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A Structured Epidemic Model Incorporating Geographic Mobility Among Regions

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ABSTRACT

A model for the spread of infectious diseases among discrete geographic regions is presented that incorporates a mobility process that describes how contact occurs between individuals from different regions. The general formulation of the mobility process is described, and it is shown that the formulation encapsulates a range of mobility behavior from complete isolation of all regions (no mobility) to permanent migration between regions. It is then shown how this mobility process fits into an SIR epidemic model, and two examples are given extending its use. The examples include a model for disease transmission in a population with two distinct mobility patterns operating and a model developed to describe a 1984 measles epidemic on the Caribbean island of Dominica.

1. INTRODUCTION

Numerous factors influence the probability of contact between susceptible and infectious people, including participation in different social activities, cultural barriers such as membership in particular ethnic groups with associated customs, or separation due to geographic distance. These factors guarantee that contact among individuals within a population is distinctly nonrandom. Results from several theoretical studies show that nonrandom mixing among subgroups has many consequences for the outcome of epidemic spread, including the time at which a disease is introduced into different subgroups and the speed of propagation and severity of an epidemic (e.g., [6, 7, 15]).

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Most recent models for the spread of infectious diseases in human populations incorporate nonrandom patterns of mixing across subgroups and include a parameter for contact between groups that depends on the home subgroups of the susceptible and infective individuals (e.g., [9, 14]). This parameter represents only the end result of the mixing process—where and when a disease spreads throughout a population—leaving implicit the mechanism by which contact occurs among individuals from different subgroups. Little attention has been paid to the mechanism by which the disease travels across space.

Sociologists, geographers, and population geneticists, on the other hand, have long been interested in modeling how characters (usually genes, ideas, or people) move across a landscape. The majority of these models view mobility as a Markov or semi-Markov process. Malecót [12], Bodmer and Cavalli-Sforza [2], and Smith [21] were interested in how human migrations among a group of villages within a population would influence the genetic structure of the population. Bodmer and Cavalli-Sforza [2] used a backward stochastic migration matrix to model the mobility process. The elements of this matrix, m_{ij}, give the probabilities that an offspring in population i has parents who came from population j. The migration matrix model is used to derive the genetic variances and covariances among populations.

One problem with the migration matrix approach of Bodmer and Cavalli-Sforza is that it assumes that each subpopulation is homogeneous with respect to migration behavior, so that migration among subpopulations can be represented as a Markov process. This assumption implies, however, that the probability of migrating is unrelated to factors such as the duration of stay in a region—an assumption that is probably not reasonable for most kinds of mobility.

Many of the advances in modeling mobility processes have been made by sociologists who detected this limitation when building models for social or labor mobility. They have recognized two possible kinds of population heterogeneity that violate the Markovian assumption. First, there can be heterogeneity in the rates at which transition events occur, but for any given transition there is homogeneity among individuals. Models that consider this kind of heterogeneity generally divide a population into subgroups according to their rates of mobility and were first developed by Blumen et al. [1], who called them mover-stayer models. In these models part of the population is assumed to remain at the original location while the remainder of the population moves according to a Markov process. The mover-stayer model was later elaborated and extended by Ginsberg [4], Henry et al. [5], McGinnis [11], Spilerman [22], and Singer and Spilerman [19, 20].

The second kind of population heterogeneity results from individual differences in the tendency to move to particular locations. In this kind of population, each person moves according to a Markov chain, but the chains vary among individuals [19]. Models dealing with this type of heterogeneity in mobility behavior have been developed by McFarland [10] and Spilerman [23].

In the following we describe a model for the transmission of infectious disease that explicitly incorporates a mobility process. Contact between individuals occurs as a result of the mobility of participants across either geographic or social space. The model is of the mover-stayer type—a population is divided into subgroups consisting of individuals who are assumed to be homogeneous in their mobility patterns. Because it is simpler to visualize, we limit our discussion here to geographic mobility. Models for behavioral or social mobility are straightforward adaptations of this process (e.g., [8, 16]).

2. MODELING THE PROCESS OF MOBILITY AMONG GEOGRAPHIC REGIONS

A. THE GENERAL MOBILITY PROCESS

Consider a population distributed into n regions. Individuals from region i leave on trips to other regions at a per capita rate σ_i per unit time. These visitors are distributed among the $n-1$ destinations with probabilities ν_{ij} to each destination j. Because the ν_{ij} give conditional probabilities of visiting another region (given that a person moves at all), $0 \leqslant \nu_{ij} \leqslant 1$ for $i \neq j$ and, by definition, $\nu_{ii} = 0$. Furthermore, $\sum_j \nu_{ij} = 1$. Persons traveling from region i to region j have a per capita return rate to region i of ρ_{ij} (Fig. 1). By definition, $\rho_{ii} = 0$.

Let $N_{ii}(t)$ be the number of residents of region i who are actually present in their home region at time t, and let $N_{ij}(t)$ be the number of residents of region i who are visiting region j at time t. Then the travel patterns of individuals among regions lead to the equations

