

TIME SCALES IN A NON-AUTONOMOUS LINEAR DISCRETE MODEL

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In this work we extend approximate aggregation methods in time discrete linear models to the case of time varying environments. Approximate aggregation consists of describing some features of the dynamics of a general system involving many coupled variables in terms of the dynamics of a reduced system with a few “global” variables.

We present a time varying discrete model in which we distinguish two processes with different time scales. By defining the global variables as appropriate linear combinations of the state variables, we transform the system into a reduced one. The variables corresponding to the original and reduced systems can be related, therefore allowing one the study of the former in terms of the latter. The property of weak ergodicity, which has to do with the capacity of a system to become asymptotically independent of initial conditions, is explored for the original and reduced systems.

The general method is also applied to aggregate a time-dependent multiregional model which appears in the field of population dynamics in two different cases: Fast migration with respect to demography and fast demography with respect to migration.

Keywords: Approximate aggregation, population dynamics, time scales, weak ergodicity, multiregional models

1. Introduction

In order to study ecological systems, one has to decide the level of complexity and detail one should incorporate into the model so as to optimize the study. Indeed any model is a compromise between generality and simplicity on the one hand

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and realism on the other. Models which include many biological details in their specification become complicated, and their analytical study is often non-viable. On the other hand, very simple models, although analytically tractable, often do not justify the assumptions needed to obtain such simplicity.

Nature offers many examples of systems with an inherent complexity. For example, communities are sets of interacting populations. Populations themselves have an internal structure, for individuals may have different ages or be in different stages. These stages may correspond to size, spatial patches, genotypes, individual activities, etc.

Aggregation methods study the relationships between a large class of complex systems, in which many variables are involved, and their corresponding reduced or aggregated systems, governed by a few variables. The basic aim of aggregation techniques is to allow one to rigorously construct, starting from a complex system, a simpler model which summarizes some characteristics of its dynamics, therefore simplifying their analytical study. The essential property of complex systems that allows their aggregation is the existence of two time scales. This allows one to think of a hierarchically organized system with a division into subsystems, in such a way that these subsystems are weakly coupled through the slow process and yet exhibit strong internal dynamics corresponding to the fast process.

In many of the complex systems found in nature, it is possible to distinguish several processes which take place with different time scales. For example, it is usually the case that processes that take place at the individual behavioral level, as migrations or changes of activity, are fast with respect to those regarding the population level, as reproduction or aging.¹ In the majority of models found in the literature, it is implicitly assumed that the fast process reaches equilibrium very fast in comparison to the time scale corresponding to the slow process, and therefore the fast dynamics is supposed to have a negligible impact on the dynamics of the system. However, by using aggregation techniques we may consider the dynamics of both the fast and the slow processes without paying a high cost in terms of the complexity of the models we have to analyze. The idea of aggregation is to choose some (usually one) global variable for each subsystem and to build a reduced system for those global variables. The aggregated system reflects in a certain way both the slow and the fast dynamics of the original system. The dynamics of the aggregated system usually corresponds to the dynamics of the original system, while the fast dynamics of the original system is reflected in the coefficients of the reduced one in such a way that it is possible to study the influences between different hierarchical levels.

Aggregation techniques have been widely studied in the context of time continuous systems with different time scales for both linear and density dependent models.^{2-5,29}

Aggregation techniques have also been extended to deal with autonomous time discrete systems in both linear and nonlinear cases, under the hypothesis that the fast process is conservative of the total number of individuals (for example migration). The complex models proposed can be classified into two groups; one in which

the time step of the model corresponds to the characteristic time of the fast process (see Refs. 6–8) and another in which the characteristic time of the slow dynamics is the time unit for the model (see Refs. 9 and 33). In previous works, the authors have extended the latter to deal with linear systems in which the fast process can have a general nature,³⁵ and also to treat systems subjected to environmental stochasticity.³⁶ In Refs. 12–14, the theoretical results are applied to a practical case regarding the study of an arborescent river network.

Non-autonomous models are important to deal with the changes in the vital rates through time as a result of environmental variation. Depending on the pattern of environmental variation we can distinguish, among others, the following types: Periodic variation, environment in process of stabilization, and general temporal variation. In the case of general temporal variation, it is interesting to study the presence or absence of weak ergodicity in the system. Weak ergodicity (see Refs. 10 and 17 for its biological significance and Ref. 37 for a mathematical discussion) has to do with the capacity of the structure of the population vector of the system to become independent of the initial conditions.

