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Limiting the spread of disease through altered migration patterns

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HIGHLIGHTS

- We examine the effect of migration patterns on the initial phase of an epidemic.
- We aim to minimise the expected growth rate and basic reproduction number.
- An explicit optimal distribution of susceptible individuals is found.
- This distribution is optimal for probability of extinction and total size of the epidemic.

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ABSTRACT

We consider a model for an epidemic in a population that occupies geographically distinct locations. The disease is spread within subpopulations by contacts between infective and susceptible individuals, and is spread between subpopulations by the migration of infected individuals. We show how susceptible individuals can act collectively to limit the spread of disease during the initial phase of an epidemic by specifying the distribution that minimises the growth rate of the epidemic when the infectives are migrating so as to maximise the growth rate. We also give an explicit strategy that minimises the basic reproduction number, which is also shown be optimal in terms of the probability of extinction and total size of the epidemic.

1. Introduction

Recently, a number of papers have been devoted to the issue of controlling disease outbreaks. Typical mechanisms for control involve treatments which speed recovery (Ndeffo Mbah and Gilligan, 2011; Rowthorn et al., 2009), culling of infected individuals (Ndeffo Mbah and Gilligan, 2010), reducing the density of disease vectors (Mpolya et al., 2014), vaccination programs (Klepac et al., 2012, 2011) and quarantine (Rowthorn et al., 2009). When the population has some spatial structure, migration also plays an important role in disease spread and provides a further control mechanism.

A common approach to incorporating spatial structure in epidemic modelling is to impose a metapopulation structure on the population (see Débarre et al., 2007; Grenfel and Harwood, 1997; Gurarie and Seto, 2009; Hess, 1996 for example). In a metapopulation, the population is divided into a number of subpopulations occupying geographically distinct locations. The disease is spread within a subpopulation by contacts between infective and susceptible individuals and is spread between subpopulations by the migration of infected individuals.

The effect of migration rates on disease spread in metapopulations has been investigated in a number of papers. Due to the complexity of these models, control strategies are often based on minimising the basic reproduction number R_0. Studying a multipatch frequency dependent SIS model, Allen et al. (2007) note that the rapid movement of infective individuals can lead to disease extinction in low risk environments. Furthermore, they conjecture that R_0 is a decreasing function of the diffusion rate for infective individuals. Hsieh et al. (2007, Theorem 4.2) note a similar result for their two-patch SEIRP model and a similar phenomenon has been observed in population models with spatially heterogeneous environments (Hastings, 1983). However, Gao and Ruan (2012,

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Section 4) have shown that for other models the dependence of R_0 on migration rates can be more complex. To investigate the effect of the migration rates on other quantities such as the number of infected individuals, numerical methods are generally required (for example Sanders et al., 2012).

In this paper, we examine how susceptible individuals can act collectively to limit the spread of disease during the initial phase of an epidemic. More specifically, we consider how susceptible individuals can distribute themselves in the metapopulation in a way that minimises the growth of the epidemic when the infectives migrate so as to maximise the growth. By formulating the problem as a minimax optimisation and focusing on the susceptible individuals, we avoid the need to distinguish between infected and susceptible individuals when applying controls to the population. This is advantageous as identification of infected individuals can be problematic due to factors such as delays in the onset of symptoms, asymptomatic carriers and costs associated with testing. Furthermore, acute disease can have a significant effect on the behaviour of animals (Hart, 1988). This is particularly true for certain parasitic diseases where the parasite attempts to force the host to act in a manner which assists the propagation of the parasite (Adamo, 2013).

In Section 2 we give our main results. Instead of using an ordinary differential equation (ODE) model for the epidemic as was done in the papers cited above, our analysis is based on a branching process model. Branching processes are known to provide a good approximation to the standard SIR and SIS Markov chain models when the number of infectives is initially small (Clancy, 1996). Using this model, we are able to give an explicit strategy that minimises the expected rate of growth under a certain condition on the recovery and infection rates. We also give an explicit strategy that minimises the basic reproduction number which does not require this extra condition. This later strategy is shown to also be optimal in terms of the probability of extinction and total size of the epidemic. In Section 3, the problem of minimising the expected growth rate is investigated numerically. The paper concludes with a discussion of how the results depend on contact rates and how they relate to ODE models.

2. Minimising disease spread in the initial stages

Consider a closed population of size N divided into m groups such that at time t group i contains $X_i(t)$ susceptibles and $Y_i(t)$ infectives. Each individual, conditional on its disease status, moves independently between groups according to an irreducible Markov process on $\{1,\dots,m\}$ with transition rate matrix R if it is susceptible and transition rate matrix Q if it is infected. The epidemic evolves as a Markov process. Contacts between individuals in the same group are assumed to be density dependent (Begon et al., 2002). More precisely, a pair of individuals in group i makes contact at the points of a Poisson process of rate β_i/N with contacts between distinct pairs of individuals being mutually independent. It is assumed that contact between an infective and a susceptible results in the infection of the susceptible. An infected individual in group i recovers with immunity at a rate γ_i. Since we are primarily concerned with the initial phase of the epidemic, our conclusions remain valid for epidemics where individuals recover without immunity.