$$\frac{dN_{ii}}{dt} = \sum_j \rho_{ij} N_{ij} - \sigma_i N_{ii}, \tag{1a}$$

$$\frac{dN_{ij}}{dt} = \sigma_i \nu_{ij} N_{ii} - \rho_{ij} N_{ij}. \tag{1b}$$

At equilibrium these terms are both equal to zero. Thus,

$$N_{ij} = \frac{\sigma_i \nu_{ij}}{\rho_{ij}} N_{ii} \tag{2}$$

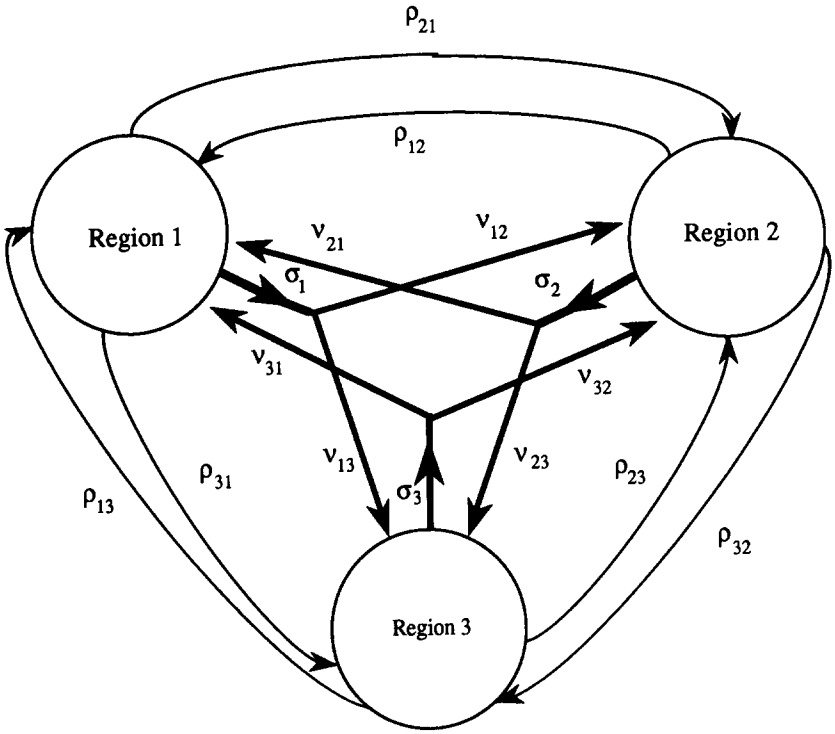

FIG. 1. Diagram of the mobility process linking three geographic regions. σ_i is the rate at which people leave region i, ν_{ij} is the probability that a person who leaves region i travels to region j, and ρ_{ij} is the rate at which persons from region i who are visiting region j return to region i.

and

$$\sum_{j\neq i} N_{ij} = \sum_{j\neq i} \frac{\sigma_i \nu_{ij}}{\rho_{ij}} N_{ii} = N_{ii}\sigma_i \sum_{j\neq i} \frac{\nu_{ij}}{\rho_{ij}} = N_{ii}\sigma_i \sum_{j} \frac{\nu_{ij}}{\rho_{ij}}, \tag{3}$$

since $\upsilon_{ii} = 0$. Let $N_i(t)$ be the total number of residents whose permanent home is in district i at time t. To avoid confusion in the following we change the index in the sum of Equation (3) to r. Then $N_i = \Sigma_{r,r\neq i} N_{ir} + N_{ii}$. This combined with Equation (3) gives

$$N_i = \sigma_i N_{ii} \sum_r \frac{\nu_{ir}}{\rho_{ir}} + N_{ii} = N_{ii}\left(1 + \sigma_i \sum_r \frac{\nu_{ir}}{\rho_{ir}}\right).$$

Thus,

$$N_{ii} = N_i\left(1 + \sigma_i \sum_r \frac{\nu_{ir}}{\rho_{ir}}\right)^{-1}. \tag{4a}$$

Combining this expression with Equation (2) gives

$$N_{ij} = N_i\left(\frac{\sigma_i \nu_{ij}}{\rho_{ij}(1+\sigma_i \Sigma_r \nu_{ir}/\rho_{ir})}\right). \tag{4b}$$

Observation of these equations shows that the terms in brackets give the fractions of permanent residents of region i who are actually present in any particular region within the population and represent the equilibrium outcome of the mobility process in the entire population.

B. SPECIAL PATTERNS OF MOBILITY

The mobility process defined here is a general process. We show that it can be used to model mobility patterns ranging from complete isolation (no travel at all) to constant traveling. The expressions that result from taking limits of Equations (4a) and (4b) under particular assumptions conform to predictions made on the basis of knowledge of a real population under those conditions.

(1) *Visiting time is short* ($\rho \to \infty$). The assumption $\rho \to \infty$ implies that the rate of return from region j to region i is instantaneous or that the length of time spent by a visitor to region j goes to 0. The limit as $\rho \to \infty$ in Equations (4a) and (4b) leads to a population with $N_{ii} \to N_i$ and $N_{ij} \to 0$ for all i and j. As expected, this means that if every person spends a minute amount of time in a region outside the home region, then at the limit all people will be found in their home region.

(2) *Waiting time between trips is infinite* ($\sigma \to 0$). This case is similar to the previous case and is equivalent to stating that nobody travels. Both logic and the analysis of Equations (4a) and (4b) as $\sigma \to 0$ confirm that the results in this case are the same as for the previous case, that is, $N_{ii} \to N_i$ and $N_{ij} \to 0$ for all i and j.

(3) *Everyone returns home at the same rate, no matter where they traveled* (*all* ρ *equal*). When all the return rates ρ are equal, then

$$N_{ii} = N_i\left(\frac{\rho}{\rho+\sigma_i}\right) \quad \text{and} \quad N_{ij} = N_i\left(\frac{\sigma_i \nu_{ij}}{\rho+\sigma_i}\right).$$

This population distribution occurs when the average time spent in each region is the same, $1/\rho$.

