m \times m$ matrix $U = [\mu_{ij}]$ the ‘mutation matrix’, representing the mutational pathway(s) allowed in the evolution of the pathogen and their probabilities.

We use the word ‘mutation’ loosely to mean any processes resulting in a change in the strain identified as a
host’s type. These processes actually occur within individual hosts, but we account for this in a phenomenological way. The most accurate interpretation of our approach would be that a host currently infected with strain $i$ transmits only strain $i$, but that each infective produced in the next generation has probability $m_{ij}$ of converting to strain $j$ over the course of infection, before any further transmission occurs. In this approach, $m_{ij}$ is an ‘effective conversion rate’ from strain $i$ to strain $j$ within one host, summarizing the results of within-host dynamics (§4.3). This is a common type of simplification involving a separation of the time scales on which within- and between-host processes occur. Antia et al. (2003) mention the possibility of strain conversion owing to mutation within a host, and André & Day (2005) explicitly model this in a phenomenological way; however, neither discuss the above considerations in any detail.

Returning to our multi-type process, the number of transmissions of each type made by a type $i$ infective with $d$ susceptible contacts now has distribution Multinomial$(d; 1 - T_i, T_iU_i)$, where $U_i$ is the $i$th row of $U$ and the probability vector is given in the order: no transmission, transmit strain 1, . . . , transmit strain $m$. The corresponding PGF for the number of transmitted infections of each type, $(X_1, \ldots, X_m)$, given $d$ susceptible contacts, is

$$E[s_1^{X_1} \cdots s_m^{X_m} | d] = \left(1 - T_i + T_i \sum_{j=1}^{m} \mu_{ij} s_j\right)^d.$$

Thus, extending the notation of §2.1, the PGF for number of infections transmitted by an initial infective of type $i$ is

$$\gamma_i(s_1, \ldots, s_m) = g \left(1 - T_i + T_i \sum_{j=1}^{m} \mu_{ij} s_j\right),$$

where $g(z)$ is the PGF for the offspring distribution of transmission.
and for a later generation infective, the PGF is

\[ \Gamma_i(s_1, \ldots, s_m) = G \left( 1 - T_i + T_i \sum_{j=1}^{m} \mu_j s_j \right). \]

Derivations of these PGFs appear in appendix C.

The probability of extinction starting from one later-generation infective of type \( i \), denoted \( q_i \), is obtained as the smallest non-negative root of the equation \( q_i = \Gamma_i(q_1, \ldots, q_m) \), solved simultaneously for all \( i \) (appendix D). More compactly, we can write this as a vector fixed-point equation: \( \vec{\Gamma}(\vec{q}) = \vec{q} \), where \( \vec{\Gamma} = (\Gamma_1, \ldots, \Gamma_m) \) and \( \vec{q} = (q_1, \ldots, q_m) \). Starting from a generation 0 infective of type \( i \), chosen uniformly at random, the overall probability of extinction is then given by \( G(1 - T_i + T_i \sum_{j=1}^{m} \mu_j q_j) = \gamma(\vec{q}) \) (appendix C). If we account for strain conversion as per the above interpretation, the only adjustment we must make in our calculations, assuming that strain \( i \) is introduced to a randomly chosen individual, is to allow the initial infective to be type \( j \) with probability \( \mu_{ji} \). We generally assume that strain 1 is, by definition, initially introduced to the host population.

In what follows, it is sometimes useful to refer to the ‘basic reproductive number of strain \( i \)’, denoted \( R_{0,i} \), and defined as the expected total number of infectious contacts made by a typical (later-generation) type \( i \) infective. Since this number is distributed as Binomial(\( d, T_i \)), we have

\[ R_{0,i} = E[d \cdot T_i] = G'(1) T_i. \]

If strain \( i \) were the only strain present, with no possibility of mutation, \( R_{0,i} \) would be the value of its basic reproductive number in the single-strain model.

We define emergence as the situation in which the pathogen escapes extinction, which necessarily requires evolution to a strain having \( R_{0,i} > 1 \). Probability of emergence is thus the complement of probability of extinction. We present numerical results for the probability of emergence beginning from one later-generation infective of type 1, \( 1 - q_1 \), but these results may be extended to account for generation 0 and/or type conversion as described above. Note that the branching process may be either indecomposable or decomposable, depending on the mutational scheme. Thus, if the epidemic persists, the complement of strains that will be present must be treated on a case-by-case basis (appendix D).

Our derivation so far is quite general, imposing no a priori restrictions on the choices of contact distribution, transmissibilities and mutation probabilities. However, in the numerical results to follow, we limit ourselves to specific examples.

Contact distributions. We consider the following contact distributions, each with mean \( \lambda \) (see also appendix B.1).

- Deterministic. Every individual has exactly \( \lambda \) contacts.
- Mixed deterministic. There are \( n \) types of individuals, where the \( k \)th type occurs in proportion \( p_k \) and has exactly \( \lambda_k \) contacts.
- Poisson.

Mixed Poisson. There are \( n \) types of individuals, where the \( k \)th type occurs in proportion \( p_k \) and has a Poisson(\( \lambda_k \)) distribution of contacts.
- Negative binomial, with dispersion \( \beta \).

Mutational schemes. We consider two broad types of mutational schemes: ‘linear’ and ‘hub-and-spoke’ (see also appendix B.2). In all cases, we assume that strain \( m \) is well adapted to the host; that is, \( T_m \) is chosen such that \( R_{0,m} > 1 \). On the other hand, any other strain \( i \) is poorly adapted to the host (\( R_{0,i} < 1 \)) unless otherwise specified.

Linear mutational schemes represent single directions through strain space, where strains 2, \ldots, \( m - 1 \) are intermediates between strains 1 and \( m \). We consider the following possibilities.

- One-step irreversible. The pathogen must acquire \( m - 1 \) point mutations, one at a time and in a fixed order. Thus, mutation occurs only from strain \( i \) to \( i + 1 \). This scheme is presented by Antia et al. (2003).
- Multi-step irreversible. Again the pathogen must acquire \( m - 1 \) point mutations in a fixed order, but now possibly simultaneously, implying that mutations can occur from strain \( i \) to any strain \( j > i \), though with diminishing probabilities.

Essentially, higher order terms are being included where they were neglected in the previous scheme. This scheme is presented by Gokhale et al. (2009), along with biological examples.

- Interchangeable and irreversible. This scheme, also presented by Gokhale et al. (2009), is similar to the preceding one, but allows the point mutations to be acquired in arbitrary order, introducing a combinatorial aspect to the probabilities. Thus, there are multiple evolutionary pathways between the first and last strains, with strain \( i \) in our model representing any ‘real’ strain having \( i - 1 \) of the required mutations. Our model thus implicitly assumes that any collection of \( i - 1 \) mutations yields the same transmissibility, \( T_i \).

- Point mutation and recombination. One-step point mutation occurs as in scheme 1, but we simplistically model an additional mechanism of more extensive genetic change (perhaps recombination or reassortment; Kuiken et al. 2006) by allowing any strain \( i \) to adapt directly to strain \( m \) with a probability not tied to that of point mutation. We neglect the chance of simultaneous mutational events, and all are irreversible.

- One-step reversible. In a modification of scheme 1, mutation can occur from strain \( i \) to either \( i + 1 \) or \( i - 1 \), representing both forward and reverse point mutation (again neglecting the chance of simultaneous mutations).

One-step irreversible mutations, coupled with a Poisson(\( \lambda \)) distribution of contacts, corresponds to the model of Antia et al. (2003), where \( R_{0,i} = \lambda T_i \).

