MULTIREGIONAL ZERO GROWTH POPULATIONS WITH CHANGING RATES

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FOREWORD

Declining rates of national population growth, continuing differential levels of regional economic activity, and shifts in the migration patterns of people and jobs are characteristic empirical aspects of many developed countries. In some regions they have combined to bring about relative (and in some cases *absolute*) population decline of highly urbanized areas; in others they have brought about rapid metropolitan growth.

The objective of the Urban Change Task in IIASA's Human Settlements and Services Area is to bring together and synthesize available empirical and theoretical information on the principal determinants and consequences of such urban growth and decline.

The study of the redistributional demographic consequences of declining rates of natural increase is complicated by the fact that virtually all of the mathematical theory of stable population growth is founded on an assumption of fixed rates of fertility, mortality, and migration. Dr. Kim suggests in this paper how the relaxation of such an assumption reveals new insights about multiregional population dynamics.

A list of publications in the Urban Change Series appears at the end of this paper.

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ABSTRACT

The theory of stable population dynamics is relatively well developed in the demographic literature, but virtually all of it is founded on the assumption of unchanging rates of fertility, mortality, and migration. The case of changing rates is relatively underdeveloped and little is known about the influence of changing rates on age composition and regional distribution. This paper considers how multiregional zero growth populations evolve over time when exposed to changing birth, death, and migration rates. It illuminates the ways in which an age-by-region composition is influenced by the pattern of recent rates and how the influence of an initial composition is lost over time.

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MULTIREGIONAL ZERO GROWTH POPULATIONS WITH CHANGING RATES

I. INTRODUCTION

In recent years, fertility in most developed countries seems to be reaching or have already reached near-replacement levels, with perturbations from time to time resulting from social and economic conditions. We are interested in describing mathematically the dynamics of such populations. To do this we begin with the result of the *weak ergodic theorem*, which states that the age structure of a population subject to an arbitrary sequence of fertility and mortality schedules over time eventually loses its dependence on the initial age distribution and comes to be a function only of its relatively recent history of fertility and mortality rates (e.g., Lopez, 1961). Nothing is said in this theorem, however, about how age structure is determined by recent vital rates or how the effect of an initial age structure is lost. This has led us to examine the dynamics of populations with arbitrarily changing vital rates but restricted to have a net reproduction rate (NRR) of unity (Kim and Sykes, 1978).

As levels and changes in levels of fertility and mortality diminish, in- and outmigration play an increasingly important role in determining the dynamics of regional populations. Rogers (1975) has developed a model of multiregional population dynamics in which migration schedules as well as mortality and fertility schedules play an important role. He thereby has extended stable population theory to include multiregional populations. Analogous to stable population theory, multiregional stable population theory states that if regional age-specific schedules of fertility, mortality, and migration are fixed for a long time, the population evolves into a multiregional stable population with fixed regional shares and regional age compositions.

Stable theory for populations with fixed rates does not extend to populations with arbitrarily changing rates over time in a predictable way. We can, however, obtain specific formulas for different attributes of such populations and see how weak ergodicity works explicitly for populations close to stationarity but with otherwise arbitrary rates. To do this we restrict the number of age groups to two for a closed population and the number of regions to two for a multiregional population without age structure. The results obtained are true *qualitatively* for populations with an arbitrary number of age groups and regions. We also follow the usual restriction of a one-sex model when age structure is considered.

In the next section we review the dynamics of closed populations with changing rates and NRR = 1. We then show how the argument can be applied to two-regional populations and, after formulating a model of biregional population dynamics with changing rates in the third section, we discuss the dynamics of populations with age groups *and* regions in the fourth section, and conclude with a brief discussion of several new interpretations of old concepts.

II. DYNAMICS OF CLOSED ZERO GROWTH POPULATIONS

In this section we summarize the results of Kim and Sykes (1978). However, the vectors and matrices describing population dynamics are here transposed back to the more conventional forms. This change makes the generalization to multiregional dynamics easier allowing one to retain the representation usually used by demographers.