(4) *Visitors tend to stay permanently at their destination* ($\rho_{ij} \to 0 \ \forall \ i,j$). This case corresponds to a migration model as opposed to a model for short-term mobility. If all $\rho_{ij} \to 0$, then Equation (1a) can be solved to give $N_{ii} = N_i \exp(-\sigma_i t)$. As $t \to \infty$, $N_{ii} \to 0$. In other words, if every resident leaves a region permanently, then at the equilibrium of the

mobility process the number of people present in that region who derived originally from the region is zero. The equilibrium value of N_{ij} as $\rho_{ij} \to 0$ and $t \to \infty$ is found by substituting the equilibrium value for N_{ii} into Equation (1b) and integrating to give $N_{ij} = \nu_{ij} N_i \ \forall \ i, j$. Because $\nu_{ii} = 0$ and $\sum_j \nu_{ij} = 1$, this equation indicates that at equilibrium the original residents of region i, N_i, are all distributed among each of the other regions and there are no original residents remaining in region i. The number found at any location is determined from the original distribution of visitors, ν. Thus, in a migration model with no chance of return to the place of origin, the equilibrium population at a given location is composed only of immigrants.

(5) *All people are always traveling* ($\sigma_i \to \infty$). Examination of Equation (4a) shows that if $\sigma_i \to \infty$, then $N_{ii} \to 0$. Interpretation of the limit of Equation (4b) is more complicated. It is easy to show that at the limit

$$N_{ij} = N_i \left[\frac{\nu_{ij}}{\rho_{ij} \sum_r (\nu_{ir} / \rho_{ir})} \right].$$

If all the ρ's are equal, then $N_{ij} = \nu_{ij} N_i$. The equation cannot be simplified further if the ρ's differ from each other. However, the term in brackets is the mean time a traveler from i spends in j relative to the total time spent traveling, and thus this equation essentially gives the fractional occupancy of different regions j by people from region i.

3. INCORPORATING THE MOBILITY PROCESS INTO AN EPIDEMIC MODEL

In order for the transmission of an infectious agent to occur, there must be direct or indirect contact between an infective individual and a susceptible individual. In the following argument, assume that the infectious agent is transmitted directly from one human to another. Extension of the argument to indirectly transmitted agents is straightforward. Assume also that the disease state of an individual (e.g., susceptible, infective, immune) does not affect either rate or pattern of mobility.

Most models for geographic spread of infectious diseases assume that the probability of transmission of a disease from an infective person to a susceptible person is a simple function of the distance between them, with the result that an epidemic diffuses smoothly out from a starting point (e.g., [13]). This may be a reasonable approach to describing

disease spread in historical times when people were more stationary, but in today's society people move far too frequently and with a higher rate of long-distance travel, so there is now less connection between the geographic distance between points and the likelihood of moving from one to the other. Models for geographic spread must allow long-distance travel. In addition, because transmission can occur in any region in which two people come into contact (which may not be the home region of either person), an epidemic model incorporating population mobility must consider both the permanent residences of the two people involved in a contact and the place where the contact occurs.

The mobility of people and the resulting nonrandom mixing can be easily incorporated into an epidemic model by adjusting the composition of a population to reflect who is actually present in a location at the time of disease transmission. Transmission of an infectious agent in a mobile population requires that the following events occur: (1) A susceptible person travels from her home village i to some village k (which may be village i if no traveling occurs), (2) an infective person travels from his home village to the same village k, (3) contact occurs among people at village k, and in some proportion β of the contacts between a susceptible person and an infectious person the infectious organism is transmitted.

The transmission term for the infection process in the ith subpopulation of a population with n regions can be represented mathematically as follows:

$$\sum_{j=1}^{n} \sum_{k=1}^{n} \kappa_k \beta_{ijk} \frac{I_{jk} S_{ik}}{N_k^*}, \tag{5}$$

where κ_k is the average number of contacts per person made in region k, β_{ijk} is the proportion of contacts in region k between a susceptible from region i and an infective from region j that actually result in transmission of the infection, I_{jk} is the number of infectives present in region k who are permanent residents of region j, S_{ik} is the number of susceptibles present in region k who are permanent residents of region i, and $N_k^* = \Sigma_m (S_{mk} + I_{mk} + R_{mk})$ is the number of people actually present in region k. In principle, the number of contacts per person could be a function of the home locations of the people involved, which might be important if, say, cultural background influenced how gregarious a person was. For simplicity's sake, we will leave it as a simple function of location of contact only.

The full epidemic model is a combination of the transmission process represented by expression (5) and terms to represent the mobility process operating in the population. Because the return rates to region i from region k, ρ_{ik}, are not equal in general to the rates at which residents leave region i to travel to region k, $\sigma_i \nu_{ik}$, it is necessary to subdivide the population into residents who are present at their home region and residents who are visiting another region. The equation for change in number of susceptible residents of region i who are actually present in that region is derived as follows:

$$\begin{aligned}\frac{dS_{ii}}{dt} &= \text{no. of residents returning home} \\ &\quad - \text{no. of residents leaving on trips} - \text{new transmissions} \\ &= \sum_k \rho_{ik} S_{ik} - \sigma_i S_{ii} - \sum_j \kappa_i \beta_{iji} \frac{S_{ii} I_{ji}}{N_i^*}.\end{aligned} \tag{6}$$

The equations for susceptible residents of region i who are visiting other regions are derived similarly and are given by

$$\frac{dS_{ik}}{dt} = \sigma_i \nu_{ik} S_{ii} - \rho_{ik} S_{ik} - \sum_j \kappa_k \beta_{ijk} \frac{S_{ik} I_{jk}}{N_k^*}. \tag{7}$$

Summing these equations for all regions gives

$$\frac{dS_i}{dt} = - \sum_k \sum_j \kappa_k \beta_{ijk} \frac{S_{ik} I_{jk}}{N_k^*}$$

and indicates that the total number of susceptibles from region i is altered only through disease transmission and not as a consequence of the mobility process. This reflects the assumption that people do not change the index of their home region (they are assigned to a particular region and do not change that assignment). Thus, technically the model does not include permanent migration unless some mechanism is included to allow changes in the index referring to home region of a person. However, as the analysis above indicated, the mobility model does lead at the limit of relevant parameters to results that are consistent with permanent migration.

