A FIRST ATTEMPT TO

COMBINE INTERREGIONAL MIGRATION

AND SPATIAL DIFFUSION MODELS

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A hybrid migration-diffusion model would be of consi-
derable interest.[1] 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.[1]

First, let us introduce the following notation and
terminology:

$X(t)$: a vector of dimension r representing the regional
distribution of population at time t;

$Y(t)$: a vector of dimension r representing the number
of knowers at time t;

P : a migration matrix operator of order n, where n
is the number of regions; an element p_{ij} 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. $\big[$ 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.$\big]$

The equation

$$X(t+1) = X(t)P \tag{1}$$

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

The equation

$$Y(t+1) = Y(t) \left[P + Q \left[\begin{array}{cccc} 1 - \dfrac{Y_1(t)}{X_1(t)} & 0 \cdots 0 \\ & \ddots & 0 \\ 0 & \ddots & 1 - \dfrac{Y_n(t)}{X_n(t)} \\ 0 \cdots 0 & \end{array} \right] \right] \tag{2}$$

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

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

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.[2]

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[1] It was Waldo Tobler who suggested to me that it might be interesting to combine the two classes of models.

[2] 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.