We consider a closed population with two age groups expressed in vector form

$$\underline{X}_t = (X_{t1}\ X_{t2})' \qquad t = 0,1,2,\ldots \qquad (2.1)$$

and introduce the 2 x 2 population projection matrix (ppm)

$$\underset{\sim}{A}_t = \begin{bmatrix} b_{t1} & b_{t2} \\ s_t & 0 \end{bmatrix} \qquad t = 1,2,\ldots \qquad (2.2)$$

(See Kim and Sykes, 1978, for a more detailed explanation of the notation used.) Since the dynamics of a population with age structure $\underline{X}_t$ at time t is given by:

$$\underline{X}_{t+1} = \underset{\sim}{A}_{t+1}\ \underline{X}_t \qquad t = 0,1,2,\ldots \qquad (2.3)$$

it follows that the age distribution at time t is

$$\underline{X}_t = \underset{\sim}{A}_t\ \underset{\sim}{A}_{t-1} \cdots \underset{\sim}{A}_2\ \underset{\sim}{A}_1\ \underline{X}_0 = \underset{\sim}{M}_t\ \underline{X}_0 \qquad (2.4)$$

where we have written the backward product of t ppm's as $\underset{\sim}{M}_t$ to avoid writing a long string of matrices frequently.

We first consider the dynamics of populations when the ppm is row-stochastic,

$$\underset{\sim}{A}_t = \begin{bmatrix} 1 - b_t & b_t \\ 1 & 0 \end{bmatrix} \qquad t = 1,2,\ldots \qquad (2.5)$$

in which fertility is split arbitrarily between the two age groups and with mortality set equal to zero. Notice that the period $NRR_t = 1$ for all t, but that the cohort $NRR_t = 1 - b_t + b_{t+1} \neq 1$. By directly multiplying the matrices, it can be shown that

$$\underset{\sim}{M}_t = \begin{bmatrix} G_t & 1 - G_t \\ G_t - \gamma_t & 1 - G_t + \gamma_t \end{bmatrix} \qquad t = 1,2,\ldots \qquad (2.6)$$

where

$$G_t = 1 - b_1 + b_1 b_2 - \cdots + (-1)^t b_1 \cdots b_t \tag{2.7a}$$

and

$$\gamma_t = (-1)^t b_1 \cdots b_t \tag{2.7b}$$

If the sequence of birth rates $\{b_t\}$ is bounded below 1 (it is a sufficient, but not a necessary condition) then

$$\lim_{t \to \infty} \gamma_t = 0$$

and

$$\lim_{t \to \infty} G_t = G \tag{2.8}$$

exist. Hence the product matrix $\underset{\sim}{M}_t$ converges to a constant matrix of rank 1, i.e.,

$$\lim_{t \to \infty} \underset{\sim}{M}_t = \begin{bmatrix} G & 1 - G \\ G & 1 - G \end{bmatrix} \tag{2.9}$$

where G satisfies

$$1 - b_1 < G < 1 - b_1 + b_1 b_2 \tag{2.10}$$

and thus is completely determined by early fertility rates. The age distribution at time t is given by, from equations (2.4) and (2.9)

$$\underline{X}_t = \left(G X_{01} + (1 - G) X_{02}\right) \underline{1} \tag{2.11}$$

for large t. The eventual population size is a weighted average of the initial population in the two age groups, with the weight determined by early vital rates, and the relative age distribution is uniform. We have seen that even with a changing fertility pattern over time, strong ergodicity holds and that all of the usual measures describing the population eventually become constant.

We next consider the dynamics of populations with column-stochastic ppms, i.e., $\underset{\sim}{A}_t$ now is of the form

$$\underset{\sim}{A}_t = \begin{bmatrix} 1 - s_t & 1 \\ s_t & 0 \end{bmatrix} \qquad t = 1,2,... \qquad (2.12)$$

In this case fertility in the second age group is constant, while that in the first age group varies with mortality. For this ppm, both period and cohort NRR are unity. By directly multiplying the ppms, it can be shown that

$$\underset{\sim}{M}_t = \begin{bmatrix} H_t & H_t - \eta_t \\ 1 - H_t & 1 - H_t + \eta_t \end{bmatrix} \qquad t = 1,2,... \qquad (2.13)$$

where

$$H_t = 1 - s_t + s_t\, s_{t-1} - \cdots + (-1)^t\, s_t \cdots s_1 \qquad (2.14a)$$