Aggregation methods in the non-autonomous linear case have been considered by the authors in Ref. 34 under the hypothesis that the fast dynamics is conservative of the total number of individuals. A time varying model is proposed and aggregated, and the relationships between the original and aggregated models are explored for the cases of periodic environmental variation, and environment in process of stabilization.

The aim of this work is to extend variables aggregation techniques in the non-autonomous case in two directions. In the first case we will propose and aggregate a time varying system with two time scales in which both the fast and the slow dynamics may correspond to any two biological processes. In particular, the fast dynamics does not need to be conservative of the total number of individuals. This allows one to aggregate systems in which, as it is the case in some situations found in the literature,^{25,26} the role of the fast process is played by demography. In the second case, we will obtain relationships between the weak ergodicity of the original and aggregated systems.

Section 2 proposes a linear time discrete model with varying coefficients which distinguishes time scales and gives a criterium to build the aggregated system. As we mentioned above, both the fast and the slow processes can be any biological processes. We just require that the fast process tends to an equilibrium in a certain sense that will be specified. The aggregated system is shown to have a structure that can easily be related to that of the slow dynamics. In fact, the entries of the matrix that represents the aggregated system are obtained as a linear combination of the ones that correspond to the slow dynamics, the coefficients of the combination being functions of the equilibrium distribution of the fast dynamics. In Sec. 2.3, we obtain relationships between the state variables and the global variables in terms of the separation of time scales between the slow and the fast processes. In Sec. 2.4, where readers interested mainly in applications may focus their attention, is devoted

to illustrate our general technique studying, through variables aggregation, some multiregional models in which we can consider that migration and demography take place with different time scales. We deal with two different situations; in the first one we consider migration to be fast with respect to demography, while in the second one we consider that the contrary happens.

Section 3 motivates and introduces the concept of weak ergodicity and its ecological significance. Some mathematical concepts and results useful in the study of weak ergodicity are presented, for the interested reader, in the appendix.

In Sec. 4, we explore the relationships between the weak ergodicity of the original and aggregated systems. We show that under wide conditions, if the separation between the time scales of the slow and fast dynamics is sufficiently high, very general sufficient conditions for weak ergodicity are simultaneously met for both systems. The results can be sharpened in some usual cases regarding the incidence matrices of the systems. Finally, the results are applied to the study of weak ergodicity for the multiregional model introduced in Sec. 2.4.

2. A Discrete Model with Different Time Scales

As it has been mentioned above, the microsystem and the aggregation procedure we propose have already been considered by the authors in Ref. 34 for the case in which the fast process is conservative of the total number of individuals in each subsystem.

2.1. Original system

We suppose a stage-structured population in which the population is classified into stages or groups in terms of any characteristic of the life cycle. Moreover, each of these groups is divided into several subgroups that can correspond to different spatial patches, different individual activities or any other characteristic that could change the life cycle parameters. The model is therefore general in the sense that we do not state in detail the nature of the population or the subpopulations.

We consider the population being subdivided into q populations (or groups). Each group is subdivided into subpopulations (subgroups) in such a way that for each $i = 1, 2, \dots, q$, group i has N_i subgroups. Therefore, the total number of subgroups is $N = N_1 + N_2 + \dots + N_q$.

We will denote x_n^{ij} the density of subpopulation j of population i at time n , with $i = 1, 2, \dots, q$ and $j = 1, 2, \dots, N_i$. In order to describe the population of group i we will use vector $\mathbf{x}_n^i = (x_n^{i1}, x_n^{i2}, \dots, x_n^{iN_i}) \in \mathbb{R}^{N_i}$, $i = 1, 2, \dots, q$. The composition of the total population is then given by vector $\mathbf{X}_n = (\mathbf{x}_n^1, \mathbf{x}_n^2, \dots, \mathbf{x}_n^q)^T \in \mathbb{R}^N$ where “T” denotes transposition.