Hub-and-spoke mutational schemes represent multiple distinct pathways through strain space. After strain 1 is introduced, mutation may proceed from
this ‘hub’ along a number of different ‘spokes’ (directions in strain space). Though still numbered sequentially for convenience, strains 2, . . ., m − 1 no longer represent intermediates on the path to strain m. For simplicity, in our results we consider only paths of length 1 (i.e. strains 2, . . ., m represent m − 1 distinct pathways), with equal probability of proceeding along any path. However, this set-up could obviously be extended to incorporate pathways of various lengths and mutation probabilities. We consider two possible scenarios.

— One-step irreversible.

— One-step reversible.

Finally, we must specify the transmissibility of each strain, T, particularly how these values relate to one another. For a given contact distribution, defining T effectively determines the pathogen’s fitness landscape. For linear mutation schemes, we will typically use the ‘jackpot model’ (Antia et al. 2003), in which strains 1 through m − 1 have identical transmissibility, and hence the same value of R0, < 1. Other biologically interesting possibilities include a fitness valley, where intermediate strains have lower fitness than strain 1, or an additive model, where fitness increases linearly with strain number (Antia et al. 2003). For hub-and-spoke schemes, we take T2, . . ., Tm−1 less than T1, representing deleterious mutations, while only Tm is greater than T1, representing a beneficial mutation.

3. RESULTS

3.1. Criticality of the process

The basic reproductive number, R0, is widely used as a predictor of when a disease has epidemic potential, as well as a descriptor of disease spread (Anderson & May 1991; Allen 2003; Brauer 2008). In branching process models, the disease has a positive probability of emergence if, and only if, R0 > 1. Other aspects of the offspring distribution affect the probability of emergence as well, and thus it is common to compare the probability of emergence across different distributions at the same value of R0 (Lloyd-Smith et al. 2005; Brauer 2008).

As clearly illustrated in the network-based approach, however, R0 is a composite quantity that is influenced by the combined processes of host-to-host contacts and disease transmission (Meyers et al. 2005; Brauer 2008). Once we decompose the process of disease spread into these mechanistic components, other comparisons suggest themselves. In particular, given that R0 itself is a critical threshold quantity for disease spread, it is natural to ask how this quantity changes across different contact distributions that have the same mean number of contacts and the same disease transmissibility. We might also ask how probability of emergence changes as a function of T rather than R0. Meyers et al. (2005) likewise argue for a focus on transmissibility, rather than R0, from the perspective of making reliable public health predictions across different host subpopulations.

Insight into the comparison between contact distributions can be gained by rewriting the equation

\[ R_0 = G(1) T. \]

Using the relationship \( G(z) = g(z)/g(1) \) gives \( R_0 = (g'(1)/g(1)) T. \) Then substituting \( g'(1) = \sigma^2 - g(1) + (g(1))^2 \), where \( \sigma^2 \) is the variance of the contact distribution, yields

\[ R_0 = (g(1) (1 + c^2) - 1) T, \]

where \( c = \sigma/g(1) \) is the coefficient of variation of the contact distribution. For a given transmissibility and mean number of contacts, the contact distribution that maximizes variance thus maximizes R0. The above equation is essentially the same as the expression for R0 given by Meyers et al. (2005), although there it is not rewritten in terms of c, and is similar to the expression for R0 used in deterministic network models (May & Lloyd 2001).

Analogously for a multi-type process, the expectation or mean matrix \( M = [a_{ij}] \), where \( a_{ij} = \partial_{T_i} g_j(T) \) is the expected number of type j progeny of one type i individual, is crucial in determining criticality of the process (Harris 1963; Allen 2003; Haccou et al. 2005). If the dominant eigenvalue of M is less than or equal to one, extinction is certain; otherwise, there is a positive probability of non-extinction and the process is classified as ‘supercritical’ (Harris 1963; Haccou et al. 2005). This threshold result holds whether the process is indecomposable or decomposable (see appendix D). The dominant eigenvalue of M is also known as the population-wide basic reproductive number.

In our multiple strain model, with contact distribution given by PGF g(z) and mutation probabilities given by matrix U = [μij], we have \( a_{ij} = G(1) T_i \mu_{ij} = (g(1) (1 + c^2) - 1) T_i \mu_{ij} \). We can thus express the mean matrix as

\[ M = (g(1) (1 + c^2) - 1) \text{diag}(T) \ U, \]

emphasizing the dependence of M—and hence its dominant eigenvalue—on the mean and variance of the contact distribution, the transmissibility of each strain and the mutation scheme.

3.2. Impact of contact distribution and transmissibility on emergence

Figure 2 illustrates, for a single strain, the impact of contact distribution on the basic reproductive number, R0, and on the probability of emergence starting from one later-generation infective, 1 − q. Figure 2a shows how R0 increases with transmissibility T: in all cases, this increase is linear, but at a different rate for each contact distribution depending on the variance in contacts. Figure 2b plots the probability of emergence versus T for each contact distribution. This probability becomes non-zero at the point where R0 passes the critical value of one, which occurs at a different value of T for each distribution (as illustrated in figure 2a). Thus, at low values of T, the disease can persist in some host contact structures but not others, despite the fact that they all have the same mean number of contacts. As T increases, however, the probability of emergence increases at different rates for different contact structures, such that the ordering is not preserved. This observation is highlighted in the inset, showing...
emergence probability over an extended range of $T$. In contrast, the ordering is consistent in figure 2c, which plots the probability of emergence versus $R_0$, comparable to Brauer’s presentation (Brauer 2008). The same value of $R_0$ has been achieved for each contact distribution by varying $T$ to compensate. We can think of the middle plot as showing the net result of opposing influences illustrated in figure 2a,c. Similar considerations and results on the impact of contact distribution and transmissibility apply to the multiple strain case.

### 3.3. Impact of mutation scheme on criticality

When there are multiple strains of pathogen, the pathways of mutation among them may also affect the threshold parameter. In the case of irreversible mutation, we can number strains such that $M$ is a triangular matrix, with its eigenvalues given simply by the entries on the main diagonal. Assuming the final strain is the best adapted, the dominant eigenvalue is then $R_{0,m} = G(1) T_m$. Hence, criticality is independent
3.4. Impact of mutation scheme on probability of emergence

We can compare not only the qualitative result of criticality, but also the quantitative probability of emergence across various supercritical branching processes. To obtain this probability, 1 \( - q_1 \) decreases, changing the criticality of the branching process. Results are illustrated for \( m = 2 \) strains, with \( T_1 = 0.01 \) and various values of \( T_2 \) spaced linearly from 0.034 (bottom curve) to 0.037 (top curve). Contact distribution is Poisson with mean 30 and forward mutation probability is \( \mu = 0.01 \).

Figure 3. As reverse mutation probability \( (\nu) \) increases, the dominant eigenvalue of the mean matrix (population \( R_0 \)) decreases, changing the criticality of the branching process. Results are illustrated for \( m = 2 \) strains, with \( T_1 = 0.01 \) and various values of \( T_2 \) spaced linearly from 0.034 (bottom curve) to 0.037 (top curve). Contact distribution is Poisson with mean 30 and forward mutation probability is \( \mu = 0.01 \).

Fixed point (see appendix D for details), and continue until the difference between successive iterations, in max norm, is less than a specified tolerance, taken to be \( 10^{-12} \) or \( 10^{-16} \) in the figures we present.