and

$$\eta_t = (-1)^t\, s_t \cdots s_1 \qquad (2.14b)$$

Although the form of H_t is superficially similar to the expression for G_t given in equation (2.7), it differs crucially in that here the recent elements of the sequence $\{s_t\}$ determine H_t. Because of this, the sequence $\{H_t\}$ has no limit as t increases, although,

$$1 - s_t < H_t < 1 - s_t + s_t\, s_{t-1} \qquad (2.15)$$

The value can be calculated to an arbitrary degree of accuracy using more terms. The sequence of product matrices $\{\underset{\sim}{M}_t\}$ satisfies

$$\lim_{t \to \infty} \left\{ \underset{\sim}{M}_t - \begin{bmatrix} H_t & H_t \\ 1 - H_t & 1 - H_t \end{bmatrix} \right\} = 0 \qquad (2.16)$$

In other words, the population at time t, for large t, is given by, from equations (2.4) and (2.16),

$$\underline{X}_t = (X_{01} + X_{02}) \begin{bmatrix} H_t \\ 1 - H_t \end{bmatrix} \qquad (2.17)$$

i.e., although the total population size is fixed at all times, the number of births and the age distribution keep constantly changing over time and are determined by the recent vital rates. See Kim and Sykes (1978) for more detailed discussion and generalization.

III. DYNAMICS OF BIREGIONAL ZERO GROWTH POPULATIONS

We now consider populations without age structure located in two regions. A major formal difference between this population and the "closed" population with two age groups is that now all four transitions are possible, whereas the contribution from the second age group to itself was zero for the closed population. When this is translated into a transition matrix (also a ppm) all four cells of the ppm have non-zero entries for the two-region (biregional) dynamics.

We can formulate the dynamics of regional populations in two alternative ways. First, we may take a period approach by using the two-region accounting relationship (Rogers, 1968):

$$\begin{bmatrix} P_1(t) \\ P_2(t) \end{bmatrix} = \begin{bmatrix} 1 + b_1(t) - d_1(t) - O_1(t) & O_2(t) \\ O_1(t) & 1 + b_2(t) - d_2(t) - O_2(t) \end{bmatrix} \begin{bmatrix} P_1(t-1) \\ P_2(t-1) \end{bmatrix}$$

$$t = 1, 2, \ldots \qquad (3.1)$$

where $P_i(t)$, $i = 1,2$, is the population size in region i at time t and $b_i(t)$, $d_i(t)$, and $O_i(t)$, $i = 1,2$, are the crude rates of birth, death, and outmigration for region i at time t. If the rates given are the usual single year rates, the time unit of equation (3.1) is also one year. If we denote the matrix in equation (3.1) as $\underset{\sim}{C}(t)$, i.e.,

$$\underset{\sim}{C}(t) = \begin{bmatrix} 1 + b_1(t) - d_1(t) - O_1(t) & O_2(t) \\ O_1(t) & 1 + b_2(t) - d_2(t) - O_2(t) \end{bmatrix} \tag{3.2}$$

then the dynamics of regional populations at time t are given by,

$$\underline{P}(t) = \underset{\sim}{C}(t)\ \underset{\sim}{C}(t-1) \cdots \underset{\sim}{C}(2)\ \underset{\sim}{C}(1)\ \underline{P}(0) \tag{3.3}$$

An alternative way of describing the dynamics of a two-region population is through a generational approach. The birth sequence in two regions satisfies the expression

$$\begin{bmatrix} B_1(t) \\ B_2(t) \end{bmatrix} = \begin{bmatrix} R_{11}(t) & R_{21}(t) \\ R_{12}(t) & R_{22}(t) \end{bmatrix} \begin{bmatrix} B_1(t-1) \\ B_2(t-1) \end{bmatrix} \qquad t = 1,2 \tag{3.4}$$

where $B_i(t)$, $i = 1,2$, is the number of births in region i at time t, and $R_{ij}(t)$, $i,j = 1,2$, is *the spatial net reproduction rate* (SNRR) in region j of women born in region i at time t-1. The $R_{ij}(t)$ is given by

$$R_{ij}(t) = \int_{\alpha}^{\beta} p_{ij}^{t}(x)\ m_j^{t}(x)\ dx \qquad i,j = 1,2 \tag{3.5}$$