In the evolution of the population we will consider two processes whose corresponding characteristic time scales, and consequently their projection intervals, are very different from each other. In order to include in our model both time scales

we will model these two processes, to which we will refer as the fast and the slow dynamics, by two different matrices.

We will choose as the projection interval of our model, that corresponding to the slow dynamics, i.e. the time elapsed between times n and $n + 1$ is the projection interval of the slow process. For simplicity, we will denote the time span $[n, n + 1)$ as Δ_n , and suppose that the coefficients of the model are constant during each of the intervals Δ_n . Notice that this hypothesis implies that the characteristics of the fast process are not allowed to vary with each projection interval associated to this process. They can only vary with each time step corresponding to the model, i.e. with each projection interval associated to the slow process.

In principle, we will make no special assumptions regarding the characteristics of the slow dynamics. Thus, for a certain fixed projection interval, the slow dynamics will be represented at time n by a non-negative projection matrix $\mathbf{M}_n \in \mathbb{R}^{N \times N}$, which in this context is usually referred to as Leftkovitch matrix,²⁴ and which we consider divided into blocks $\mathbf{M}_{ij}(n)$, $1 \leq i, j \leq q$. We have then

$$\mathbf{M}_n = \begin{pmatrix} \mathbf{M}_{11}(n) & \mathbf{M}_{12}(n) & \cdots & \mathbf{M}_{1q}(n) \\ \mathbf{M}_{21}(n) & \mathbf{M}_{22}(n) & \cdots & \mathbf{M}_{2q}(n) \\ \vdots & \vdots & \ddots & \vdots \\ \mathbf{M}_{q1}(n) & \mathbf{M}_{q2}(n) & \cdots & \mathbf{M}_{qq}(n) \end{pmatrix}, \tag{2.1}$$

where each block $\mathbf{M}_{ij}(n) = [M_{ij}^{ml}(n)]$ has dimensions $N_i \times N_j$ and characterizes the rates of transference of individuals from the subgroups of group j to the subgroups of group i at time n . More specifically, for each $m = 1, 2, \dots, N_i$ and each $l = 1, 2, \dots, N_j$, $M_{ij}^{ml}(n)$ represents the rate of transference due to the slow process of individuals from subgroup l of group j to subgroup m of group i , at time n .

As far as the behavior of the fast dynamics is concerned, the following assumptions are made:

- (a) the fast dynamics is an internal process for each group, i.e. there is no transference of individuals from one group to another group. Therefore, if we consider a fixed projection interval, the fast dynamics of group i will be represented, during interval Δ_n , by a non-negative matrix $\mathbf{P}_i(n)$ of dimensions $N_i \times N_i$ for each $i = 1, \dots, q$ and $n = 1, 2, \dots$
- (b) For each i and n , matrix $\mathbf{P}_i(n)$ has spectral radius equal to one.
- (c) For each i and n , matrix $\mathbf{P}_i(n)$ is irreducible and primitive.

We will come back to the justification and interpretation of these hypotheses later on.

The matrix which represents the fast dynamics for the whole population during interval $[n, n + 1)$ is

$$\mathbf{P}_n = \text{diag}(\mathbf{P}_1(n), \mathbf{P}_2(n), \dots, \mathbf{P}_q(n)). \tag{2.2}$$

As stated above, the projection interval of the model is that corresponding to matrices \mathbf{M}_n . Therefore we need to approximate the effect of the fast dynamics over a time interval much longer than its own. In order to do so we will suppose that during each interval Δ_n , matrix \mathbf{P}_n has operated k times, where k is a large enough integer that can be interpreted as the ratio between the projection intervals corresponding to the slow and fast dynamics. Therefore, the fast dynamics during interval Δ_n will be modeled by \mathbf{P}_n^k and the proposed model will consist of the following system of N linear difference equations that we will denote as “microsystem” or “original system”:

$$\mathbf{X}_{n+1} = \mathbf{M}_n \mathbf{P}_n^k \mathbf{X}_n. \tag{2.3}$$

Hypothesis (b), by which the spectral radius of the $\mathbf{P}_i(n)$ is one, has a clear biological justification. Indeed, if the spectral radius of any $\mathbf{P}_i(n)$ were smaller or greater than one then, if the separation between the two time scales is large enough, the fast process in group i during interval Δ_n would lead the total population of this group to zero or infinity, respectively, before the slow process has time to act. Therefore, the dynamics of the system during Δ_n would be controlled by the fast process and the distinction of two processes in the modeling of the system would be unnecessary.

