

Mathematics 4MB3/6MB3 Mathematical Biology
2017 Project Spatial epidemics dynamics: Synchronization

Group Name: Model Students

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1 Abstract

2 Background/Introduction

Many diseases, specifically childhood diseases, exhibit recurrent epidemics illustrated by a prevalence curve with peaks that dampen out, yet persist into the modern era (Lloyd, 1996). Using the standard susceptible, exposed, infective, and removed (SEIR) model, there exist two equilibrium points characterized whose stability is determined by the basic reproduction number \mathcal{R}_0 . As a result if $\mathcal{R}_0 > 1$, the system approaches the endemic equilibrium via damped oscillations. Part A goes here Explain synchro and extinction here

3 Methods

SIR model

Sinusoidal forcing

Spatial dynamics (n patches each has its own SIR system)

Assumptions:

Population the same for all patches

Pop is constant (death == birth) (all patches)

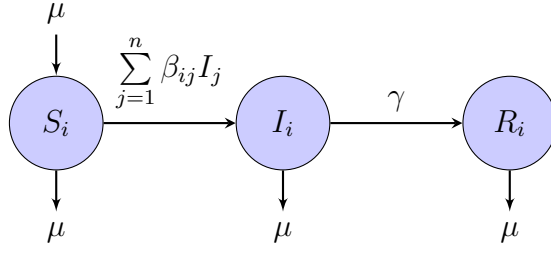
No migration between patches

Visitations are allowed (inter patch dynamics can be described as such)

Recovery rate is the same for all (same health care)

INSERT FLOW CHART HERE (and corresponding equations)

The spatial SIR model consists of n identical patches (which represent cities) with identical population sizes. The population is constant in each patch and there is no migration between patches. Intra-patch dynamics are given by the standard SIR model with vital dynamics and sinusoidal seasonal forcing. Connectivity between patches is represented by disease transmission. Infecteds can infect people from other patches. This models individuals visiting other patches, creating additional sources of infection in the visited patch. A visualization of the dynamics in a single patch i is shown by



The equations describing the dynamics in a single patch are

$$\begin{aligned}
 \frac{dS_i}{dt} &= \mu - S_i \sum_{j=1}^n \beta_{ij}(t) I_j - \mu S_i \\
 \frac{dI_i}{dt} &= S_i \sum_{j=1}^n \beta_{ij}(t) I_j - \gamma I_i - \mu I_i \\
 \frac{dR_i}{dt} &= \gamma I_i - \mu R_i
 \end{aligned} \tag{1}$$

where S is the proportion of the population that is susceptible to infection, I is the proportion of the population that is infectious, and R is the proportion of the population that has recovered from the disease (and have lifelong immunity) or who have died as a result of the disease. μ is the birth/death rate, γ is the recovery rate, and $\beta_{ij}(t)$ are the elements of the $n \times n$ matrix $\beta(t)$:

$$\beta(t) = \langle \beta \rangle (1 + \alpha \cos(2\pi t)) M \tag{2}$$

$\langle \beta \rangle (1 + \alpha \cos(2\pi t))$ is the standard sinusoidal forced transmission rate. M is a matrix describing the connectivity between patches. Its diagonals are all ones (transmission rates within patches are the same as in a single patch SIR model) and its off-diagonal elements are generally less than one since transmission between patches is usually assumed to be much lower than transmission within patches. M is assumed to be symmetric - i.e. patches affect each other in the same way. The row sums of M (and thus the column sums too) are all equal. This ensures that coherent solutions remain coherent. Two different M matrices are used in this paper. The first is equal coupling where all patches are equally connected, i.e. all off-diagonal elements of M are equal. This parameter is called m .

$$M = \begin{bmatrix} 1 & m & m & m \\ m & 1 & m & m \\ m & m & 1 & \\ m & & & \dots \end{bmatrix}$$

The second motif is nearest neighbor coupling. In this case it is assumed that the patches reside on a ring and can only affect their two nearest neighbors.

$$M = \begin{bmatrix} 1 & m & 0 & 0 & \dots & m \\ m & 1 & m & 0 & & \vdots \\ 0 & m & 1 & & & \\ 0 & 0 & & \ddots & & \\ \vdots & & & & \ddots & m \\ m & & \dots & m & 1 & \end{bmatrix}$$

Let rate be..