where $p_{ij}^{t}(x)$ is the probability of surviving to age x in region j for those born in region i at time t, and $m_j^t(x)$ is the age-specific fertility rate for age x in region j at time t. Note that although Rogers and Willekens (1976a, equation 4.2; 1976b, equation 3) have expressions similar to equation (3.4), they restricted themselves to the limiting stationary birth sequence of populations with constant rates of no growth. Also note that $R_{ij}(t)$ in equations (3.4) and (3.5) is ${}_iR_j(0)$ at time t in the notation of Rogers and Willekens. The total population at time t may be expressed as

$$\begin{bmatrix} Y_1(t) \\ Y_2(t) \end{bmatrix} = \begin{bmatrix} e_{11}(t) & e_{21}(t) \\ e_{12}(t) & e_{22}(t) \end{bmatrix} \begin{bmatrix} B_1(t) \\ B_2(t) \end{bmatrix} \tag{3.6}$$

where $Y_i(t)$, i = 1,2, is the population size in region i at time t, and $e_{ij}(t)$, i,j = 1,2, represents the number of years lived in region j, on the average, by individuals born in region i at time t. Note that $e_{ij}(t)$ is ${}_ie_j(0)$ at time t in the notation of Rogers (1975). From equations (3.4) and (3.6) the dynamics of total populations is given by

$$\underline{Y}(t) = \underset{\sim}{e}(t)\ \underset{\sim}{R}(t)\ \underset{\sim}{e}^{-1}(t-1)\ \underline{Y}(t-1) \tag{3.7}$$

and hence by writing

$$\underset{\sim}{N}(t) = \underset{\sim}{e}(t)\ \underset{\sim}{R}(t)\ \underset{\sim}{e}^{-1}(t-1) \tag{3.8}$$

which may be called the *spatial net reproduction rate for a population* (SNRRP), we rewrite equation (3.7) as

$$\begin{bmatrix} Y_1(t) \\ Y_2(t) \end{bmatrix} = \begin{bmatrix} N_{11}(t) & N_{21}(t) \\ N_{12}(t) & N_{22}(t) \end{bmatrix} \begin{bmatrix} Y_1(t-1) \\ Y_2(t-1) \end{bmatrix} \tag{3.9}$$

It follows that the regional population distribution at time t is given by

$$\underline{Y}(t) = \underset{\sim}{N}(t)\ \underset{\sim}{N}(t-1) \cdots \underset{\sim}{N}(2)\ \underset{\sim}{N}(1)\ \underline{Y}(0) = \underset{\sim}{M}_t\ \underline{Y}(0) \tag{3.10}$$

Hence, the dynamics of total populations is formally identical to that of the birth sequence in the generational model, and also to the dynamics of populations in the period model.

Before exploring the dynamics of regional populations with changing rates, let us briefly summarize the dynamics of stable stationary populations (e.g., Rogers and Willekens, 1976b). When the rates are constant over time, the limiting distribution is determined by the maximal eigenvalue and the corresponding eigenvectors of the ppm. A stationary multiregional population results if the maximal eigenvalue is unity, i.e., in a case of a 2 x 2 matrix

$$N = \begin{bmatrix} a & b \\ c & d \end{bmatrix}$$

if the elements satisfy the relationship

$$(1 - a)(1 - d) = bc \qquad (3.11)$$

A special case of equation (3.11) is a row-stochastic matrix, which may be written as

$$\underset{\sim}{N} = \begin{bmatrix} 1 - b & b \\ c & 1 - c \end{bmatrix} \qquad (3.12)$$

An example of this form is given by Rogers and Willekens (1976b:8). The limiting stationary distribution becomes

$$\underline{Y} = \left(\frac{bY_1(0) + cY_2(0)}{b + c} \right) \underline{1} \qquad (3.13)$$

which states that the two regions will have an equal number of persons, and the ultimate population size will be determined by a weighted average of the initial populations in the two regions.

Another special case of equation (3.11) is a column-stochastic matrix (Rogers and Willekens, 1976b:7)

$$\underset{\sim}{N} = \begin{bmatrix} 1 - c & b \\ c & 1 - b \end{bmatrix} \qquad (3.14)$$

When the matrix is of this form, the limiting stationary distribution is given by

$$\underline{Y} = \Big(Y_1(0) + Y_2(0)\Big) \begin{bmatrix} \dfrac{b}{b+c} \\ \\ \dfrac{c}{b+c} \end{bmatrix} \qquad (3.15)$$

so that the ratio of regional shares in two regions will be b/c.

