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A FIRST ATTEMPT TO COMBINE INTERREGIONAL MIGRATION AND SPATIAL DIFFUSION MODELS

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## A first Attempt to Combine Interregional Migration and Spatial Diffusion Models

A hybrid migration-diffusion model would be of considerable interest.<sup>1</sup> The synthesis of two dynamic spatial models has much appeal -- too often we unwittingly generate and extend models independently of other models even though they are describing very closely related processes. More specifically, it is clear that the diffusion of information is often undertaken by agents who are shifting locations. For example, firms relocate or establish branch plants; opinion leaders change their place of residence. Thus the spatial diffusion process is often doubly dynamic -- information is spread according to an information field operator, but from one time period to the next, the distribution of the population (both knowers and non-knowers) is itself changing. On the face of it, diffusion processes of this type would appear to be highly relevant in a regional development context. This note represents a first crude attempt to model such systems.<sup>1</sup>

First, let us introduce the following notation and terminology:

- P : a migration matrix operator of order n, where n is the number of regions; an element p<sub>ij</sub> denoting the probablility of a person currently in i moving to j by the next time period;

Q : an information diffusion operator or order n, an element  $q_{ij}$  denoting the probability that someone in region i at the beginning of a time period will tell someone in j by the end of the period. [In this formulation, no more than one "telling" per knower is allowed in any unit time interval (i.e.,  $\sum_{j} q_{ij} \leq 1.0$ ); it is also assumed the contacts are made at the beginning of each time period, i.e., before migration occurs.]

The equation

$$X(t+1) = X(t)P$$

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describes the expected sequence of the total population distribution over time.

The equation

$$Y(t+1) = Y(t) \begin{bmatrix} P + Q \begin{bmatrix} 1 - \frac{Y_{1}(t)}{X_{1}(t)} & 0 \dots 0 \\ 0 & \ddots & 0 \end{bmatrix} \\ \vdots & \ddots & 1 - \frac{Y_{n}(t)}{X_{n}(t)} \end{bmatrix}$$
(2)

describes the expected sequence of the distribution of knowers over time.

Let the elements of the diagonal matrix be denoted by  $r_{ij}(t)$  -- this is the probability that a contacted person in j is one of those who does not yet know about the innovation. Equation (2) can then be written more simply as

$$Y(t+1) = Y(t) \left[P + QR(t)\right]$$
(2a)

Equations (1) and (2a) describe the expected trajectories of the total population and the knowers subgroup. (Non-knowers trajectories are of course simply the difference between (1) and (2a)). The above model makes a number of undoubtedly unwarranted assumptions about both the migration and diffusion processes. As it stands, it represents only a first approximation of such systems. In fact, the model represents to a large degree little more than an accounting framework which links simple migration and diffusion models. There are innumerable ways in which the model could be extended and enriched. Perhaps the most obvious modification would be to make the MIF operators embedded in Q a function of the population distribution X -- a decline in the population of a place would generally be expected to make contacts from all other locations less likely. A gravity type relationship could be postulated, estimated, and incorporated into the model.<sup>2</sup>

> Ross D. MacKinnon, March 5th, 1975.

<sup>1</sup> It was Waldo Tobler who suggested to me that it might be interesting to combine the two classes of models.

<sup>2</sup> After writing this note, the genetics literature was brought to my attention. (See for example, Jacquard, 1974) There are a number of models which describe processes where populations are migrating and simultaneously mutations are occurring. These processes are rather simpler than the ones described above in that mutations occur according to probability distributions which are independent of the population group (region). In the migration-spatial diffusion model the probabilities of successful contacts and the nature of the spread of information is highly conditioned by location -location of both innovators and potential adopters. In spite of their comparative simplicity, the migration-mutation models of genetics are under review to determine their relevance to the above problem. In addition, the theory of epidemics and Markov random fields may offer some methodological clues.