Figure 4 illustrates the probability of emergence across various linear mutation schemes with the same contact distribution. Here, \( T_m \) is far from the critical threshold, and reverse mutation, even at a high rate equal to that of forward mutation, makes a negligible impact on the probability of emergence. This agrees with Sagitov and Serra’s result that reverse mutation is negligible in a similar model with an arbitrary offspring distribution (Sagitov & Serra 2009), and with the neglect of pathways to the escape mutant exceeding the minimum length in the work of Iwasa et al. (2003, 2004). On the other hand, results are highly sensitive to the path of forward mutation that is assumed to be possible. Allowing jumps directly to strain \( m \) tends to make a particularly large difference, with this effect most pronounced when early strains have very low transmissibility. Simultaneous point mutations, though extremely rare, also make a significant contribution to the probability of emergence. In general, similar trends were observed for larger \( T_m \) with the probability of emergence scaled up but the relationships among mutation schemes the same. Probability of emergence reaches a plateau, presumably at the
probability of the well-adapted strain $m$ ever appearing, as $T_m$ becomes very large (results not shown).

We can also consider the impact of mutation scheme when intermediate strain fitness (as determined by transmissibility for fixed contact structure) varies. Although we have typically used the jackpot model, one might also consider other choices of transmissibilities. As one would expect, the higher the intermediate strain fitness, the higher the probability of emergence as observed by Antia et al. (2003). Now that we have generalized the mutation scheme, we can investigate whether this effect is more pronounced for some schemes than for others. For instance, a decrease in intermediate strain transmissibility (creating a fitness valley) hurts the pathogen’s chance of emergence more if only one-step forward mutation is possible, as opposed to a jump directly to the final strain through recombination (results not shown). This is in agreement with an observation by Iwasa et al. (2004).

### 3.5. Impact of mutation probabilities and number of strains

For any given mutation scheme, we can gain greater insight into the effect of mutation probabilities and number of strains by estimating the probability of emergence analytically. As other authors (Antia et al. 2003; Iwasa et al. 2003, 2004; Serra & Haccou 2007; Sagitov & Serra 2009) have considered analytical approximations for this model (or special cases of it) in detail, we keep our remarks brief.

Using an intuitive argument, Antia et al. derived the following approximation for the probability of evolution to strain $m$ (starting from strain 1) in the case of a Poisson-distributed number of infectious transmissions and one-step irreversible mutation (Antia et al. 2003):

$$\Pr(\text{evo}) \approx \prod_{i=1}^{m-1} \frac{\mu_{R_{0,i}}}{1 - R_{0,i}} = \mu^{m-1} \prod_{i=1}^{m-1} \frac{R_{0,i}}{1 - R_{0,i}}.$$  

This approximation, which holds for $\mu \ll 1$ and $R_{0,i}$ not too close to 1, makes it clear that probability of emergence, which is proportional to the probability of evolution in this estimation, is expected to scale $\sim \mu^{m-1}$ (Antia et al. 2003). The derivation in fact proceeds without reference to any features of the offspring distribution besides its mean, and figure 5 confirms that the prediction holds for all our sample contact distributions. Differences among contact distributions are primarily due to our comparison at fixed $T$, rather than fixed $R_{0,i}$.

More generally, Serra & Haccou (2007) give a formal derivation for probability of ‘escape’ (or emergence), showing that (in our notation)

$$1 - q_i \approx \frac{R_{0,i}}{1 - R_{0,i}} \sum_{j=1, j \neq i}^{m} \mu_j (1 - q_j)$$

under quite general conditions, including the scenarios considered by Antia et al. (2003) and Iwasa et al. (2003, 2004). Specifically, this approximation is valid under the following assumptions.

- Total offspring distribution for each type is arbitrary, provided its variance is finite. The mean of the distribution for type $i$ is $R_{0,i}$. Mutations occur independently among the offspring.
- There is a single ‘escape’ type (which we denote $m$) having $R_{0,m} > 1$; all other types $i \neq m$ have $R_{0,i} < 1$.
- There are no mutations away from the escape type; thus, $q_m$ can be computed independently and substituted into the above approximation for $q_i$, $i \neq m$.
- All mutation probabilities $\mu_{ij}$, $i \neq j$, are of $O(u)$.

Under these conditions, the above approximation has error of $O(u^2)$. However, the neglected error term increases as $R_{0,i} \to 1$, implying that the approximation will break down if strain fitness approaches the critical threshold. Iwasa et al. (2004) present approximations valid for various choices of $R_{0,i}$, including the near-critical case, though only for a specific offspring distribution.

As an example, consider our ‘mutation and recombination’ scheme. Either by applying an Antia-like argument to this specific scenario or by substituting mutation probabilities into Serra and Haccou’s result, we can show that the probability of emergence starting from a type 1 individual $(1 - q_i)$ scales as $O(\mu^{m-1}) + O(\rho)$, where $\mu$ is the probability of one-step forward ‘point mutation’ and $\rho$ is the probability of jump-to-$m$ ‘recombination’. Figure 6 supports this prediction for an example with $m = 3$ strains, illustrating the relative contributions of the different adaptive pathways. When $\rho \gg \mu^2$, the probability of emergence is almost constant in $\mu$ and scales approximately linearly in $\rho$. When $\rho \ll \mu^2$, the probability of emergence is almost constant in $\rho$ and scales proportionally to $\mu^2$.

Despite the availability of these useful analytical results, there is still a place for numerical solutions when looking for subtle differences among cases (e.g. different contact distributions) or where the assumptions underlying these approximations are broken or pushed to their limits (e.g. relatively large mutation probabilities), as we will encounter in the next subsection.

### 3.6. Impact of increasing overall mutation rate

The same biological mechanisms (e.g. nucleotide substitution rate, error-correcting mechanisms) contribute to all mutation rates, not only those for beneficial mutations. Given this constraint, it is not immediately clear whether pathogens with the highest mutation rates will have the largest or smallest probability of emergence. We explore this question for two mutational schemes in which deleterious steps are possible: one-step reversible mutation and hub-and-spoke irreversible mutation.

For simplicity, with one-step reversible mutation, we use only two strains (implying that linear and hub-and-spoke schemes are equivalent), the poorly adapted strain 1 and the well-adapted strain 2. Mutation from 1 to 2 occurs with probability $\mu$, and from 2 to 1 with...
probability $v$, which we scale proportionally to $\mu$. Results demonstrate a non-monotonic relationship between mutation rate and probability of emergence (figure 7). The probability of emergence increases with mutation rate over a wide range, before abruptly crashing to zero. This occurs because the branching process becomes subcritical once reverse mutation rate is too high, even when forward mutation rate is similarly high (§3.3). Note, however, that the crash does not occur if $T_2$ is well above the critical threshold.

With an irreversible hub-and-spoke mutation scheme, we assume that the initial strain is equally likely to mutate to any other, but only one mutational pathway is beneficial. As an extreme case, we set transmissibility of all deleterious strains to be zero. Figure 8 plots the probability of emergence versus $T_1$ for various mutation probabilities. When $T_1$ is well below the critical threshold (at which $R_{0,1}$ reaches 1), emergence probability increases linearly with mutation probability, as we would predict from analytical approximations (§3.5). Although this figure plots results for $m = 10$ strains, a virtually identical increase in emergence probability versus $\mu$ at fixed small $T_1$ was observed for $m = 2, 3, 5$ as well (results not shown). This indicates that regardless of how high the risk of deleterious steps, a pathogen that is guaranteed to go extinct unless it acquires a beneficial mutation (evolves to strain $m$) is always better off having a large mutation rate. Near the critical threshold, emergence probability shows a sharp jump; once strain 1 is sufficiently fit to escape extinction without further evolution, mutation probability makes only a small difference in results. Shortly after this point, a very high mutation probability becomes detrimental to the pathogen, even while strain 1 is not as well adapted as strain $m$. The risk of mutating to a poorly adapted strain now outweighs the potential benefit of mutating to a better adapted strain. Adding reverse mutation at a probability equal to that of forward mutation makes negligible difference to quantitative results (results not shown), as also observed with linear mutation schemes where $R_{0,m}$ is not too close to one. We might suspect...
that increasing reverse mutation probability independently of forward mutation probability could provide a benefit to the pathogen if the transmissibility of deleterious strains is non-zero, such that mutation could ‘rescue’ the pathogen by a return to strain 1 (the hub). However, this does not appear to be the case within tested parameter ranges (results not shown): increasing reverse mutation probability decreases probability of emergence, though only marginally when $R_{0,m}$ is well above one.