Equations for the other disease classes are derived similarly. The complete SIR epidemic model with population mobility is

$$\frac{dS_{ii}}{dt} = \sum_k \rho_{ik} S_{ik} - \sigma_i S_{ii} - \sum_j \kappa_i \beta_{iji} \frac{S_{ii} I_{ji}}{N_i^*}, \tag{8a}$$

$$\frac{dS_{ik}}{dt} = \sigma_i \nu_{ik} S_{ii} - \rho_{ik} S_{ik} - \sum_j \kappa_k \beta_{ijk} \frac{S_{ik} I_{jk}}{N_k^*}, \tag{8b}$$

$$\frac{dI_{ii}}{dt} = \sum_k \rho_{ik} I_{ik} - \sigma_i I_{ii} + \sum_j \kappa_i \beta_{iji} \frac{S_{ii} I_{ji}}{N_i^*} - \gamma I_{ii}, \tag{8c}$$

$$\frac{dI_{ik}}{dt} = \sigma_i \nu_{ik} I_{ii} - \rho_{ik} I_{ik} + \sum_j \kappa_k \beta_{ijk} \frac{S_{ik} I_{jk}}{N_k^*} - \gamma I_{ik}, \tag{8d}$$

$$\frac{dR_{ii}}{dt} = \sum_k \rho_{ik} R_{ik} - \sigma_i R_{ii} + \gamma I_{ii}, \tag{8e}$$

$$\frac{dR_{ik}}{dt} = \sigma_i \nu_{ik} R_{ii} - \rho_{ik} R_{ik} + \gamma I_{ik}, \tag{8f}$$

where γ is the rate of recovery from the disease. This model can be modified in standard ways to allow for vital dynamics, other disease states, or additional details specific to a particular disease.

4. APPLICATIONS OF THE MODEL

The general structure of the mobility process can be used in models for a number of different kinds of diseases, and in addition the model can be extended to allow for more than one type of mobility within a population. We next describe two examples with multiple mobility patterns: (1) a general epidemic model in a population with two types of mobility and (2) an example of the method applied to the spread of measles on a Caribbean island. The last example includes different mobility patterns at different ages.

The extension to multiple mobility types is limited to populations with static structural groups that do not change over time. Consider a population with two static structural groups, *a* and *b*. At equilibrium,

$$\frac{dN_{ii}^a}{dt} = 0, \qquad \frac{dN_{ii}^b}{dt} = 0, \qquad \frac{dN_{ij}^a}{dt} = 0, \qquad \text{and} \qquad \frac{dN_{ij}^b}{dt} = 0.$$

Using the derivation above, it is easily shown that one can derive equations analogous to Equations (4a) and (4b) but with group-specific elements.

In general, if the mobility process is linked to dynamic structural groups such as age, so that both the structural group and the consequent mobility of individuals vary over time, either one must assume that the time course of the disease is so short that people do not change age classes (which changes the dynamic class to a static class, as in our second example), or one must use a different kind of model. We comment on the latter problem in the final section.

A. *A GENERAL EPIDEMIC MODEL FOR A NONSEXUALLY TRANSMITTED DISEASE IN A POPULATION WITH TWO TYPES OF MOBILITY*

In a population divided into two distinct groups, there can be both within-group contact and between-group contact. Thus, a susceptible individual can become infected by either an infective with the same mobility pattern or an infective with a different mobility pattern. Because the groups are static and independent of one another, the contact probabilities of the susceptible person with each kind of infective person can be summed. This results in the following model equations for susceptibles with mobility type a:

$$\frac{dS_{ik}^a}{dt} = \sigma_i{}^a \nu_{ik}^a S_{ii}^a - \rho_{ik}^a S_{ik}^a - \sum_{j=1}^{n} \kappa_k \beta_{ijk} \frac{S_{ik}^a \left(I_{jk}^a + I_{jk}^b\right)}{N_k^*}, \tag{9a}$$

$$\frac{dS_{ii}^a}{dt} = \sum_{k=1}^{n} \rho_{ik}^a S_{ik}^a - \sigma_i{}^a S_{ii}^a - \sum_{j=1}^{n} \kappa_i \beta_{iji} \frac{S_{ii}^a \left(I_{ji}^a + I_{ji}^b\right)}{N_i^*}, \tag{9b}$$

where $N_i^* = \Sigma_m (S_{mi}^a + I_{mi}^a + R_{mi}^a + S_{mi}^b + I_{mi}^b + R_{mi}^b)$ is the total number of people of all types present at location i. Equations for susceptibles of type b and for the infective and removed classes are derived similarly. This model can easily be generalized to an arbitrary number of mobility types. In all cases, as long as the groups are defined on the basis of static characteristics, the general model includes transmission terms that are sums of the interactions among people of different types. Each of the individual interactions has the form of Equation (5) but with parameters specific to the groups involved in a contact. For example, in Equation (9a), the transmission term is

$$\sum_j \kappa_k \beta_{ijk} \frac{S_{ik}^a I_{jk}^a}{N_k^*} + \sum_j \kappa_k \beta_{ijk} \frac{S_{ik}^a I_{jk}^b}{N_k^*}.$$

B. A MODEL FOR THE TRANSMISSION OF MEASLES IN THE COMMONWEALTH OF DOMINICA, WEST INDIES

Our second example incorporating the mobility process into an epidemic model relates to an actual epidemic on the West Indian island of Dominica. Dominica is a 300 square mile island in the Lesser Antilles with a population of around 70,000. In 1984 there was a major measles epidemic on the island, with over 200 reported cases distributed throughout the seven health districts. The geographic distribution of measles cases during the epidemic has been linked to observed mobility patterns among the regions on the island [17]. Mathematical modeling of such an epidemic can proceed using the kind of model described here.