The primitivity of the $\mathbf{P}_i(n)$, together with assumption (b), guarantees that for a separation of the two time scales sufficiently high, the fast process during each Δ_n approaches an equilibrium distribution. The use of primitive matrices is a common feature in the modeling of most biological processes.^{10,11}

In Ref. 34 the authors propose a model very similar to that considered here but in which the fast process is conservative for the total number of individuals in each of the groups, as it is the case with processes like migration or changes of activity. In that work, matrices $\mathbf{P}_i(n)$ are supposed to be stochastic and primitive, and trivially verify hypotheses (b) and (c). In this way, the model here presented can be considered a generalization of the above-mentioned to take into account fast processes of a general kind.

Let $i = 1, \dots, q$ and n be fixed and consider the positive vectors defined by

$$\begin{aligned} \mathbf{P}_i(n) \mathbf{v}_i(n) &= \mathbf{v}_i(n), & \mathbf{u}_i^T(n) \mathbf{P}_i(n) &= \mathbf{u}_i^T(n) \\ \mathbf{1}^T \mathbf{v}_i(n) &= 1, & \mathbf{u}_i^T(n) \mathbf{v}_i(n) &= 1, & \mathbf{v}_i(n) > 0, & \mathbf{u}_i(n) > 0, \end{aligned} \tag{2.4}$$

where $\mathbf{1} = (1, 1, \dots, 1)^T$. Therefore, $\mathbf{v}_i(n)$ and $\mathbf{u}_i(n)$ are, respectively, the positive right and left eigenvectors of $\mathbf{P}_i(n)$ associated to eigenvalue one and verifying some normalization conditions. Notice that, since $\mathbf{P}_i(n)$ is primitive, eigenvalue one is simple and therefore $\mathbf{v}_i(n)$ and $\mathbf{u}_i(n)$ are defined in a unique way by conditions (2.4).

Vectors $\mathbf{v}_i(n)$ and $\mathbf{u}_i(n)$ can be interpreted in the following way in terms of the fast dynamics of group i in interval Δ_n . Let us consider a hypothetical situation in which the system were governed by the fast process exclusively. Suppose, moreover, that Δ_n is long enough with respect to the projection interval corresponding to the

fast process for this to reach its equilibrium conditions during Δ_n . Then, for any “initial condition” of the system at time n , the structure of the population of group i at the end of Δ_n would be defined by $\mathbf{v}_i(n)$, meanwhile the reproductive value¹⁰ of the individuals of that group would be characterized by $\mathbf{u}_i(n)$.

Therefore, for each n , the matrices that characterize the fast process equilibrium in each Δ_n for each group i and for the whole population would be $\bar{\mathbf{P}}_i(n)$ and $\bar{\mathbf{P}}_n$ respectively, where

$$\begin{aligned} \bar{\mathbf{P}}_i(n) &= \lim_{k \rightarrow \infty} \mathbf{P}_i^k(n) = \mathbf{v}_i(n)\mathbf{u}_i^T(n) > 0 \\ \bar{\mathbf{P}}_n &= \text{diag}(\bar{\mathbf{P}}_1(n), \bar{\mathbf{P}}_2(n), \dots, \bar{\mathbf{P}}_q(n)). \end{aligned} \tag{2.5}$$

We define matrices

$$\begin{aligned} \mathbf{V}_n &= \text{diag}(\mathbf{v}_1(n), \mathbf{v}_2(n), \dots, \mathbf{v}_q(n)) \\ \mathbf{U}_n &= \text{diag}(\mathbf{u}_1^T(n), \mathbf{u}_2^T(n), \dots, \mathbf{u}_q^T(n)), \end{aligned} \tag{2.6}$$

whose interpretation is immediate bearing in mind what we pointed out about $\mathbf{v}_i(n)$ and $\mathbf{u}_i(n)$.