Now we consider dynamics of populations in two regions with changing rates specified by either equation (3.1) or (3.9). Before going into the details, we first summarize and interpret useful theorems on backward products of row-stochastic matrices given by Chatterjee and Seneta (1977). For backward products

$$\underset{\sim}{M}_t = \underset{\sim}{A}_t \, \underset{\sim}{A}_{t-1} \cdots \underset{\sim}{A}_2 \, \underset{\sim}{A}_1$$

of row-stochastic matrices $\{\underset{\sim}{A}_t\}$, weak and strong ergodicity are equivalent, i.e.,

$$\lim_{t \to \infty} \underset{\sim}{M}_t = \underline{1} \, \underline{P}' \qquad (3.16)$$

where $\underline{P}'$ is necessarily a probability vector that depends on the elements of early matrices (Theorem 1). A sufficient condition for ergodicity is

$$\lim_{t \to \infty} \sum_{k=1}^{t} \varepsilon_k = \infty \qquad (3.17)$$

where ε_k is the minimum element of the matrix $\underset{\sim}{N}_t$ (Corollary of Theorem 4).

Although the limit theorem given in equation (3.16) is known, it does not tell us anything about how the sequence converges, or what the elements of the limiting matrix are. To see the specifics of the convergence, we proceed directly, as in the previous section.

When the changing matrices in equations (3.1) or (3.9) are of the form

$$\underset{\sim}{A}_t = \begin{bmatrix} 1 - a_t & a_t \\ c_t & 1 - c_t \end{bmatrix} \qquad t = 1,2,\ldots \qquad (3.18)$$

row elements sum to one. This condition is equivalent to

$$d_i(t) + o_i(t) = b_i(t) + o_j(t) \qquad i,j = 1,2 \qquad (3.19)$$

for the period model of equation (3.1), and to

$$N_{ii}(t) + N_{ji}(t) = 1 \qquad i,j = 1,2 \qquad (3.20)$$

for the generational model of equation (3.9). By directly multiplying the matrices, we obtain

$$\underset{\sim}{M}_1 = \underset{\sim}{A}_1 = \begin{bmatrix} 1 - a_1 & a_1 \\ c_1 & 1 - c_1 \end{bmatrix}$$

$$\underset{\sim}{M}_2 = \underset{\sim}{A}_2\ \underset{\sim}{A}_1 = \begin{bmatrix} 1 - \left(a_1 + a_2\left[1 - (a_1 + c_1)\right]\right) & a_1 + a_2\left[1 - (a_1 + c_1)\right] \\ c_1 + c_2\left[1 - (a_1 + c_1)\right] & 1 - \left(c_1 + c_2\left[1 - (a_1 + c_1)\right]\right) \end{bmatrix}$$

$$\vdots$$

It can be shown that the upper-righthand corner element of $\underset{\sim}{M}_t$ is given by

$$\begin{aligned} G_t = a_1 &+ a_2\left(1 - (a_1 + c_1)\right) + a_3\left(1 - (a_1 + c_1)\right)\left(1 - (a_2 + c_2)\right) \\ &+ \cdots + a_t\left(1 - (a_1 + c_1)\right)\cdots\left(1 - (a_{t-1} + c_{t-1})\right) \quad , \end{aligned} \qquad (3.21)$$

for all t. Since $0 < |1 - (a_t + c_t)| < 1$, for all t, the sequence $\{G_t\}$ converges to some value G, i.e.,

$$\lim_{t \to \infty} G_t = G \tag{3.22}$$

exists and, hence, we have that

$$\lim_{t \to \infty} \underset{\sim}{M}_t = \begin{bmatrix} 1 - G & G \\ 1 - G & G \end{bmatrix}$$

The value of G can be calculated explicitly to any arbitrary degree of accuracy by equation (3.21) using only the early rates. The speed of convergence depends on the values of a_t and c_t; more specifically, we see from equation (3.21) that the smaller the value of $|1 - (a_t + c_t)|$, $t = 1,2,\ldots$ the faster is the convergence. Consequently the regional population is given by

$$\lim_{t \to \infty} \begin{bmatrix} y_1(t) \\ y_2(t) \end{bmatrix} = \begin{bmatrix} (1 - G)\ y_1(0) + G\ y_2(0) \end{bmatrix} \begin{bmatrix} 1 \\ 1 \end{bmatrix} \tag{3.23}$$