Measles transmission in Dominica and elsewhere is closely tied to the school system [3, 18]. In addition, children in Dominica travel to different regions as a consequence of school-related activities. Thus, it is important to divide the population into separate age classes, among which the mobility patterns differ.

Age is a dynamic characteristic rather than a static characteristic. However, Dominica is not a large enough island to maintain measles in an endemic state. The disease enters the island, runs its course, and then goes extinct. The 1984 epidemic began around the middle of August, and by early January 1985 there were no more cases of the disease reported to the health authorities. The disease apparently did not appear again on the island for several months. Thus, although people do move into new age classes, a single epidemic process for a disease like measles takes so little time that it is safe to assume in a model for this process that age is a static characteristic, that people remain in the age class to which they were assigned for the duration of the epidemic.

Based on knowledge about the population structure of Dominica, the population is divided into seven districts (corresponding to the seven health districts on the island), each of which is further divided into three age classes: infants (0–2 yr, represented by the superscript b), school age (2–15 yr, represented by the superscript s), and adults (> 15, represented by the superscript a). These age classes differ in their mobility patterns. We consider three types of mobility, with associated parameters σ, ρ, and ν. These patterns include (1) adult mobility resulting from work-related and recreational travel (indicated below by the superscript w), (2) general children's mobility resulting from recreational travel (indicated below by the superscript c), and (3) childhood travel related to school events such as field trips and sporting activities (indicated below by the superscript f). School-related trips do not

follow the adult pattern and tend to be biased toward those districts with significant educational features.

The contact processes for the three age classes can be derived in an analogous way to the examples above. Infants can become infected with the measles virus as a result of their family-related travel and the consequent contact with an infected adult or child from the same or another region. School-aged children become infected as a consequence of either family- or school-related travel. Adults become infected after contacts resulting from family-related travel.

The model equations for infants and adults have similar structures but with group-specific parameters. However, because schoolchildren can contract an infection through more than one type of activity (either recreational travel or school-related travel), the model equations for schoolchildren must consider both the multiple mobility processes and the consequent differences in mixing populations during which disease transmission can occur (since schoolchildren are assumed to mix with other schoolchildren only on school-related trips). This scenario results in the following measles transmission model [with the superscript (b,a) indicating that the equation is valid for either infants (b) *or* adults (a) and with the superscript (c,w) indicating that the equation is valid for either a child's *or* an adult's mobility—b and c always appear together in the same equation, as do a and w]:

$$\frac{dS_{ik}^{(b,a)}}{dt} = \sigma_i^{(c,w)}\nu_{ik}^{(c,w)}S_{ii}^{(b,a)} - \rho_{ik}^{(c,w)}S_{ik}^{(b,a)} - \sum_{j=1}^{7}\beta_{ijk}\kappa_k\left[S_{ik}^{(b,a)}\left(\frac{I_{jk}^b + I_{jk}^s + I_{jk}^a}{N_k^*}\right)\right], \tag{10a}$$

$$\frac{dS_{ii}^{(b,a)}}{dt} = \sum_{k=1}^{7}\rho_{ik}^{(c,w)}S_{ik}^{(b,a)} - \sigma_i^{(c,w)}S_{ii}^{(b,a)} - \sum_{j=1}^{7}\beta_{iji}\kappa_i\left[S_{ii}^{(b,a)}\left(\frac{I_{ji}^b + I_{ji}^s + I_{ji}^a}{N_i^*}\right)\right], \tag{10b}$$

$$\frac{dS_{ik}^s}{dt} = \sigma_i^c\nu_{ik}^c S_{ii}^s - \rho_{ik}^c S_{ik}^s - \sum_{j=1}^{7}\beta_{ijk}\kappa_k\left[S_{ik}^s\left(\frac{I_{jk}^b + I_{jk}^s + I_{jk}^a}{N_k^*}\right)\right] + \sigma_i^f\nu_{ik}^f S_{ii}^s - \rho_{ik}^f S_{ik}^s - \sum_{j=1}^{7}\beta_{ijk}\kappa_k^s\left(\frac{S_{ik}^s I_{jk}^s}{N_k^{s*}}\right), \tag{10c}$$

$$\frac{dS_{ii}^s}{dt} = \sum_{k=1}^{7}\rho_{ik}^c S_{ik}^s - \sigma_i^c S_{ii}^s - \sum_{j=1}^{7}\beta_{iji}\kappa_i\left[S_{ii}^s\left(\frac{I_{ji}^b + I_{ji}^s + I_{ji}^a}{N_i^*}\right)\right]$$

$$+ \sum_{k=1}^{7} \rho_{ik}^{f} S_{ik}^{s} - \sigma_i^{f} S_{ii}^{s} - \sum_{j=1}^{7} \beta_{iji} \kappa_i^{s} \left(\frac{S_{ii}^{s} I_{ji}^{s}}{N_i^{s*}} \right), \tag{10d}$$

$$\frac{dI_{ik}^{(b,a)}}{dt} = \sigma_i^{(c,w)} \nu_{ik}^{(c,w)} I_{ii}^{(b,a)} - \rho_{ik}^{(c,w)} I_{ik}^{(b,a)} + \sum_{j=1}^{7} \beta_{ijk} \kappa_k \left[S_{ik}^{(b,a)} \left(\frac{I_{jk}^{b} + I_{jk}^{s} + I_{jk}^{a}}{N_k^{*}} \right) \right] - \gamma I_{ik}^{(b,a)}, \tag{10e}$$

