PATCH SIR MODELS ON THE K-REGULAR GRAPH

D. I. WALLACE *, E. HU-WANG and M. CHEN

Department of Mathematics, Dartmouth College,
Hanover, NH 03755, U.S.A.
**E-mail: dwallace@math.dartmouth.edu*

The epidemiology of person-to-person communicable disease in large, homogeneous populations is modeled by three ordinary differential equations. These represent the susceptible, infectious and recovered individuals. For smaller populations an agent-based model can capture the inhomogeneous nature of human interactions by modeling each individual as a node in a network, or vertex in a graph. In this model we look at a set of large homogeneous populations, each modeled as a classic SIR epidemic (the patches), but which have immigration between them (the graph). We use this approach to simulate the spread of influenza during an outbreak and compare results of the simulation with available data.

It is a mathematically interesting and epidemiologically useful question to ask which aspects of disease transmission are controlled by the local properties of each SIR model, and which are controlled by the global connectivity of the graph. We prove that, for a general class of patch SIR models, the stability of the disease free equilibrium is a local property.

Keywords: SIR models, patch models, regular graphs, epidemiology

1. Introduction and Models

The classic model of an infectious disease is given by three coupled ordinary differential equations for susceptible, infectious and recovered individuals (SIR models).[1] This model is appropriate for large homogeneous well-mixed populations. Models for diseases that spread from city to city consider populations that are separated into patches, each of which is described by an SIR model, with migration between patches given as a linear term. Equations 1-3 below give the general form for patch SIR models.

$$S_i' = f(S_i) - \beta S_i I_i - \Sigma_{j\sim i}(i,j) m_{(i,j)} S_i + \Sigma_{j\sim i} m_{(j,i)} S_j \qquad (1)$$

$$I_i' = \beta S_i I_i - (v + b + \alpha) I_i - \Sigma_{j\sim i} m_{(i,j)} I_i + \Sigma_{j\sim i} m_{(j,i)} I_j \tag{2}$$

$$R_i' = v I_i - b R_i - \Sigma_{j\sim i} m_{(i,j)} R_i + \Sigma_{j\sim i} m_{(j,i)} R_j \tag{3}$$

Here $f(S_i)$ is the birth rate of the susceptible population, as any function of S_i only, b and v are birth and death rates, α is the death rate of the disease only, β is the transmission coefficient, $m_{(i,j)}$ is the relative rate of travel from vertex i to vertex j, assumed to be equal for susceptible, infectious and recovered populations at vertex i. Sums denoted by $j \sim i$ indicate vertices adjacent to the ith vertex. Note the $f(S_i)$ is not the most general form that could be taken, but it is good enough for many applications.

Such models can be considered hybrids between spacial models incorporating partial differential equations and single agent models evolving on graphs whose vertices represent individual members of a population. Patch models enable one to delineate local properties depending on the dynamics inside a patch from global properties depending on properties of the graph. For example, some graphs, such as Ramanujan graphs,[2] are known to be good propagators of information for their size. These properties should play a role in propagation of disease in patch models.

2. A Simulation of the U.S. influenza outbreak in 2009-2010

Six major U.S. areas connected by large airports (CA, CO, TX, GA, IL, NY) were used as a basis for parametrizing the model in equations 1-3. For this simulation, $f(S_i)$ was set to $a(1 - S_i/k_i) - dS_i$. The birth rate, a, and death rate, d, were taken as the U.S. average[3,4] and k_i was chosen to give an equilibrium population at the disease free equilibrium corresponding to the actual population of each city.[5] The transmission and death rates from this particular strain can be estimated from commonly known statistics[6] and the recovery rate can be estimated from data.[7] The graph between patches was the complete graph on six vertices, with migration rates estimated from airport data.[8] The resulting simulation was then compared with the patient data from clinics in each area (Regions 2,4,5,6,8,9) that report to the Center for Disease Control. The data gives the percent of those patients who, having presented with flu-like symptoms, tested positive for influenza.[9] Early cases were detected in California and Texas.[10] These were taken as initial conditions in the model, with disease incidence at all other locations taken to be zero. The resulting projections for all cities are shown in Figure

1, as well as the percent positive disease data for the U.S. as a whole. Figure 2 shows the projection for California plotted against the percent positive disease data for California.

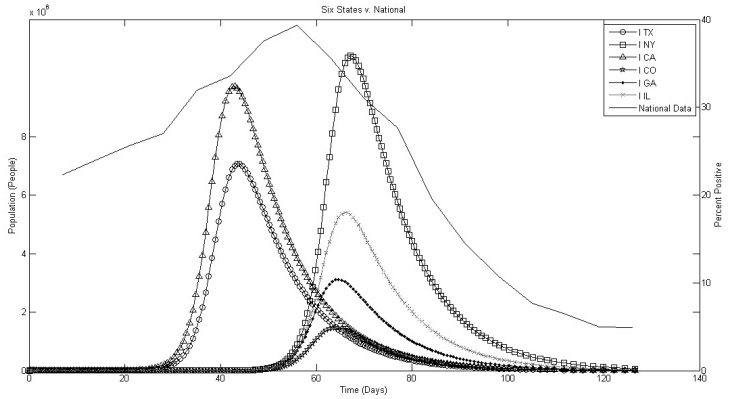

Fig. 1. Model predictions of all six cities, scale on left. National disease incidence (percent positive) data, scale on right.