4. DISCUSSION

We have linked phenomenological and contact network-based approaches to modelling disease spread as a branching process, clarifying how they may be viewed within a common framework. By explicitly considering the number of contacts along with a model of how transmission occurs to these contacts, a network-based model offers more detailed insights into factors contributing to pathogen fitness and probability of emergence. Such a model lends itself to comparison of the relative impact of various public health interventions, which may act by reducing either number of contacts or probability of transmission per contact (Meyers et al. 2005; Brauer 2008).

Expressing the basic reproductive number as $R_0 = (g'(1)(1 + c^2) - 1)T$—where $g'(1)$ is the mean of the contact distribution, $c$ is its coefficient of variation and $T$ is transmissibility—highlights the contributions of both ecological factors (contact structure) and epidemiological factors (transmissibility) to pathogen fitness. That is, a pathogen’s fitness depends on the particular host population in which it circulates, an observation that has been made more generally for pathogen fitness measures (Antolin 2008). Similarly, in the multi-type process, we can express the mean matrix as $M = (g'(1)(1 + c^2) - 1)\text{diag}(\overline{T})U$, where $\overline{T}$ is the vector of strain transmissibilities and $U$ is the mutation matrix. These expressions make it clear that for fixed transmissibilities, mean number of contacts and mutation scheme, maximizing pathogen fitness is equivalent to maximizing the variance of the host population’s contact distribution; this agrees with the general observation that increasing heterogeneity among hosts increases $R_0$ (Antolin 2008). Furthermore, in the multi-type process, we see that criticality is independent of mutation probabilities if mutation is uni-directional; however, if mutation is bi-directional then this can push the process into a subcritical range (figure 3).

We have argued that the comparison of emergence probability across contact distributions should be made at given pathogen transmissibility, rather than at given pathogen fitness ($R_0$). This comparison more easily lends itself to questions about the sort of host population contact structure that is associated with greatest risk of disease emergence. In contrast, holding $R_0$ fixed in comparisons requires that we simultaneously alter pathogen transmissibility when altering the contact distribution, thereby confounding these two factors.

4.1. What are the most risky contact structures?

The contact distribution associated with highest risk of emergence is not always the same, but rather depends on the transmissibility, i.e. the particular pathogen involved. Especially large differences among contact distributions occur near the critical threshold for the branching process. Recall figure 2b: at a transmissibility of 0.03, probability of emergence ranges from 0 to
approximately 0.7, depending on contact distribution, even when all distributions have the same mean. This suggests that certain pathogens, having a transmissibility near the critical threshold, will be able to cause an epidemic in some host populations, but not others.

Although previous authors have often found that increased population heterogeneity increases the probability of extinction (e.g. Caraco et al. 1998; Lloyd-Smith et al. 2005), in phenomenological models this heterogeneity is necessarily introduced directly to the offspring distribution. In contrast, the heterogeneity we introduce through contacts in our more mechanistic model has the counteracting effect of raising the chances of getting the disease is correlated with the number of opportunities to pass it on. (Recall the distinction between degree and excess degree distribution.) Through comparison of contact distributions at given transmissibility, we found that heterogeneity can in fact increase the risk of emergence over a significant range.

4.2. What are the most risky mutational processes?

Probability of emergence is highly sensitive to the mutational pathway(s) by which the pathogen may possibly evolve (figure 4). Provided we are not too close to the critical threshold, reverse mutation has very limited impact on this probability and may reasonably be neglected. On the other hand, the possibility of taking large adaptive steps through either simultaneous point mutations or another mechanism of genetic change can have a dramatic impact. Given the finding on simultaneous mutations, it may be worth including higher order terms in other mutation schemes as well. As in the case of contact distribution, however, the ‘most risky’ mutational pathway depends on the pathogen’s initial transmissibility. Given a mutational scheme, probability of emergence is also sensitive to mutation probabilities and number of intermediate strains in an analytically predictable manner (figures 5 and 6).

We also considered more realistic situations where deleterious as well as beneficial evolutionary steps are available to the pathogen, either by reverse mutation or by including multiple pathways in strain space. Here, we constrained all types of mutations to occur with proportional probabilities, based on some overall mutation rate of the pathogen. We found that, when the pathogen was initially poorly adapted, increasing overall mutation rate was usually beneficial to an emerging pathogen (i.e. riskier to the host). On the other hand, as the pathogen’s initial fitness increases beyond the critical threshold where survival without adaptation is possible, the risk of deleterious mutations comes to outweigh the benefit of potential mutation to a more fit strain, and a high mutation rate becomes a liability (figure 8). Thus, our results largely provide support for the hypothesis that the statistically higher propensity of RNA viruses to emerge is due to their high mutation rate (Cleaveland et al. 2001; Woolhouse et al. 2005). However, an exception occurs with pathogens for which the fully adapted strain has a basic reproductive number only slightly above one. In this situation, when allowing for reverse mutation, we observed another phenomenon in which emergence probability has a non-monotonic relationship with overall mutation rate (figure 7). If this rate passes a critical point, excessive back mutation to poorly adapted strains implies that the pathogen can no longer sustain itself. This result parallels the phenomenon of ‘error catastrophe’ observed in viral quasi-species models, which offer a theoretical explanation for experimental success in inducing lethal mutagenesis in viruses (Eigen 2002; Anderson et al. 2004; Clementi 2008). Although the required ‘mutation’ rate may at first appear unrealistically high, it is important to remember that it does not represent the probability of point mutation during a single replication event, but actually incorporates all factors involved in strain conversion, including genetic changes arising during multiple rounds of replication and within-host strain competition. Taken together, our results suggest that any attempt to alter a pathogen’s mutation rate for host benefit should be undertaken with careful consideration of the pathogen’s initial fitness and the availability of mutations, both beneficial and deleterious. An attempt to induce lethal mutagenesis seems liable to backfire if the pathogen has significant adaptive potential, as in the case of many emerging pathogens.

4.3. Future directions

We have modelled the spread of an emerging pathogen following its introduction to a new host species. This model does not incorporate the dynamics of the introduction itself (or possibly multiple introductions), such as interspecific interactions (Woolhouse et al. 2005; Day et al. 2006; Kuiken et al. 2006; Woolhouse & Gaunt 2007; Lloyd-Smith et al. 2009). Indeed, although a better understanding of the dynamics of cross-species transmission is likely to be important in dealing with emerging diseases, few models to date have considered multiple species and phases in cross-over (Lloyd-Smith et al. 2009). (However, see Day et al. (2006) and Reluga et al. (2007) for models incorporating ongoing interactions with animal reservoirs.) Putting our model in a broader context could elucidate the impact of additional risk factors such as pathogen–host range (Cleaveland et al. 2001; Taylor et al. 2001).

Within the context of transmission in a single-host population, there are several common but potentially significant limitations of our modelling approach. Given the importance of contact structure that we and others have predicted, consideration of more realistic networks may be an important next step. Using a branching process neglects higher order network features, such as loops that persist even in large populations, thus implicitly assuming that the availability of susceptibles is not limited by local saturation. Clustering of contacts is expected to limit disease spread owing to reduction in the availability of susceptibles (Keeling & Eames 2005), and including features such as triangles in networks may have a dramatic impact in decreasing the probability of a large-scale epidemic (Trapman 2007). Thus, we expect...
the branching process approach to provide an upper bound on the risk of emergence. On the other hand, a recent analysis addressing some apparent inconsistencies in the literature suggests that the impact of clustering on the probability of an epidemic is in fact negligible unless degree is typically small or host-based heterogeneities are large (Miller 2009), providing some support for conclusions drawn from a branching process approach. While some authors (e.g. Ball & Neal 2002; Trapman 2007; Miller 2009) have made progress in modelling stochastic single-strain disease spread with more complicated contact structures, to our knowledge such approaches have not yet been extended to multiple strains.