$$\frac{dI_{ii}^{(b,a)}}{dt} = \sum_{k=1}^{7} \rho_{ik}^{(c,w)} I_{ik}^{(b,a)} - \sigma_i^{(c,w)} I_{ii}^{(b,a)} + \sum_{j=1}^{7} \beta_{iji} \kappa_i \left[S_{ii}^{(b,a)} \left(\frac{I_{ji}^{b} + I_{ji}^{s} + I_{ji}^{a}}{N_i^{*}} \right) \right] - \gamma I_{ii}^{(b,a)}, \tag{10f}$$

$$\frac{dI_{ik}^{s}}{dt} = \sigma_i^{c} \nu_{ik}^{c} I_{ii}^{s} - \rho_{ik}^{c} I_{ik}^{s} + \sum_{j=1}^{7} \beta_{ijk} \kappa_k \left[S_{ik}^{s} \left(\frac{I_{jk}^{b} + I_{jk}^{s} + I_{jk}^{a}}{N_k^{*}} \right) \right] + \sigma_i^{f} \nu_{ik}^{f} I_{ii}^{s} - \rho_{ik}^{f} I_{ik}^{s} + \sum_{j=1}^{7} \beta_{ijk} \kappa_k^{s} \left(\frac{S_{ik}^{s} I_{jk}^{s}}{N_k^{s*}} \right) - \gamma I_{ik}^{s}, \tag{10g}$$

$$\frac{dI_{ii}^{s}}{dt} = \sum_{k=1}^{7} \rho_{ik}^{c} I_{ik}^{s} - \sigma_i^{c} I_{ii}^{s} + \sum_{j=1}^{7} \beta_{iji} \kappa_i \left[S_{ii}^{s} \left(\frac{I_{ji}^{b} + I_{ji}^{s} + I_{ji}^{a}}{N_i^{*}} \right) \right] + \sum_{k=1}^{7} \rho_{ik}^{f} I_{ik}^{s} - \sigma_i^{f} I_{ii}^{s} + \sum_{j=1}^{7} \beta_{iji} \kappa_i^{s} \left(\frac{S_{ii}^{s} I_{ji}^{s}}{N_i^{s*}} \right) - \gamma I_{ii}^{s}, \tag{10h}$$

$$\frac{dR_{ik}^{(b,a)}}{dt} = \sigma_i^{(c,w)} \nu_{ik}^{(c,w)} R_{ii}^{(b,a)} - \rho_{ik}^{(c,w)} R_{ik}^{(b,a)} + \gamma I_{ik}^{(b,a)}, \tag{10i}$$

$$\frac{dR_{ii}^{(b,a)}}{dt} = \sum_{k=1}^{7} \rho_{ik}^{(c,w)} R_{ik}^{(b,a)} - \sigma_i^{(c,w)} R_{ii}^{(b,a)} + \gamma I_{ii}^{(b,a)}, \tag{10j}$$

$$\frac{dR_{ik}^{s}}{dt} = \sigma_i^{c} \nu_{ik}^{c} R_{ii}^{s} - \rho_{ik}^{c} R_{ik}^{s} + \sigma_i^{f} \nu_{ik}^{f} R_{ii}^{s} - \rho_{ik}^{f} R_{ik}^{s} + \gamma I_{ik}^{s}, \tag{10k}$$

$$\frac{dR_{ii}^{s}}{dt} = \sum_{k=1}^{7} \rho_{ik}^{c} R_{ik}^{s} - \sigma_i^{c} R_{ii}^{s} + \sum_{k=1}^{7} \rho_{ik}^{f} R_{ik}^{s} - \sigma_i^{f} R_{ii}^{s} + \gamma I_{ii}^{s}. \tag{10l}$$

In this model, $S_i^{(b,s,a)}$, $I_i^{(b,s,a)}$, and $R_i^{(b,s,a)}$ are the numbers of susceptible, infective, and recovered individuals, respectively, of a particular age class in district i, $N_k^{*} = \sum_l \sum_{\bullet=b,s,a} (S_{lk}^{\bullet} + I_{lk}^{\bullet} + R_{lk}^{\bullet})$ is the number of people actually present in district k at time t, N_k^{s*} is the number of schoolchildren present in district k for school-related activities at time t and is a function of the number of schoolchildren from

each region and their school-related mobility patterns, β_{ijk} is the proportion of contacts between a susceptible from district i and an infective from district j that occur in district k and result in transmission of the virus, κ_k is the average number of contacts made by a person while visiting location k, κ_k^s is the average number of contacts made by a schoolchild while visiting location k for a school-related activity, and γ is the recovery rate from measles. The different mobility patterns are represented by the parameters σ, ρ, and ν, with superscript c referring to general children's mobility, superscript w referring to adult mobility, and superscript f referring to school-related mobility. For a disease like measles, it may very well be that the transmission fraction β_{ijk} varies depending on the ages of people involved in an interaction (B. Bolker, personal communication). We assume here that this does not happen, although it could be included by simply separating the (additive) transmission terms in Equations (9a)–(9h) into expressions with variable β's.

Although this model is highly complex, most of the parameters can be estimated from easily collected data. For example, data on daily activities and short-term travel patterns on the island have been collected for estimation of the adult mobility patterns [17]. In addition, observations of children's activities and interviews with head teachers at all secondary schools and several primary schools and preschools can be used to make assumptions about the mobility of children. Because these data are relatively easy to collect, the inclusion of the additional structure in the model does not limit its practical use.

Knowledge of the mobility patterns linking regions can help to explain observed patterns of geographic spread of an epidemic. Weekly incidence data by health district of the 1984 measles epidemic on Dominica are available. These data indicate that the epidemic probably began in the Portsmouth district at the north end of the island (Figure 2). Early epidemic peaks occur in the St. Joseph, La Plaine, and Marigot Health Districts, with the epidemic reaching a peak in the Castle Bruce Health District 2–3 weeks later. Grand Bay, with only two early cases of the disease, appears to have missed the epidemic. Although actual weekly incidence data are lacking for the Roseau Health District, nurses in the district believe that the majority of the cases from Roseau occurred late in the epidemic.