Some of the properties of these matrices are gathered in the following lemma, whose proof is straightforward:

Lemma 1. *Matrices \mathbf{P}_n , $\bar{\mathbf{P}}_n$, \mathbf{V}_n and \mathbf{U}_n verify, for all n :*

- (a) $\bar{\mathbf{P}}_n\mathbf{P}_n = \mathbf{P}_n\bar{\mathbf{P}}_n = \bar{\mathbf{P}}_n\bar{\mathbf{P}}_n$,
- (b) $\mathbf{P}_n\mathbf{V}_n = \bar{\mathbf{P}}_n\mathbf{V}_n = \mathbf{V}_n$,
- (c) $\mathbf{U}_n\bar{\mathbf{P}}_n = \mathbf{U}_n$, $\mathbf{U}_n\mathbf{V}_n = \mathbf{I}_q$, $\bar{\mathbf{P}}_n = \mathbf{V}_n\mathbf{U}_n$.

Let us introduce some concepts and notation which will be useful in the subsequent developments. A non-negative matrix \mathbf{A} is said to be column allowable (row allowable) if it has at least a nonzero element in each of its columns (rows). \mathbf{A} is said to be allowable if it is both column and row allowable. The product of row (column) allowable matrices is row (column) allowable. Notice that an irreducible matrix is allowable. It is easy to prove that if \mathbf{A} is row (column) allowable and \mathbf{B} is a positive matrix, then $\mathbf{AB} > 0$ ($\mathbf{BA} > 0$) as long as the product is defined.

The incidence matrix of a non-negative matrix \mathbf{A} will be denoted by $i(\mathbf{A})$, and we will write $\mathbf{A} \sim \mathbf{B}$ to denote that \mathbf{A} and \mathbf{B} have the same incidence matrix.

Lemma 2. *The incidence matrices of $\bar{\mathbf{P}}_n$, \mathbf{V}_n and \mathbf{U}_n are the same for all n , i.e. for all n and n' we have $\bar{\mathbf{P}}_n \sim \bar{\mathbf{P}}_{n'}$, $\mathbf{V}_n \sim \mathbf{V}_{n'}$ and $\mathbf{U}_n \sim \mathbf{U}_{n'}$. Besides, those incidence matrices are independent of the incidence matrix of the \mathbf{P}_n and are allowable for all n .*

Proof. Trivial from the definition of these matrices and the fact that the $\bar{\mathbf{P}}_i(n)$, $\mathbf{v}_i(n)$ and $\mathbf{u}_i(n)$ are positive. □

2.2. Aggregated model

In this section we will approximate the microsystem (2.3), consisting of N variables (microvariables) associated to the different subgroups, by an aggregated system (or macrosystem) of q variables (global variables), each of them associated to one group.

In general it is not possible to perfectly aggregate²² the microsystem, i.e. it is not possible to define a set of global variables as functions of the microvariables $\mathbf{Y}_n = f_n(\mathbf{X}_n)$ in such a way that the microsystem depends solely on these global variables. Biological systems can be perfectly aggregated only in some cases and for very particular values of the parameters involved, so perfect aggregation has only a theoretical interest.

As a general technique, in order to aggregate the microsystem we will resort to approximate aggregation. For this we will consider an auxiliary system which approximates the dynamics of the general system and that is susceptible of being perfectly aggregated. This auxiliary system is defined by

$$\mathbf{X}_{n+1} = \mathbf{M}_n \bar{\mathbf{P}}_n \mathbf{X}_n, \tag{2.7}$$

and can be interpreted as the microsystem when we substitute the fast process corresponding to each interval Δ_n by the equilibrium characteristics of the fast process in Δ_n . In other words, we are letting $k \rightarrow \infty$ in the expression of the microsystem, supposing that Δ_n is long enough with respect to the projection interval of the fast process for the fast dynamics to reach equilibrium. Since $\lim_{k \rightarrow \infty} \mathbf{P}_n^k = \bar{\mathbf{P}}_n$ and $\mathbf{M}_n \mathbf{P}_n^k = \mathbf{M}_n \bar{\mathbf{P}}_n + \mathbf{M}_n (\mathbf{P}_n^k - \bar{\mathbf{P}}_n)$, we can consider matrix $\mathbf{M}_n \mathbf{P}_n^k$ as being a perturbation of matrix $\mathbf{M}_n \bar{\mathbf{P}}_n$ (notice that we are using the same notation for the variables in the general and auxiliary system).