A second major assumption in our model is that hosts are homogeneous in terms of their epidemiological characteristics. That is, the same transmissibility applies to every host infected with a given strain of pathogen. However, host-based factors are predicted to play a role in emergence risk (Woolhouse et al. 2005; Woolhouse & Gaunt 2007), suggesting value in a more realistic model. This would incorporate variability in host characteristics contributing to transmissibility, such as infectivity and susceptibility (Yates et al. 2006; Miller 2007). Analysis in the single-strain case predicts that such heterogeneities reduce the probability of an epidemic (Miller 2007, 2009).

Furthermore, both the level of transmissibility ($T$) and the strain conversion process have been treated only phenomenologically in our present between-host model. We (and other authors) have implicitly assumed that any conversion of strains within an individual is instantaneous, with no possibility for co-infection. We have also ignored variation in the precise number of pathogen copies in the body. Realistically, once a mutation arises in a host there will be some dynamical process leading to fixation or loss over time, with coexistence of strains at least temporarily. Both André & Day (2005) and Handel et al. (2006) also raise this issue, the latter suggesting that the difficulty of obtaining direct estimates of parameters in the between-host

Figure 8. Probability of emergence $(1 - q)$ in the irreversible hub-and-spoke mutation scheme. Contact distribution is Poisson with mean 30. There are 10 strains, with mutation occurring with equal probability $\mu$ from strain 1 to each other strain. $T_m = 0.05$ while $T_i = 0$ for $i = 2, \ldots, m - 1$. (a) We plot versus $\mu$ for various values of $T_1$ ranging from 0.01 (bottom) to 0.05 (top), in increments of 0.01. (b) We plot versus $T_1$ for various values of $\mu$: $10^{-3}$ (light grey), $10^{-1}$ (dark grey) and $10^{-1}$ (black). The vertical dashed line indicates the critical threshold at which $R_{0,1}$ reaches one.

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model (e.g. $R_0$ and conversion rates) supports a move to
modelling at the within-host level.

An important avenue for future work will thus be to
develop an explicit model of within-host processes, and
then to link the within- and between-host scales. In
recent years, a number of authors have developed
such ‘nested models’ (reviewed in Mideo et al. 2008);
however, these are typically deterministic, whereas we
suggest that stochasticity may be important at both
levels. A pathogen may then increase its fitness via
multiple routes (Antolin 2008), with potential for
conflicting selection at different scales (Gilchrist &
Coombs 2006; Coombs et al. 2007). We anticipate
that antagonistic selection at the within- versus
between-host scales would tend to reduce the prob-
ability of population-level emergence, as the more
transmissible strain (better able to avoid extinction
between hosts) is thwarted by dominance of other
strain(s) within the host. By extending our model to
the within-host scale, we can address these sorts of
trade-offs in greater detail, offering further perspectives
on risk factors contributing to evolutionary emergence.

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APPENDIX A. CORRESPONDENCE OF
APPROACHES (SINGLE-STRAIN MODELS)
The parallels and subtle differences between the
phenomenological and network-based approaches suggest
several questions regarding when models are equivalent
and whether one may be recovered as a special case of
another. We explore these questions in the following
subsections.

A.1. Can $g(z)$ be recovered from $G(z)$?
Not all models deal with generation 0 infectives, or we
may only have information for ‘typical’ (later-
generation) infectives. To connect such cases to a con-
tact network framework, we may ask: given the excess
degree distribution, $G(z)$, can we work backwards to
determine the degree distribution, $g(z)$?

We have the relationship

$$G(z) = \frac{g'(z)}{g'(1)}.$$  

Integrating both sides yields

$$\int_0^z G(s) \, ds = \frac{1}{g'(1)} \int_0^z g'(s) \, ds = \frac{1}{g'(1)} (g(z) - p_0)$$

$$\Rightarrow g(z) = p_0 + g'(1) \int_0^z G(s) \, ds.$$  

Thus, given only $G(z)$, $g(z)$ is under-determined: once a
disease is being passed among those who are connected
to the contact network, we have no way of knowing how
many additional individuals are in the population but
have no contacts at all. To determine $g(z)$, we must
impose an additional assumption. Note that the prop-
ties of a PGF imply $g(1) = 1$; thus, we have the relation
ship

$$g(1) = p_0 + g'(1) \int_0^1 G(s) \, ds = 1$$

$$\Rightarrow g'(1) = \frac{1 - p_0}{\int_0^1 G(s) \, ds}.$$  

Thus, we can find $g(z)$ if we specify either $p_0$, the prob-
ability of having zero contacts, or $g'(1)$, the mean number
of contacts. We can calculate the other
quantity from the above relationship, subject to the
restriction that $p_0 \in [0,1]$ and hence $g'(1) \in [0,1/\int_0^1 G(s) \, ds]$.

A.2. Under what conditions is $g(z) = G(z)$?
Phenomenological models do not typically distinguish
between generation 0 and later-generation infectives.
In what case(s) will this perspective be exactly equiva-
 lent to a network-based model? That is, suppose every
infective, whether in the initial or later generations,
have exactly the same distribution of still-susceptible
contacts: $g(z) = G(z)$. What restrictions does this
impose on the possible distribution of contacts?

Since $G(z) = g'(1)/g'(1)$, the condition that $g(z) =
G(z)$ leads to the ordinary differential equation

$$g'(z) = g'(1)g(z),$$  

which, using the constraint that $g(1) = 1$, has the
unique solution

$$g(z) = \exp(g'(1)(z - 1)).$$  

Since a PGF uniquely identifies a distribution, we can
deduce that the contact distribution is Poisson, with
only the mean $g'(1)$ left to our discretion. Thus, the
distinction between generations of infectives is in fact
irrelevant in many phenomenological models, which
specify a Poisson distribution. Note that if we only
require that the number of still-susceptible contacts
should have the same type of distribution in each gen-
eration, but not necessarily with the same parameter(s),
then other types of distributions are possible: for
instance, a negative binomial degree distribution with
mean $\lambda$ and dispersion $\beta$ leads to a negative binomial
excess degree distribution with mean $\lambda(\beta + 1)/\beta$ and
dispersion $\beta + 1$.

A.3. Can $G(z)$ be recovered from $\Gamma(s)$?
Recall that authors taking phenomenological
approaches (e.g. Antia et al. 2003; Lloyd-Smith et al.
2005) specify only the distribution of infectious con-
tacts. Once we separate contact structure from
transmissibility in a network-based approach (as in
Brauer 2008), is there more than one distribution of
contacts that will achieve the same distribution of infec-
tious contacts? For consistency among models, in
the remainder of this section, we will treat all infectives
alike, and work only with $G(z)$ and $\Gamma(s)$. The same

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Table 1. Names and associated PGFs of distributions used in numerical results. Listed parameters are the mean for deterministic and Poisson; number of trials and probability of success for binomial; mean and dispersion for negative binomial; proportion of each type and mean for each type for mixed deterministic and mixed Poisson; and proportion of each type, number of trials for each type, and probability of success for mixed binomial. The PGF for a Poisson distribution is given by Brauer (2008) and the PGF for a negative binomial distribution is given by Lloyd-Smith et al. (2005).