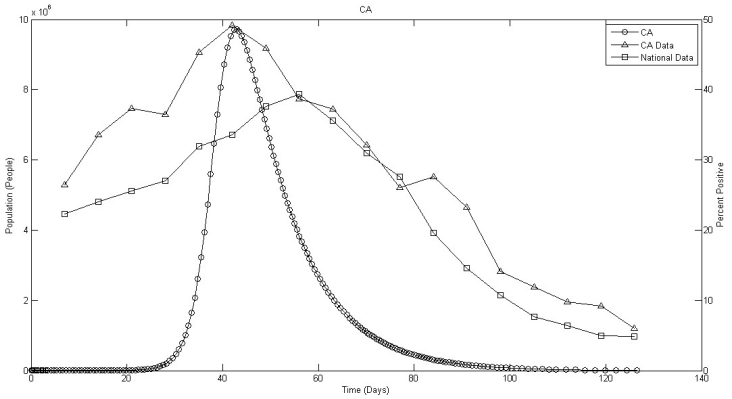

Fig. 2. Model prediction for California, scale on left. National and California disease incidence (percent positive) data, scale on right.

Data is not available for, nor is it easy to estimate, the actual number

of influenza cases in a geographic region. However we might hope for a reasonable representation of timing of an outbreak, as measured by percent positive data. In Figure 1 the national average for the data sits right between the two projected peaks. The early peaks are for California and Texas, where the disease was presumed to start. The later peaks are for the other states, after migration brings them the disease. In Figure 2 the peak of the simulation for California lines up well with the peak of the data, as did the simulation for the New York region. The other four simulations (CO, GA, IL, TX) all peaked a week or two later than the data for the respective region.

3. A General Theorem for Homogeneous Systems on the k-regular Graph

Theorem 3.1. *Let a patch model on a graph be given by equations 1-3. Assume that $m_{(i,j)} = m$ for all edges. Assume that the graph is regular, with n vertices and k edges at each vertex. Assume that, at the disease free equilibrium all S_i^* are equal to S^*. Let $f'(S^*)$ denote the partial derivative of f with respect to S_i at the disease free equilibrium. Let A denote the adjacency matrix for the graph and let $diag(c_i)$ denote the n by n diagonal matrix with diagonal elements c_i. Assume further that*

(1) the eigenvalues of $diag(\beta S^* - (v+b+\alpha) - km) + mA)$ are distinct from those of $diag((f'(S^*) - \beta I_i - km) + mA$, and
(2) the eigenvalues of $diag(\beta S^* - (v+b+\alpha) - km) + mA)$ are distinct from those of $diag(-b - km) + mA$

Then the stability of the disease free equilibrium does not depend on n, k, m or any other properties of the graph. The stability of the DFE depends only on $\beta, v, b, \alpha,$ and $f'(S_i*)$.

Proof.

With assumptions and notation as above, the Jacobian, J, at the disease free equilibrium is given by:

$$\begin{pmatrix} diag((f'(S^*) - \beta I_i - km) + mA & diag(-\beta S_i) & 0 \\ 0 & diag(\beta S_i - (v+b+\alpha) - km) + mA) & 0 \\ 0 & diag(v) & diag(-b - km) + mA \end{pmatrix}. \tag{4}$$

For simplicity we will assign labels to each n by n submatrix as below.

$$\begin{pmatrix} M & P & 0 \\ 0 & Q & 0 \\ 0 & R & N \end{pmatrix}. \tag{5}$$

It is clear that

(1) vectors of the form $(V, 0, 0)^t$, where V is an eigenvector of M, and
(2) vectors of the form $(0, 0, W)^t$, where W is an eigenvector of N

are eigenvectors of J.

Let U^t be an eigenvector of Q with eigenvalue λ. Then $(A, U, B)^t$ is an eigenvector of J provided

(1) $MA^t + PU^t = \lambda A^t$, or equivalently $A^t = (\lambda I - M)^{-1} PU^t$
(2) $RU^t + NB^t = \lambda B^t$, or equivalently $B^t = (\lambda I - N)^{-1} RU^t$

Vectors A and B may be constructed because the matrices $(\lambda I - M)$ and $(\lambda I - N)$ are invertible under the hypotheses of the theorem. Thus we have that the eigenvalues of J are given by the eigenvalues of M, Q and N. For stability of the disease free equilibrium it suffices to show that the largest eigenvalue of any of these matrices is negative. In each case, the largest eigenvalue is bounded by the maximum of $(diag(f'(S^*) - km) + m\Lambda, diag(\beta S^* - (v + b + \alpha) - km) + m\Lambda, diag(-b - km) + m\Lambda)$, where Λ is the largest eigenvalue of A. For k-regular graphs this is known to be k, so the largest eigenvalue of J is therefore bounded by the maximum of $(diag(f'(S^*)), diag(\beta S^* - (v + b + \alpha)), diag(-b))$.

This gives the result. □

4. Summary

In this paper we give a general form for a patch SIR model with migration between connected patches represented as a graph with adjacency matrix A. The population growth term for each patch is given as any general function of the susceptible population. Often this is taken as a constant recruitment rate that is offset by a relative death rate. An even more general setting would allow population growth to be a function of the total population. However the assumption in the models here fits well with diseases that pass relatively quickly through a population, such as influenza.

A version of the general form is used as the basis of a numerical simulation of the influenza outbreak of 2010 using airport traffic data for six regions to estimate migration rates. The simulation shows a very good match

in timing of outbreaks in two of six cities, and a somewhat late timing (compared to percent positive clinical data) in the other four. It suggests that simulations based on airport traffic data may be useful in bracketing the timing of outbreaks within a given period. Further, the peak of the outbreak for the U.S. as a whole sits neatly between the earliest and latest peaks of the simulation.

In a special case of the general model we take the patches to be identical, all migration rates to be identical, and the graph to be regular. For this situation we prove that the stability of the disease free equilibrium is a local property. It depends only on the parameters associated to birth, death, transmission and recovery for a single patch.

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