Matrix $\mathbf{M}_n \bar{\mathbf{P}}_n$ has the following expression in terms of the blocks corresponding to the slow and fast processes:

$$\mathbf{M}_n \bar{\mathbf{P}}_n = \begin{pmatrix} \mathbf{M}_{11}(n) \bar{\mathbf{P}}_1(n) & \mathbf{M}_{12}(n) \bar{\mathbf{P}}_2(n) & \cdots & \mathbf{M}_{1q}(n) \bar{\mathbf{P}}_q(n) \\ \mathbf{M}_{21}(n) \bar{\mathbf{P}}_1(n) & \mathbf{M}_{22}(n) \bar{\mathbf{P}}_2(n) & \cdots & \mathbf{M}_{2q}(n) \bar{\mathbf{P}}_q(n) \\ \vdots & \vdots & \ddots & \vdots \\ \mathbf{M}_{q1}(n) \bar{\mathbf{P}}_1(n) & \mathbf{M}_{q2}(n) \bar{\mathbf{P}}_2(n) & \cdots & \mathbf{M}_{qq}(n) \bar{\mathbf{P}}_q(n) \end{pmatrix}. \tag{2.8}$$

In order to show that (2.7) can be perfectly aggregated, let us multiply both sides by matrix \mathbf{U}_{n+1}

$$\mathbf{U}_{n+1} \mathbf{X}_{n+1} = \mathbf{U}_{n+1} \mathbf{M}_n \bar{\mathbf{P}}_n \mathbf{X}_n = \mathbf{U}_{n+1} \mathbf{M}_n \mathbf{V}_n \mathbf{U} \mathbf{X}_n,$$

where we have used Lemma 1. Therefore, if we define the vector of global variables by

$$\mathbf{Y}_n = \mathbf{U}_n \mathbf{X}_n, \tag{2.9}$$

we see that (2.7) can be expressed as a function of the global variables exclusively. In this way, the aggregated system is defined by

$$\mathbf{Y}_{n+1} = \bar{\mathbf{M}}_n \mathbf{Y}_n, \tag{2.10}$$

where matrix $\bar{\mathbf{M}}_n \in \mathbb{R}^{q \times q}$ is given by $\bar{\mathbf{M}}_n = \mathbf{U}_{n+1} \mathbf{M}_n \mathbf{V}_n$, and has the form

$$\bar{\mathbf{M}}_n = \begin{pmatrix} \mathbf{u}_1^T(n+1) \mathbf{M}_{11}(n) \mathbf{v}_1(n) & \cdots & \mathbf{u}_1^T(n+1) \mathbf{M}_{1q}(n) \mathbf{v}_q(n) \\ \vdots & \ddots & \vdots \\ \mathbf{u}_q^T(n+1) \mathbf{M}_{q1}(n) \mathbf{v}_1(n) & \cdots & \mathbf{u}_q^T(n+1) \mathbf{M}_{qq}(n) \mathbf{v}_q(n) \end{pmatrix}. \quad (2.11)$$

Therefore, for each time n , the element of row i and column j of the matrix of the aggregated model is $\mathbf{u}_i^T(n+1) \mathbf{M}_{ij}(n) \mathbf{v}_j(n) = \sum_{m,l} u_i^m(n+1) v_j^l(n) M_{ij}^{ml}(n)$ which is a linear combination of the coefficients of the slow dynamics at time n corresponding to the transference from group j to group i . Notice that the coefficients are defined by the equilibrium characteristics of the fast dynamics for intervals Δ_n and Δ_{n+1} and that the aggregated system does not depend on the value of k used in the modeling of the general system.

The following lemma, which is a trivial consequence of (2.11) and of the fact of vectors $\mathbf{v}_i(n)$ and $\mathbf{u}_i(n)$ being positive for all i and n , allows one to relate the incidence matrix of matrices \mathbf{M}_n and $\bar{\mathbf{M}}_n$.

Lemma 3. *For all n , $\bar{\mathbf{M}}_n$ is a non-negative matrix in which the element of row i and column j of $\bar{\mathbf{M}}_n$ is nonzero if and only if matrix $\mathbf{M}_{ij}(n)$ is not zero.*

From this last result we have that the pattern of nonzero elements in $\bar{\mathbf{M}}_n$ coincides with the pattern of nonzero blocks $\mathbf{M}_{ij}(n)$ for the slow dynamics.