| contact (degree) distribution         | excess degree distribution | offspring distribution (single strain) |
|---------------------------------------|----------------------------|----------------------------------------|
| deterministic(λ)                     | deterministic(λ - 1)       | binomial(λ - 1, T)                     |
| Poisson(λ)                            | Poisson(λ)                 | Poisson(λ(T))                          |
| negative binomial(λ, β)              | negative binomial(λ(β + 1)/β, β + 1) | negative binomial(λ(β + 1)/β, β + 1) |
| mixed deterministic(μ, λ)            | mixed deterministic(μλ/λ, λ, λ - 1) | mixed Poisson(μλ/λ, λ, λ - 1) |
| mixed Poisson(μ, λ)                  | mixed Poisson(μλ/λ, λ, λ - 1) | mixed Poisson(μλ/λ, λ, λ - 1) |

Table 2. Contact distributions used in numerical results, along with their variance and the expression for the basic reproductive number $R_0$ for the single-strain model in each case.

| contact (degree) distribution         | variance                  | $R_0$                     |
|---------------------------------------|---------------------------|---------------------------|
| deterministic(λ)                     | 0                         | $λ(1 - 1)T$               |
| Poisson(λ)                            | $λ$                       | $λT$                      |
| negative binomial(λ, β)              | $λ(1 + λ/β)$              | $λT(β + 1)/β$             |
| mixed deterministic(μ, λ)            | $μλ/λ - λ)^2$             | $(1/λ)μλ/λ - λ)^2 (λ - 1)T$|
| mixed Poisson(μ, λ)                  | $λ + μλ/λ - λ)^2$         | $(1/λ)μλ/λ - λ)^2 T$      |

results apply if we replace $G(z)$ with $g(z)$ and $Γ(s)$ with $γ(s)$.

Given a distribution $Γ(s)$ for number of infectious contacts, we can always obtain a distribution $G(z)$ for number of still-susceptible contacts that satisfies $Γ(s) = G(1 - T + Ts)$, trivially, by taking $T = 1$ and $G(z) = Γ(z)$. More generally, for arbitrary $T$, we require that $G(1 - T + Ts) = Γ(s)$, if $Γ(s)$ exists for this choice of $Γ(s)$. Rearranging $s = (z - (1 - T))/T$. Thus, $G(z) = Γ(z - (1 - T))/T$ if $G(z)$ exists; that is, if this expression yields a valid PGF. Taking $z \in [0,1]$ as we would usually evaluate a PGF leads to $s = (z - (1 - T))/T \in [1 - (1 - T)/T, 1]$ and $Γ(s)$ may not be a valid PGF on this range. Taking $Γ(s)$ to be, say, binomial or negative binomial leads to a valid PGF for $G(z)$, for any $T \in [0,1]$. But taking $Γ(s) = s^N$ (exactly $N$ infections transmitted by every infective) only gives a valid PGF if $T = 1$, not surprisingly. These examples illustrate that some, but not all, distributions of infectious transmissions can be traced back to contact distributions for arbitrary $T$. This limitation is to be expected, given that we have constrained the number of transmissions from an individual to be distributed binomially with total number of ‘trials’ equal to the number of contacts. Precise conditions on $Γ(s)$ yielding a valid contact distribution $G(z)$ in this or other models of transmission is an interesting mathematical question, but lies beyond the scope of the present work.

APPENDIX B. DETAILED DESCRIPTIONS OF CONTACT DISTRIBUTIONS AND MUTATIONAL SCHEMES

B.1. Contact distributions

The following contact distributions are used in our numerical results. In all cases, $λ$ denotes the mean of the distribution. Tables 1 and 2 summarize these distributions with the corresponding PGFs and expressions for $R_0$.

Deterministic. Every individual has a fixed number of contacts. This leads to a binomial offspring distribution.

Poisson. This distribution is appropriate ‘if contacts between members of the population are random, corresponding to the assumption of mass action in the transmission of disease’ (Brauer 2008, p. 142). The degree and excess degree distributions are the same. Using a Poisson-distributed number of contacts also leads to a Poisson-distributed number of infectious contacts (offspring distribution), as used in several phenomenological models (e.g. Antia et al. 2003; Yates et al. 2006; Reluga et al. 2007). In fact, since a Poisson distribution is fully determined by its mean, disease outbreak properties in this situation are fully determined by $R_0$ (or $R_{0_s}$ for multiple strains), regardless of whether $R_0$ is influenced through contacts or transmissibility. However, for other distributions, the parameters involved in the model do not appear only in the combination $R_{0_s}$, that is, for a fixed
choice of $R_0$, the probability of emergence still varies depending on the chosen parameters. Here, the separation of ecological and epidemiological influences is significant.

**Negative binomial.** This type of distribution arises in Lloyd-Smith et al. (2005) by taking a Poisson distribution with mean drawn from a Gamma distribution. We might interpret this distribution as arising from an infective making contacts at a constant rate (i.e. at points of a Poisson process) over a Gamma-distributed duration of infection. Variance decreases as dispersion ($\beta$) increases; in the limit as $\beta \to \infty$, we get a Poisson distribution.

**Mixed distributions.** This choice of distribution is motivated by the existence in the host population of ‘superspreaders’, who contribute an unusually large number of transmission events (Lloyd-Smith et al. 2005; Meyers et al. 2005; Day et al. 2006; Yates et al. 2006; Brauer 2008). We introduce this heterogeneity through number of contacts, an ecological effect, similarly to examples in Brauer (2008). Another possibility is that superspreading is due to higher-than-normal transmissibility among certain members of the population (Yates et al. 2006), an epidemiological effect that might be incorporated through an extension to our model (§4.3). While phenomenological models directly specifying the distribution of infections contacts would not distinguish the two cases, which both simply raise $R_0$ (e.g. Lloyd-Smith et al. 2005), these situations may lead to very different results (Meyers et al. 2005). Some authors distinguish the two cases by labelling hosts with a large number of contacts ‘superspreaders’, and those with high transmissibility ‘supershedders’ (Meyers et al. 2005).

In general, a mixed distribution specifies $n$ types of individuals, in proportions $p_1, \ldots, p_n$. Each type has a characteristic distribution of contacts, which we take to be either deterministic (the $k$th type has exactly $k$ contacts) or Poisson ($k$th type has a Poisson($k$) distribution of contacts), where $\sum_{k=1}^{n} p_k k = \lambda$. These cases lead to a mixed binomial or a mixed Poisson offspring distribution, respectively. For our numerical examples, we have taken $n = 2$, representing a less-frequent class of superspreaders among more-frequent ‘normal’ spreaders.

**B.2. Mutational schemes**

Schemes are numbered and interpreted as in §2.2. Each is characterized by the mutation matrix $U = [\mu_{ij}]$, where $\mu_{ij}$ is the probability that an infection transmitted by a type $i$ is of type $j$. We denote the probability of one-step forward point mutation by $\mu$, of one-step reverse point mutation by $\nu$ and of jump-to-strain-$m$ genetic change (e.g. recombination) by $\rho$.