Data from both interviews with residents of the island and counts of traffic at several locations on the island were used to construct networks showing links among regions (Figure 3). Several conclusions about the Dominican transportation system can be drawn from these diagrams. First, both sets of data show the overriding importance of the capital, Roseau, to the island. Second, there is a clear distinction between the

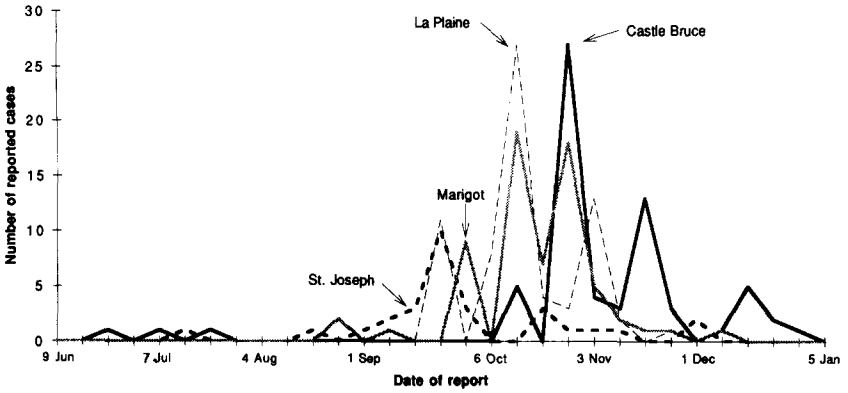

FIG. 2. Weekly incidence during the latter half of 1984 of measles by health district on the island of Dominica, West Indies. Graph does not include early cases in the Grand Bay district and does not include the Roseau or Portsmouth districts because of lack of weekly incidence data.

Caribbean coastal districts (Roseau, St. Joseph, and Portsmouth) and the districts on the Atlantic side (Marigot, Castle Bruce, La Plaine, and Grand Bay), with both sets of data indicating much more frequent travel associated with the Caribbean side of the island. Third, frequencies of both vehicular travel and travel of respondents between Grand Bay and Roseau were the second highest on the island, but other data show mostly local travel of Grand Bay natives to Roseau and back and indicate that Grand Bay is relatively isolated physically and socially from the rest of the island.

The measles incidence data reflect the social and geographic isolation of the Grand Bay district. There were only two reported cases of measles for the entire year, even though all other districts on the Atlantic side of the island had major outbreaks of the disease. It is possible that people from Grand Bay went to the Roseau health center for treatment instead of the Grand Bay center (J. Astaphan, personal communication) or that diagnoses of the disease were not officially made at the time of the epidemic, but the general isolation of the area suggests that the observed patterns may reflect the actual course of events. Data also indicate that the Castle Bruce district, which includes a Carib Indian reservation, is relatively weakly connected to other districts. This may help to explain the later epidemic peak in this district.

Simulations of the model presented here with the mobility data collected on Dominica have not yet been done. However, the data

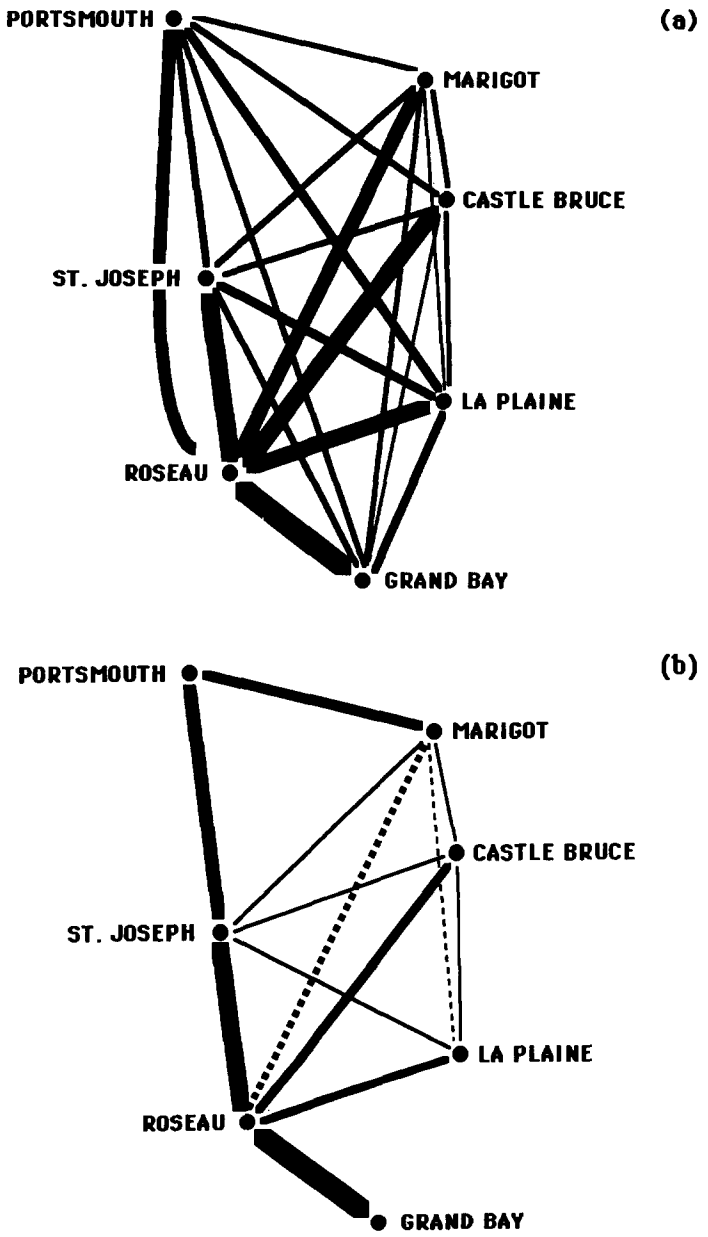

FIG. 3. Network diagrams showing links among health districts. (a) Derived from health center interviews. (b) Derived from data on frequency and direction of vehicular travel. Line thickness indicates relative frequency of travel between nodes. Dashed lines are used to indicate that the roads between Roseau and Marigot and between La Plaine and Marigot pass through a village in the St. Joseph district, resulting in a link that is not technically direct.

presented here suggest that the mobility patterns have influenced significantly the epidemic patterns, so that a model developed to explain the observed epidemic and predict future epidemics should incorporate population mobility among regions.