The global variables $\mathbf{Y}_n = (y_n^1, \dots, y_n^q)^T$, defined by (2.9), have the following expression in terms of the variables \mathbf{X}_n of the auxiliary system:

$$y_n^i = \mathbf{u}_i^T(n) \mathbf{x}_n^{iT} = u_i^1(n) x_n^{i1} + u_i^2(n) x_n^{i2} + \cdots + u_i^{N_i}(n) x_n^{iN_i}, \quad i = 1, \dots, q. \quad (2.12)$$

As a consequence:

- y_n^i is a linear combination of the microvariables corresponding to group i , being the coefficients of the combination the components of vector $\mathbf{u}_i(n)$. Recall that, as it was specified in the previous section, $\mathbf{u}_i(n)$ is a vector of reproductive values for the fast process in group i during interval Δ_n . Therefore, for each $j = 1, \dots, N_i$ the microvariable x_n^{ij} corresponding to subgroup j has a relative weight which is proportional to $u_i^j(n)$, i.e. proportional to the contribution to the total population at time $n + 1$ that the “initial” population at time n of group i and subgroup j would have in the case that the system were governed by the fast process exclusively and this process reached equilibrium within Δ_n . In this way, the higher the relative value of $u_i^j(n)$ in vector $\mathbf{u}_i(n)$ is, the higher the relative contribution of x_n^{ij} to y_n^i .
- the macrovariables are conservative for the fast process. Indeed, suppose that the fast process is the only one acting in the system. Then, the microvariables \mathbf{X}_t would be transformed, for a projection interval $[t, t + 1)$ corresponding to the fast process and belonging to Δ_n , in $\mathbf{X}_{t+1} = \mathbf{P}_n \mathbf{X}_t$. Aggregating, and using Lemma 1, we have $\mathbf{Y}_{t+1} = \mathbf{U}_n \mathbf{P}_n \mathbf{X}_t = \mathbf{U}_n \mathbf{X}_t = \mathbf{Y}_t$ as we wanted to show.

In this work, we will say that a given property holds “for k large enough”, when there exists an integer k_0 such that for all $k \geq k_0$ that property holds.

2.3. Relationships between micro and macrovariables

If $\mathbf{z}_0 \neq \mathbf{0}$ is the initial condition for a system of non-autonomous difference equations of the kind

$$\mathbf{z}_{n+1} = \mathbf{A}_n \mathbf{z}_n, \tag{2.13}$$

then, for every $n \geq 0$, $\mathbf{z}_n = \mathbf{T}_n \mathbf{z}_0$, where $\mathbf{T}_n = \mathbf{A}_{n-1} \cdots \mathbf{A}_1 \mathbf{A}_0$. Therefore, the dynamics of the system is characterized by the behavior of the matrix products \mathbf{T}_n . In particular, in order to study the asymptotic behavior of the system we have to deal with infinite backwards products of non-negative matrices.

For each $p \geq 0$ and each $n > p$ we define the following matrix products, which will be useful in the sequel:

$$\begin{aligned} \mathbf{\Pi}_{n,p}(k) &= \mathbf{M}_{n-1} \mathbf{P}_{n-1}^k \cdots \mathbf{M}_{p+1} \mathbf{P}_{p+1}^k \mathbf{M}_p \mathbf{P}_p^k, \\ \mathbf{\Pi}'_{n,p} &= \mathbf{M}_{n-1} \bar{\mathbf{P}}_{n-1} \cdots \mathbf{M}_{p+1} \bar{\mathbf{P}}_{p+1} \mathbf{M}_p \bar{\mathbf{P}}_p, \\ \bar{\mathbf{\Pi}}_{n,p} &= \bar{\mathbf{M}}_{n-1} \cdots \bar{\mathbf{M}}_{p+1} \bar{\mathbf{M}}_p \end{aligned} \tag{2.14}$$

and we have the following expression for the original and aggregated system in terms of the vector of initial conditions:

$$\begin{aligned} \text{original system: } \mathbf{X}_n &= \mathbf{\Pi}_{n,0}(k) \mathbf{X}_0, \\ \text{auxiliary system: } \mathbf{X}_n &= \mathbf{\Pi}'_{n,0} \mathbf{X}_0, \\ \text{aggregated system: } \mathbf{Y}_n &= \bar{\mathbf{\Pi}}_{n,0} \mathbf{Y}_0. \end{aligned} \tag{2.15}$$