**One-step irreversible:**

$$ U = \begin{bmatrix} 1 - \mu & \mu & 0 & \ldots & 0 & 0 & 0 \\ 0 & 1 - \mu & \mu & \ldots & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & \ldots & 1 - \mu & \mu \\ 0 & 0 & 0 & \ldots & 0 & 0 & 1 \end{bmatrix} $$

**Multi-step irreversible:** following Gokhale et al. (2009),

$$ \mu_{ij} = \begin{cases} \mu^{j-i}(1 - \mu)^{m-j} & \text{for } i < j \leq m, \\ 1 - \sum_{k=i+1}^{m} \mu^{j-i}(1 - \mu)^{m-k} & \text{for } j = i, \\ 0 & \text{otherwise}. \end{cases} $$

**Interchangeable and irreversible:** following Gokhale et al. (2009),

$$ \mu_{ij} = \begin{cases} \binom{m-i}{j-i} \mu^{j-i}(1 - \mu)^{m-j} & \text{for } i \leq j \leq m, \\ 0 & \text{otherwise}. \end{cases} $$

**Point mutation and recombination:**

$$ U = \begin{bmatrix} 1 - \mu - \rho & \mu & 0 & \ldots & 0 & 0 & \rho \\ 0 & 1 - \mu - \rho & \mu & \ldots & 0 & 0 & \rho \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & \ldots & 1 - \mu - \rho & \mu + \rho \\ 0 & 0 & 0 & \ldots & 0 & 1 & 1 \end{bmatrix}. $$

**One-step reversible:**

$$ U = \begin{bmatrix} \frac{1 - \mu}{\nu} & \frac{\mu}{\nu} & 0 & \ldots & 0 & 0 & 0 \\ \frac{\nu}{1 - \mu} & 1 - \nu - \frac{\mu}{\nu} & \mu & \ldots & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & \ldots & 1 - \nu & \nu \\ 0 & 0 & 0 & \ldots & 0 & 1 - \nu & \nu \end{bmatrix}. $$

**Hub-and-spoke, irreversible:**

$$ U = \begin{bmatrix} 1 - (m-1)\mu & \mu & \mu & \ldots & \mu & \mu \\ 0 & 1 & \ldots & 0 & 0 & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & \ldots & 1 & 0 \\ 0 & 0 & 0 & \ldots & 0 & 1 \end{bmatrix}. $$

**Hub-and-spoke, reversible:**

$$ U = \begin{bmatrix} 1 - (m-1)\mu & \mu & \mu & \ldots & \mu & \mu & \nu & 1 - \nu \\ \nu & 1 - \nu & 0 & \ldots & 0 & 0 & \nu & 1 - \nu \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \vdots \\ \nu & 0 & 0 & \ldots & 0 & 1 - \nu & 0 & \nu \end{bmatrix}. $$

**APPENDIX C. DERIVATION OF PGFs FOR THE MULTI-TYPE MODEL**

Here, we present a derivation of the PGFs used in our network-based multi-type model. First consider the PGF for number of infections of each type, $X = (X_1, \ldots, X_m)$, transmitted by a type $i$ infective, given $d$ susceptible contacts. The number of each type of transmission (including ‘failed’ transmissions) has a multinomial distribution with $d$ independent ‘trials’; possible outcomes are transmission of type $j$ (probability $T_{\mu_{ij}}$), for some $j = 1, \ldots, m$, or no
transmission (probability \( 1 - T_i \)). Thus,

\[
E[s_X s_X^{(0)} \cdots s_X^{(m)} | d] = \sum_{d=0}^{\infty} \Pr(d \text{ susceptible contacts}) \left\{ \begin{array}{ll}
\Pr(\bar{X}) = (x_1, x_2, \ldots, x_m) | D = d) \\
\times \Pr(\text{ext} | \bar{X} = (x_1, \ldots, x_m))
\end{array} \right.
\]

\[
= \sum_{d=0}^{\infty} \Pr(d \text{ susceptible contacts}) \left\{ \begin{array}{ll}
\Pr(\bar{X}) = (x_1, x_2, \ldots, x_m) | D = d) \\
\times \Pr(\text{ext} | \bar{X} = (x_1, \ldots, x_m))
\end{array} \right.
\]

\[
= \sum_{d=0}^{\infty} \Pr(d \text{ susceptible contacts}) \left\{ \begin{array}{ll}
\Pr(\bar{X}) = (x_1, x_2, \ldots, x_m) | D = d) \\
\times \Pr(\text{ext} | \bar{X} = (x_1, \ldots, x_m))
\end{array} \right.
\]

\[
= \sum_{d=0}^{\infty} \Pr(d \text{ susceptible contacts}) \left\{ \begin{array}{ll}
\Pr(\bar{X}) = (x_1, x_2, \ldots, x_m) | D = d) \\
\times \Pr(\text{ext} | \bar{X} = (x_1, \ldots, x_m))
\end{array} \right.
\]

\[
\times (T_1 \mu_{11}^{(0)} \cdots (T_m \mu_{m1})^{(0)}(1 - T_i)^{d - x_1 - \cdots - x_m}) q_1^{x_1} \cdots q_m^{x_m}
\]

\[
= \sum_{d=0}^{\infty} \left[ 1 - T_i + T_i \sum_{j=1}^{m} \mu_{ij} q_j \right]^d
\]

\[
= g \left[ 1 - T_i + T_i \sum_{j=1}^{m} \mu_{ij} q_j \right] .
\]

**APPENDIX D. TECHNICAL RESULTS FOR MULTI-TYPE BRANCHING PROCESSES**

In this section, we present more detailed technical results relevant to the methods applied to our multi-type branching process. As in the main text, we denote by \( \vec{\Gamma} = (\Gamma_1, \Gamma_2, \ldots, \Gamma_m) \) the vector of type-specific offspring distribution PGFs. First, we make the reasonable assumption that our process is never singular. Singular processes are those in which every individual has exactly one offspring (Harris 1963), and are often excluded from analyses.

Results for multi-type branching processes are usually stated for indecomposable processes, in which ‘each type of individual eventually may have progeny of any other type’ (Haccou et al. 2005, p. 26), also known as irreducible processes (Mode 1971). Such a process can be identified from the expectation matrix, \( M \): the process is indecomposable if, for every pair of types \((i, j)\), there exists a positive integer \( n \) such that \( M^n(i,j) > 0 \); or equivalently, there is a non-zero probability of producing at least one type \( j \) in generation \( n \), given that the process starts with one type \( i \) (Mode 1971; Haccou et al. 2005). If \( n \) is independent of the types \((i, j)\), the process is called positively regular (Mode 1971). Only periodic processes are indecomposable, but fail to be positively regular (Mode 1971); however, a periodic process can be represented by a non-periodic process through a transformation of time scale (Haccou et al. 2005). Thus, from here on, we take indecomposable to mean positively regular. In our model, whenever mutation is reversible and all types are transmissible, we have an indecomposable process.

On the other hand, we may be dealing with a decomposable process, in which there are ‘distinct groups of types that do not produce types in other groups’ (Haccou et al. 2005, p. 27). In our model, whenever mutation is irreversible, the mutation matrix \( U \) is upper triangular; hence, the expectation matrix \( M \) and any positive power \( M^n \) are also upper triangular and we have a decomposable process. We also encounter decomposable processes whenever there are non-transmitting types, leading to an all-zero row in \( M \).

We say that extinction of the process occurs when the population of every type reaches zero at some generation. Analogously to the single-type case, there is a threshold theorem for multi-type processes stating when non-extinction is possible; now, the threshold parameter is the dominant eigenvalue \( \rho \) of the expectation matrix \( M \). In the indecomposable case, extinction occurs with probability one from any starting type if and only if \( \rho \leq 1 \) (Harris 1963; Mode 1971; Athreya & Ney 1972; Allen 2003; Haccou et al. 2005). In the decomposable case, we must consider classes of types that communicate, i.e., any type within a class can give rise to any other type in the class after some number of generations (Harris 1963; Mode 1971). Then, provided there is no type that produces in the next generation exactly one offspring in its class with probability one, the threshold theorem continues to hold in the decomposable case (Harris 1963; Mode 1971). We will assume that this condition, which is
essentially an extension of the definition of non-singularity (Mode 1971), always holds in processes we consider.

Applying this theorem to our model, clearly the possibility of non-extinction requires that some type is supercritical in isolation, i.e. \( R_{0,i} > 1 \) for some \( i \).