Explain the beta matrix in terms of the sin forcing which is then multiplied by the connectivity matrix (talk about the properties that it showcases)

Deterministic vs stochastically

How to detem???

Gillespie alg (very brief)

4 Results

Graphs, code

Bifurcation diagram

Show the corresponding plots for different R_0 values (deterministic pop)

Initial conditions here


(reproduce the diagrams from paper here)

5 Discussion:

Talk about how the prop of M affect the results

How the results show this: extinction and synchronization

Discuss the changes in period of the relationship

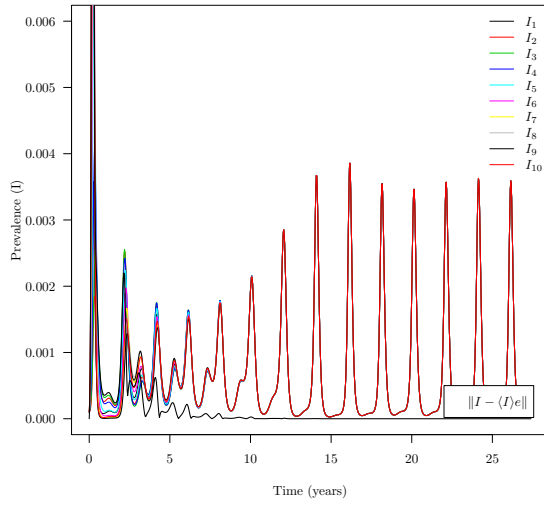
Solutions to (1) were calculated using the  deSolve package. The following figures are the solutions for $n = 10$, a 50 year life expectancy, a 13 day mean infectious period, nearest neighbor coupling, and seasonal forcing amplitude $\alpha = 0.1$. Figure 1 shows the affect of the strength of connectivity, m .

At low enough m the solutions do not become coherent. Figure 2 shows the affect R_0 has on the period of oscillations and nature of the cycles.

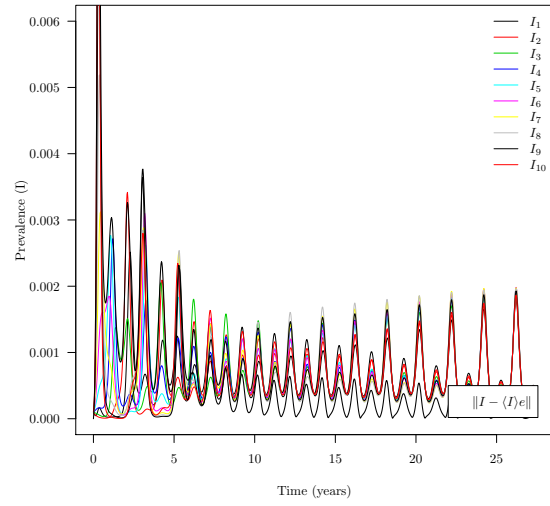
A stochastic version of this model was simulated using the Gillespie algorithm with $n = 10$, a population size of 1000, a 50 year life expectancy, a 13 day mean infectious period, equal coupling, $R_0 = 17$, $m = 0.2$, and seasonal forcing amplitude $\alpha = 0.1$. See Figure 3.