5. ADVANTAGES AND LIMITATIONS OF THE MOBILITY MODEL

One major advantage of the mobility model is that it allows for the simultaneous consideration of both epidemic and behavioral processes and therefore can be used to look at interactions between these processes. When the mobility process is at an equilibrium, the model collapses to a standard SIR epidemic model for a structured population, and when there is no disease the model is just a simple mobility process. The behavior of the standard SIR model has been well studied, and the analysis above describes the equilibrium behavior of the mobility model. Analysis of the complete model will allow one to study what happens within the region bounded by these two processes and will lead to a greater understanding of how mobility and disease transmission interact with one another.

A second advantage of the mobility model is that because it builds the process of contact between a susceptible individual and an infective individual into a dynamic model, it allows one to look not just at the fact that person A came into contact with person B, but at how, when, and where that contact occurred. Since the model includes the key element of location of a contact, parameters related to the probability of transmission, such as β, the proportion of contacts that result in transmission, and κ, the number of contacts per person per unit time, can be made a function not only of where people come from but also of where the contact occurs. Consequently, for example, the probability that American travelers to tropical regions of Africa will become infected by malaria can be linked to both their general susceptibility given that they are from the United States and their increased probability of getting bitten by a sporozoite-carrying mosquito. Since the transmission probabilities and contact numbers can be specific to the location of contact, the formulation allows one to specify different transmission risks for a disease like influenza for someone traveling to a high-density city like Hong Kong at the peak of an influenza outbreak and someone traveling to the deserts of Death Valley, even if the two people are identical in all other respects.

Environmental factors associated with the location of contact can have important effects on transmission risk. For example, the risks of transmission of intestinal helminths or hookworm, which have life

stages in the soil or water, are strongly influenced by the general sanitation of an area where people are interacting and are perhaps even more dependent on these factors than on the general susceptibility of an uninfected person or the infectious stage of an infected person.

Environmental risk factors can vary greatly over very short distances. The island of Dominica, West Indies, has an area of approximately 300 square miles, the size of many counties within the United States. Even in this small area there is marked variation across districts of three environmental variables—water supply, population density, and banana production (a measure of the importance of agriculture to an area). These variables almost certainly influence the risk of transmission of different kinds of infectious disease.

Unlike factors related to the biology of the parasite, the physiological effects of an infection on a host, or the susceptibility or resistance of a host to infection, environmental risk factors are often relatively easy to measure. Many of these factors are routinely gathered by public health officials, in national censuses, and by utility companies. They do not require the extensive clinical and laboratory studies necessary to study parasite biology and the factors underlying variability in host susceptibility and resistance. Thus, the use of a model that allows this variability may prove more practical than one that assumes that it is negligible.

Data needed to estimate the mobility matrix, although not widely available, are also relatively easy to collect. Records on who enters or leaves a country are usually kept by immigration authorities. Airline companies collect data on the number of passengers leaving from a particular location and traveling to other locations. Rvachev and Longini [14] used such data to describe the global spread of influenza. On a more local scale, standard ethnographic techniques, such as surveys and participant observation, can be used to collect data on the daily behavior of individuals in a population. Counters can be set up across roads to enumerate the numbers of vehicles traveling along the roads. The main difficulty with all of these methods is the intensity of effort required to collect the data.

The major limitation of the mobility model has been alluded to earlier—it must be based on groups defined by static characteristics that do not change over time. While this constraint may not be a problem for some diseases and populations, it presents major problems when mobility patterns are linked to dynamic characteristics such as age. In a model with static groups, the mobility patterns of different groups are independent of one another, with the result that the model consists of sums of contact terms all of which have the same basic structure. If the mobility patterns are linked to changing variables, then

the effects of different groups cannot be separated. It should be possible to describe the mobility process in such a situation, but the methods used would differ from those of a model for static subgroups, and it is not clear that the resulting model would have a structure analogous to that found for the static population.

The mobility model as presented here assumes that a person who travels to a region must return *directly* to the region of origin and is not allowed to travel to other regions first. This is a simplifying assumption that is not particularly realistic, since there are many examples in real populations of circular mobility or of trips with more than one destination. A generalization of the model that relaxes this assumption is in preparation.

A third limitation of the mobility model is that it increases the complexity of structured population models. Because of this, careful assessment of the problem being addressed by the model should be made to determine whether the additional complexity is needed. In most cases, however, although data are not widely available at the present time to estimate the additional parameters, they are generally more easily collected than data on physiological characteristics such as susceptibility or infectivity.

The development of mathematical models for the geographic spread of infectious diseases has lagged behind other areas of mathematical modeling. Yet one of the most obvious characteristics of many diseases is their marked spread across a landscape. The model presented here provides one method that may prove useful in better tying mathematical epidemiology to these patterns of infectious disease spread across space and time.

We dedicate this work to Stavros Busenberg, who would no doubt have had major and interesting contributions to this paper if he had lived long enough to enjoy a collaboration that was just barely beginning.

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