The result of equation (3.23) should be interpreted with $y_i(t)$, a_t and c_t replaced by $P_i(t)$, $O_2(t)$ and $O_1(t)$ in the period model, and by $Y_i(t)$, $N_{21}(t)$ and $N_{12}(t)$ in the generational model. We have just seen that despite constantly changing rates over time, the regional population will come to have a constant (stationary) distribution: the population will have equal regional shares and the size of the population will be a weighted average of the initial population distribution, where the weights (spatial reproductive values) are given by equation (3.22).

The condition of row-stochastic ppm's merits some discussion. In the period model, equation (3.19) shows that as long as the number leaving a region by death and outmigration is equal to the number arriving in the region by birth and inmigration, strong ergodicity results. In the generational model, equation (3.20) shows that if, regardless of origin, the SNRRP at the destination is unity, strong ergodicity results.

We next consider the dynamics of populations when the ppm is column-stochastic, i.e.,

$$\underset{\sim}{A}_t = \begin{bmatrix} 1 - a_t & c_t \\ a_t & 1 - c_t \end{bmatrix} \qquad t = 1,2,\ldots \qquad (3.24)$$

This condition is equivalent to

$$b_i(t) = d_i(t) \qquad i = 1,2 \qquad (3.25)$$

with arbitrary $O_i(t)$ for the period model, and to

$$N_{ii}(t) + N_{ij}(t) = 1 \qquad i,j = 1,2 \qquad (3.26)$$

for the generational model. Letting H_t denote the upper-righthand element of the product matrix, $\underset{\sim}{M}_t$, and multiplying directly, we obtain

$$H_1 = c_1$$

$$H_2 = c_2 + c_1 \left[1 - (a_2 + c_2)\right]$$

$$\vdots$$

and, in general

$$H_t = c_t + c_{t-1} \left[1 - (a_t + c_t)\right] + c_{t-2} \left[1 - (a_t + c_t)\right]\left[1 - (a_{t-1} + c_{t-1})\right]$$
$$+ \cdots + c_1 \left[1 - (a_t + c_t)\right] \cdots \left[1 - (a_2 + c_2)\right] \qquad (3.27)$$

for all t.

Since $0 < |1 - (a_t + c_t)| < 1$, for all t, the value of H_t depends only on the most recent rates. Although H_t has no limit, the product matrix $\underset{\sim}{M}_t$ satisfies

$$\lim_{t \to \infty} \left\{ \underset{\sim}{M}_t - \begin{bmatrix} H_t & H_t \\ 1 - H_t & 1 - H_t \end{bmatrix} \right\} = 0 \qquad (3.28)$$

(In fact, it is a transpose of a non-homogeneous Markov chain.) For large t, the population in two regions is given by,

$$\begin{bmatrix} y_1(t) \\ y_2(t) \end{bmatrix} = \Big(y_1(0) + y_2(0)\Big) \begin{bmatrix} H_t \\ 1 - H_t \end{bmatrix} \tag{3.29}$$

The size of the total population is fixed with uniform spatial reproductive values, but regional shares keep changing constantly over time. This occurs when the period rate of natural increase in each region is zero with an arbitrary interregional migration rate in the period model, and when the SNRRP in the origin region is unity, where N_{ii} is given in the region of origin and $N_{ij} = 1 - N_{ii}$ is given in the other region in the generational model.

IV. DYNAMICS OF ZERO GROWTH MULTIREGIONAL POPULATIONS

The dynamics of multiregional populations with a recognition of age structure may be written as Rogers (1975:122-123)

$$\underline{K}^{(t)} = \underset{\sim}{G}(t)\ \underline{K}^{(t-1)} \tag{4.1}$$

or

$$\underline{\overline{K}}^{(t)} = \underset{\sim}{H}(t)\ \underline{\overline{K}}^{(t-1)} \tag{4.2}$$

where the multiregional ppm's now depend on time t, in contrast to the fixed multiregional ppm's of Rogers. (See Rogers, 1975, for a description of the elements of the vectors and matrices.) When we consider populations with two age groups and two regions, equations (4.1) and (4.2) become