When mutation is irreversible, the eigenvalues of \( M \) are simply given by the entries on the main diagonal, and assuming that the final strain \( m \) is best adapted, the dominant eigenvalue is \( R_{0,m} \). Thus, the process is guaranteed to go extinct from every initial type if and only if \( R_{0,m} \leq 1 \). Otherwise, there is a positive probability that the process does not go extinct, at least from some initial type. In fact, any initial type will suffice, provided the probability of forward mutation is positive and every strain is transmissible. For reversible mutation, again assuming strain \( m \) is best adapted, having \( R_{0,m} > 1 \) is a necessary, but not sufficient, condition to obtain a positive probability of non-extinction (cf. figure 3). Finally, if any type is non-transmissible (as we sometimes consider with hub-and-spoke schemes), clearly a process initiated by such a type is guaranteed to go extinct. Starting from any other type, we can simply ignore any production of non-transmissible types to define a process fitting into one of the aforementioned cases.

Let \( q_i \) denote the extinction probability of a multi-type branching process initiated by one type \( i \) individual. It is a well-known result for an indecomposable process that \( \tilde{q} = (q_1, \ldots, q_m) \) is a fixed point of the vector equation \( \tilde{V} \tilde{q} = \tilde{q} \), i.e. \( V(i)q_i = q_i \), \( \forall i \) (Harris 1963; Athreya & Ney 1972; Kimmel & Axelrod 2002; Allen 2003; Haccou et al. 2005). However, the argument for reaching this conclusion in fact applies to any branching process (Mode 1971); some further deductions depend on irreducibility. First note that \( \tilde{I} \) (the vector of length \( m \) containing all ones) is always a fixed point of \( \tilde{V} \); there may be other solutions too.

For an indecomposable process, \( \tilde{q} \) is the smallest non-negative fixed point of \( \tilde{V} \); if \( \rho \leq 1 \), then \( \tilde{q} \) is \( \tilde{I} \), as guaranteed by the threshold theorem; while if \( \rho > 1 \) (the supercritical case), \( 0 \leq q_i < 1 \), \( \forall i \) (Harris 1963; Mode 1971; Athreya & Ney 1972; Kimmel & Axelrod 2002; Allen 2003; Haccou et al. 2005). Furthermore, the only solutions to the fixed-point equation with \( 0 \leq s_i \leq 1 \), \( \forall i \), are \( \tilde{I} \) and \( \tilde{q} \), and fixed-point iteration beginning with any \( \tilde{s} \) (\( 0 \leq s_i < 1 \), \( \forall i \)) converges to \( \tilde{q} \) (Harris 1963; Mode 1971; Athreya & Ney 1972). This suggests a simple way to compute extinction probabilities to arbitrary accuracy, and is indeed the method we use for our numerical results (§3.3).

For a decomposable process, the threshold theorem again implies that \( \tilde{q} = \tilde{I} \) if \( \rho \leq 1 \). However, for a supercritical process (\( \rho > 1 \)), the uniqueness of fixed-point solutions \( \tilde{s} \neq \tilde{I} \) does not necessarily hold, nor must every \( q_i \) be less than one even when \( \tilde{q} \neq \tilde{I} \). For any situation we consider, we can argue (see below) that our computational method finds the ‘right’ solution \( \tilde{q} \) representing the probability that the entire process (i.e. every type) goes extinct; see also Reluga et al. (2007) for interpretations of multiple solutions.

We first assume that all types are transmissible, so \( M \) has no all-zero row. Suppose mutation is irreversible and hence \( M \) is upper triangular. This implies that \( \Gamma(s) \) is in fact independent of \( s_j \) for all \( j < i \). Thus, we can solve for any fixed point \( \tilde{s} \) by working backwards through types \( m, m-1, \ldots, 1 \), substituting solutions for those \( j \) already found and leaving an equation in one variable only. Assuming type \( m \) is supercritical (\( R_{0,m} > 1 \)), according to results for single-type branching processes, \( \Gamma_m(s_m) = s_m \) has two solutions: \( s_m = 1 \) and \( s_m = q_m < 1 \) (the extinction probability of the process initiated by a type \( m \)). We can then solve for \( s_{m-1} \) in each case. \( \Gamma_{m-1}(s_{m-1}, 1) \) is the PGF of the number of type \( m - 1 \)’s produced by a type \( m - 1 \), defining a single-type branching process. In most cases we consider, \( R_{0,m-1} < 1 \), and hence this will be a subcritical branching process, yielding a unique fixed point on \([0, 1]\), \( s_{m-1} = 1 \). Occasionally (e.g. figure 8), we will consider a case where \( R_{0,m-1} > 1 \) and the process may be supercritical: in this case, we obtain two fixed points, \( s_{m-1} = 1 \) and \( s_{m-1} = q_{m-1} < 1 \). On the other hand, \( \Gamma_{m-1}(s_{m-1}, q_m) \) is an increasing, concave-up function satisfying \( \Gamma_{m-1}(0, q_m) > 0 \) and, assuming \( \mu_{m-1,m} > 0 \) (i.e. \( \Gamma_{m-1}(\tilde{s}) \) is not independent of \( s_m \)), \( \Gamma_{m-1}(1, q_m) < 1 \); therefore, there is a unique solution \( q_{m-1} < 1 \) satisfying \( \Gamma_{m-1}(q_{m-1}, q_m) = q_{m-1} \). The argument proceeds identically as we continue to work backwards through types. To summarize, in most cases, we will have \( R_{0,m} > 1 \) and \( R_{0,i} < 1 \) \( \forall i \neq m \); this yields two solutions to the vector fixed-point equation: \( \tilde{s} = 1 \) and \( \tilde{s} = \tilde{q} \), the extinction probability, where \( q_i < 1 \), \( \forall i \). Furthermore, fixed-point iteration beginning with any \( \tilde{s} \) with all components <1 will converge to the latter solution, since iteration of \( \Gamma_m(s_m) \) converges to \( q_m \). In the occasional case that we have more than one supercritical type, there will be more than two solutions, corresponding to different subsets of types persisting in the case of non-extinction (Reluga et al. 2007). However, only one solution \( \tilde{q} \) will have all components <1, and this can readily be identified as the vector of probabilities that the entire process (every type) goes extinct, based on arguments presented above. Again, this is the solution that will be reached by fixed-point iteration beginning with any \( \tilde{s} \) such that \( s_i < 1 \), \( \forall i \), which is the method we apply in computations. In more complicated mutational schemes (not considered here), for instance if certain pathways are reversible and others are not, classes in a decomposable process may consist of more than one type; here we can write \( M \) in a block triangular form and apply results from Mode (1971) to make similar arguments.

If any type \( i \) is not transmissible, its corresponding PGF is clearly \( \Gamma_i(s) = 1 \), with unique fixed point \( s_i = 1 \). Substituting this solution into all other equations yields PGFs that effectively neglect any production of type \( i \), and we can then proceed as described above.

Finally, recall that the probability of extinction starting from a generation 0 infective of type \( i \), chosen uniformly at random with respect to degree, is given by \( g(1 - t_i + T \sum_{j=1}^m \mu_{ij} q_j) = \gamma(\tilde{q}) \). This probability is less than one if and only if \( q_i < 1 \) for some \( j \) for which \( \mu_{ij} > 0 \), simply meaning that extinction is guaranteed in this process if it is guaranteed in the processes initiated by later-generation infectives of types accessible by mutation.
If the branching process escapes extinction, we may be interested in the complement of types present in the long term. In indecomposable processes, all types will persist, and their populations grow asymptotically at a geometric rate $\rho$ (Haccou et al. 2005). However, this is not necessarily the case in decomposable processes. A simple inductive argument can be used to show that only supercritical types can persist if mutation is irreversible; so, in most cases we consider, ‘emergence’ means that only type $m$ is present in the long term. More detailed limit theorems can be found in Mode (1971).

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