In the absence of infective individuals, the entirely susceptible population evolves following a closed (linear) migration process with per-capita migration rates R. If the population is in equilibrium, then the probability that an individual is in group i is given by π_i where π is the unique solution to $\pi R=\mathbf{0}$ subject to the constraint $\pi\mathbf{1}=1$.

We consider the spread of the disease from a small number of initial infective individuals. Clancy (1996, Theorem 2.1) shows that, when N is large, the epidemic can be approximated by a multitype branching process. Assuming that the susceptible population is in equilibrium, the branching process for the number of infective individuals is given by

$$(Y_1,\dots,Y_m)\to(\dots,Y_i+1,\dots,Y_j-1,\dots) \qquad \text{at rate } Q_{ji}Y_j, \tag{1}$$

$$(Y_1,\dots,Y_m)\to(\dots,Y_i+1,\dots) \qquad \text{at rate } \beta_i\pi_iY_i, \tag{2}$$

$$(Y_1,\dots,Y_m)\to(\dots,Y_i-1,\dots) \qquad \text{at rate } \gamma_iY_i. \tag{3}$$

Note that the branching process depends on R only through the equilibrium distribution π.

Suppose that the susceptible population aims to minimise some quantity $f(\pi,Q)$, calculated from the branching process determined by (1)–(3). Let $\mathcal{S}$ denote the relative interior of the $(m-1)$-simplex and let $\mathcal{Q}$ be the set of irreducible migration rate matrices. Without imposing any constraints on the movements of the infectives, the susceptible population can choose π such that, for any $\epsilon>0$, a value no larger than $\inf_{\pi\in\mathcal{S}}\sup_{Q\in\mathcal{Q}}f(\pi,Q)+\epsilon$ is attained. On the other hand, the infectives can migrate in such a way that, for any $\epsilon>0$, a value no smaller than $\sup_{Q\in\mathcal{Q}}\inf_{\pi\in\mathcal{S}}f(\pi,Q)-\epsilon$ is attained. In general,

$$\sup_{Q\in\mathcal{Q}}\inf_{\pi\in\mathcal{S}}f(\pi,Q)\le\inf_{\pi\in\mathcal{S}}\sup_{Q\in\mathcal{Q}}f(\pi,Q)$$

(Petrosjan and Zenkevich, 1996, Lemma in Section 1.2.2). A pair $(\pi^*,Q^*)\in\mathcal{S}\times\mathcal{Q}$ such that

$$f(\pi^*,Q)\le f(\pi^*,Q^*)\le f(\pi,Q^*),$$

for all $\pi\in\mathcal{S}$ and all $Q\in\mathcal{Q}$ is called a saddle point for f. If a saddle point exists, then

$$\min_{\pi\in\mathcal{S}}\sup_{Q\in\mathcal{Q}}f(\pi,Q)=\max_{Q\in\mathcal{Q}}\inf_{\pi\in\mathcal{S}}f(\pi,Q)$$

(Petrosjan and Zenkevich, 1996, Theorem in Section 1.3.4). The susceptibles can attain this value by distributing themselves amongst the groups according to π^*. When a saddle point for f does not exist, there may still be an ϵ-saddle point, that is, for every $\epsilon>0$ there exists a pair $(\pi^\epsilon,Q^\epsilon)\in\mathcal{S}\times\mathcal{Q}$ such that

$$f(\pi^\epsilon,Q)-\epsilon\le f(\pi^\epsilon,Q^\epsilon)\le f(\pi,Q^\epsilon)+\epsilon,$$

for all $\pi\in\mathcal{S}$ and all $Q\in\mathcal{Q}$. The existence of an ϵ-saddle point implies that

$$\inf_{\pi\in\mathcal{S}}\sup_{Q\in\mathcal{Q}}f(\pi,Q)=\sup_{Q\in\mathcal{Q}}\inf_{\pi\in\mathcal{S}}f(\pi,Q)=\lim_{\epsilon\to0}f(\pi^\epsilon,Q^\epsilon)$$

(Petrosjan and Zenkevich, 1996, Theorem in Section 2.2.5). In the following, we determine the (ϵ)-saddle points for four quantities derived from the branching process (1)–(3).

As mentioned in the Introduction, this formulation avoids the need to distinguish between susceptible and infected individuals in the application of controls. To illustrate this point, suppose that susceptible individuals normally move between groups following a Markov process with migration rate matrix R. The optimal distribution of susceptibles π^* can be obtained by border controls where a migrating individual from group j going to group i is given admittance with probability p_{ji} and otherwise returned to group j. Detailed balance equations show that the optimal distribution for susceptibles is obtained if the admittance probabilities satisfy

$$R_{ji}p_{ji}\pi_j^*=R_{ij}p_{ij}\pi_i^*,$$

for all i,j. Although the border controls will have an effect on the migration rate of infected individuals if they are applied to the population as a whole, the optimal distribution for susceptible individuals ensures that the growth of the epidemic can be no greater than $\min_{\pi\in\mathcal{S}}\sup_{Q\in\mathcal{Q}}f(\pi,Q)$.