$$\left[\begin{array}{c} \overset{t}{K}_1(1) \\ \overset{t}{K}_2(1) \\ \hline \overset{t}{K}_1(2) \\ \overset{t}{K}_2(2) \end{array}\right] = \left[\begin{array}{cc:cc} \overset{t}{b}_{11}(1) & \overset{t}{b}_{21}(1) & \overset{t}{b}_{11}(2) & \overset{t}{b}_{21}(2) \\ \overset{t}{b}_{12}(1) & \overset{t}{b}_{22}(1) & \overset{t}{b}_{12}(2) & \overset{t}{b}_{22}(2) \\ \hdashline \overset{t}{s}_{11} & \overset{t}{s}_{21} & 0 & 0 \\ \overset{t}{s}_{12} & \overset{t}{s}_{22} & 0 & 0 \end{array}\right] \left[\begin{array}{c} \overset{t-1}{K}_1(1) \\ \overset{t-1}{K}_2(1) \\ \hdashline \overset{t-1}{K}_1(2) \\ \overset{t-1}{K}_2(2) \end{array}\right] \tag{4.3}$$

and

$$\left[\begin{array}{c} K_1^t(1) \\ K_1^t(2) \\ \hline K_2^t(1) \\ K_2^t(2) \end{array}\right] = \left[\begin{array}{cc|cc} b_{11}^t(b) & b_{11}^t(2) & b_{21}^t(1) & b_{21}^t(2) \\ s_{11}^t & 0 & s_{21}^t & 0 \\ \hline b_{12}^t(t) & b_{12}^t(2) & b_{22}^t(1) & b_{22}^t(2) \\ s_{12}^t & 0 & s_{22}^t & 0 \end{array}\right] \left[\begin{array}{c} K_1^{t-1}(1) \\ K_1^{t-1}(2) \\ \hline K_2^{t-1}(1) \\ K_2^{t-1}(2) \end{array}\right] \tag{4.4}$$

respectively, where $K_i^t(j)$ denotes the number of persons in region i, in age group j at time t, $b_{ij}^t(k)$ is the number of persons in the first age group in region j at time t, per person in region i, in age group k at time t-1, and s_{ij}^t is the proportion surviving in the second age group in region j at time t per person in the first age group in region i at time t-1. Since the arrangement of equation (4.1) seems to be simpler to manipulate we shall use it henceforth. The dynamics of multiregional population at time t is given by

$$\begin{aligned} \underline{K}^{(t)} &= \underset{\sim}{G}(t)\ \underset{\sim}{G}(t-1) \cdots \underset{\sim}{G}(2)\ \underset{\sim}{G}(1)\ \underline{K}^{(0)} \\ &= \underset{\sim}{M}(t)\ \underline{K}^{(0)} \end{aligned} \tag{4.5}$$

and hence the dynamics are completely determined by the backward product $\underset{\sim}{M}(t)$ of multiregional ppm's $\{\underset{\sim}{G}(t)\}$.

As a special case of zero growth dynamics, we first consider the case of row stochastic multiregional ppm's. Since the multiregional ppm $\underset{\sim}{G}(t)$ is regular, from the theorems of Chatterjee and Seneta given by equation (3.16), we conclude that

$$\lim_{t \to \infty} \underset{\sim}{M}(t) = \underline{1}\ \underline{p}'$$

holds, so that

$$\lim_{t \to \infty} \underline{K}^{(t)} = \left(\underline{p}, \underline{K}^{(0)}\right) \underline{1} \tag{4.6}$$

where $(\underline{p},\underline{K}^{(0)})$ represents the inner product of the vectors $\underline{p}$ and $\underline{K}^{(0)}$. Notice that the elements of the vector $\underline{p}$ represent spatial reproductive values. Thus when fertility, mortality, and migration rates change over time with the constraints

$$\begin{cases} \sum_{j=1}^{m} \sum_{k=1}^{n} b_{ji}^{t}(k) = 1 & i = 1,2,\ldots,m \\ \\ \sum_{j=1}^{m} s_{ji}^{t}(k) = 1 & \begin{array}{l} i = 1,2,\ldots,m \\ k = 1,2,\ldots,n-1 \end{array} \end{cases} \tag{4.7}$$

for populations with n age groups and m regions, the population evolves into a multiregional stationary population with constant age distribution and regional shares.