6 Conclusion

Figure 1: $\mathcal{R}_0 = 17$

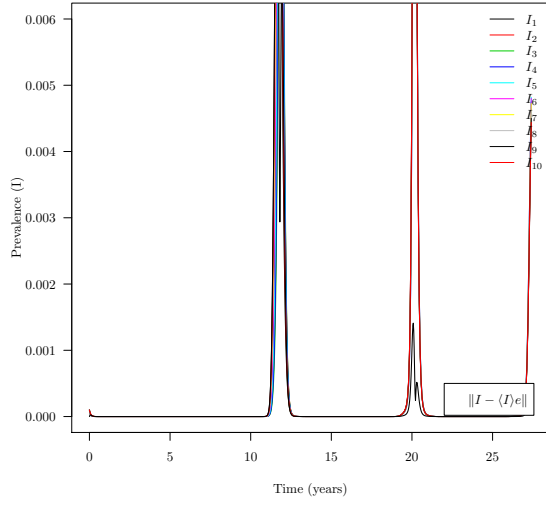


(a) $m = 0.2$

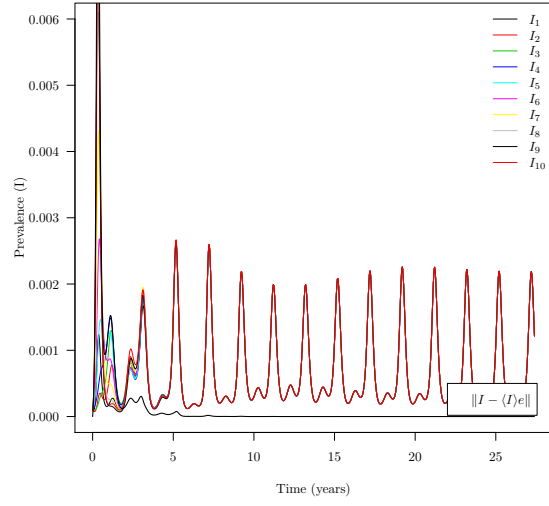


(b) $m = 0.01$

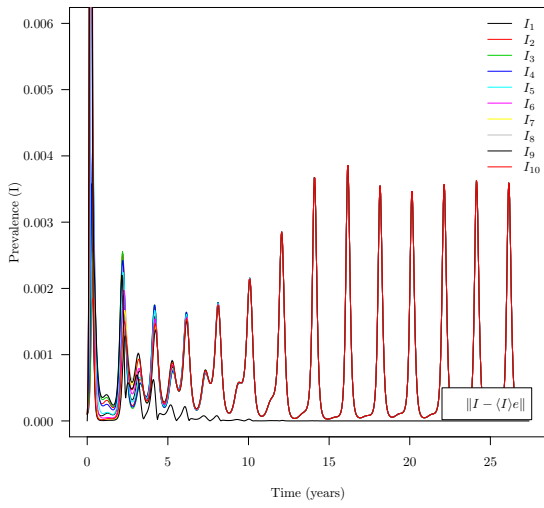
Figure 2: $m = 0.2$



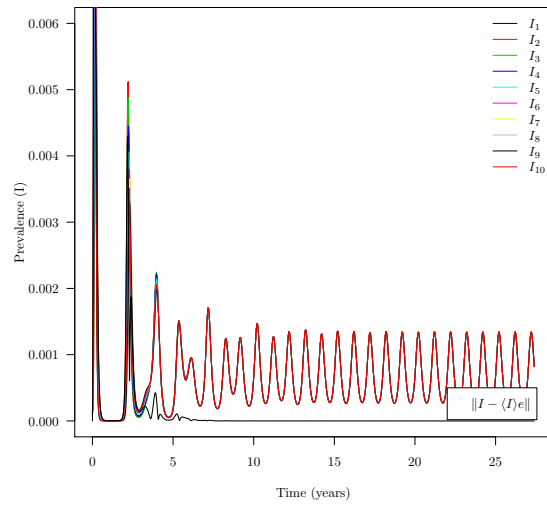
(a) $\mathcal{R}_0 = 4$



(b) $\mathcal{R}_0 = 12$



(c) $\mathcal{R}_0 = 17$



(d) $\mathcal{R}_0 = 25$

Figure 3: A stochastic simulation.