Next when the multiregional ppm $\underset{\sim}{G}(t)$, is column-stochastic, for all t, the sequence of product matrices $\{\underset{\sim}{M}(t)\}$ is a transpose of a non-homogeneous Markov chain, so that

$$\lim_{t \to \infty} \left\{ \underset{\sim}{M}(t) - \underline{h}_t \, \underline{1}' \right\} = 0 \tag{4.8}$$

holds and hence, for large t, the multiregional population becomes

$$\underline{K}^{(t)} = \left(\underline{1}, \underline{K}^{(0)} \right) \underline{h}_t \quad , \tag{4.9}$$

where the inner product $(\underline{1},\underline{K}^{(0)})$ gives the initial total population size, and the vector $\underline{h}_t$ satisfies $(\underline{1},\underline{h}_t) = 1$. Here the vector $\underline{h}_t$ is determined by recent rates. The result of equation (4.9) holds when, for all t,

$$\sum_{j=1}^{m} \left[b_{ij}^{t}(k) + s_{ij}^{t}(k) \right] = 1 \qquad \begin{array}{l} i = 1,2,\ldots,m \\ k = 1,2,\ldots,n-1 \end{array} \tag{4.10}$$

for populations with n age groups and m regions.

V. DISCUSSION

We have seen that the dynamics of populations (both single-regional and multiregional) with a sequence of row-stochastic ppm's results in strong ergodicity, while that of populations with a sequence of column-stochastic ppm's results in only weak ergodicity. Specific expressions originally obtained for populations with two age groups in a single region were first extended to populations without age structure in two regions. With these expressions we can see explicitly how strong and weak ergodicity work. The dynamics of populations with n age groups and m regions is qualitatively the same, although we cannot give explicit formulas in such general cases.

Populations without age structure in two regions were formulated in two alternative ways: a period formulation which involves crude rates of birth, death, and migration in each period, and a generational formulation which involves SNRRPs. For the generational model, the dynamics of population change are formally identical to the dynamics of birth sequences, although due to constantly changing mortality and migration schedules they have to be treated separately when the rates change over time.

Demographic interpretations of row- and column-stochastic ppm's merit some more discussion. For populations with two age groups in a single region, if mortality is fixed, and if a lifetime fertility of unity is split arbitrarily into two age groups (only period NRR = 1), all measures of interest about the population eventually become constant. When fertility in the first age group and survivorship adjust themselves for the sum to be unity, with fertility in the second age group being unity (both period and cohort NRR = 1), then the birth sequence and the age structure keep changing over time.

In the period formulation of the evolution of two-regional populations without age structure, when the number leaving a region by death and outmigration is the same as that arriving in the region by birth and inmigration, then strong ergodicity holds with constant regional shares. In the generational formulation, if the SNRRP at the destination is unity (this may be stated as "location SNRRP = 1", or the "location replacement alternative"), then strong ergodicity holds. On the other hand, in the period formulation, if the rate of natural growth in each region is zero, with arbitrary interregional migration rates, only weak ergodicity holds and, hence, regional shares keep changing constantly to reflect recent migration patterns. In the generational model, when the SNRRP at the origin is unity (this may be defined to be "cohort SNRRP = 1", or the "cohort replacement alternative" (Rogers and Willekens, 1976b:6)), then weak ergodicity results. The conditions (4.7) and (4.10) for populations with n age groups in m regions may be interpreted similarly.

Finally, the main advantage of having specific formulas for the 2 x 2 ppm's, in addition to the limit theorems, is that we can see the particular workings of strong and weak ergodicity, and see how they specialize to the stable stationary case. For example, in equations (3.21) and (3.27), if $a_t = a$ and $c_t = c$ for all t, G_t for large t reduces to

$$G = a\left[1 + \left[1 - (a + c)\right] + \left[1 - (a + c)\right]^2 + \cdots\right]$$

$$= \frac{a}{a + c} \quad ,$$

and H_t, for large t, reduces to

$$H = c\left[1 + \left[1 - (a + c)\right] + \left[1 - (a + c)\right]^2 + \cdots\right]$$

$$= \frac{c}{a + c}$$

thus giving the results of equations (3.13) and (3.15).

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