For each n , let the eigenvalues of \mathbf{P}_n (i.e. the union of the eigenvalues of the $\mathbf{P}_i(n)$) ordered by decreasing modulus be

$$1 = \lambda_1(n) = \cdots = \lambda_q(n) > |\lambda_{q+1}(n)| \geq \cdots \geq |\lambda_N(n)|,$$

and let δ verify the condition

$$\begin{aligned} \delta &= 1 \quad \text{if } \sup_n \{|\lambda_{q+1}(n)|\} = 1 \\ 1 > \delta > \sup_n \{|\lambda_{q+1}(n)|\} & \quad \text{if } \sup_n \{|\lambda_{q+1}(n)|\} < 1. \end{aligned} \tag{2.16}$$

From this definition we see that δ is greater than the modulus of the subdominant eigenvalue of matrices \mathbf{P}_n . Then we have:

Proposition 1. *For all n we have $\mathbf{P}_n^k = \bar{\mathbf{P}}_n + o(\delta^k)$; $k \rightarrow \infty$, where δ is given by (2.16).*

Proof. Let n be fixed and let us consider a Jordan canonical decomposition of \mathbf{P}_n . Eigenvalue 1 is simple and strictly dominant for each of the $\mathbf{P}_i(n)$ and is associated

to right and left eigenvectors $\mathbf{v}_i(n)$ and $\mathbf{u}_i(n)$. Therefore, for matrix \mathbf{P}_n eigenvalue 1 is strictly dominant, semisimple and has multiplicity q . Besides, the columns of \mathbf{V}_n and the rows of \mathbf{U}_n are bases of its associated right and left eigenspaces, respectively. Since $\mathbf{U}_n \mathbf{V}_n = \mathbf{I}_q$, a Jordan decomposition of \mathbf{P}_n with eigenvalues ordered by decreasing modulus will have the form

$$\mathbf{P}_n = (\mathbf{V}_n | \mathbf{V}'_n) \operatorname{diag}(\mathbf{I}_q, \mathbf{H}_n) \begin{pmatrix} \mathbf{U}_n \\ \mathbf{U}'_n \end{pmatrix},$$

where \mathbf{V}'_n and \mathbf{U}'_n are appropriate matrices and \mathbf{H}_n corresponds to Jordan blocks associated to eigenvalues $\lambda_{q+1}(n), \dots, \lambda_N(n)$ (of modulus strictly less than δ). Therefore, taking into account that $\bar{\mathbf{P}}_n = \mathbf{V}_n \mathbf{U}_n$ we have

$$\mathbf{P}_n^k = \bar{\mathbf{P}}_n + (\mathbf{V}_n | \mathbf{V}'_n) \operatorname{diag}(0, \mathbf{H}_n^k) \begin{pmatrix} \mathbf{U}_n \\ \mathbf{U}'_n \end{pmatrix},$$

from where

$$\frac{\mathbf{P}_n^k - \bar{\mathbf{P}}_n}{\delta^k} = (\mathbf{V}_n | \mathbf{V}'_n) \operatorname{diag}\left(0, \left(\frac{\mathbf{H}_n}{\delta}\right)^k\right) \begin{pmatrix} \mathbf{U}_n \\ \mathbf{U}'_n \end{pmatrix},$$

and the desired result follows taking limits $k \rightarrow \infty$. □

The following proposition provides a relationship between the micro and the macrovariables and, besides, characterizes the relationship between the matrix products in (2.14).

Proposition 2. *Let $p \geq 0$ and $n \geq p$. Then:*

- (a) $\mathbf{\Pi}'_{n+1,p} = \mathbf{M}_n \mathbf{V}_n \bar{\mathbf{\Pi}}_{n,p} \mathbf{U}_p$, $\bar{\mathbf{\Pi}}_{n,p} = \mathbf{U}_n \mathbf{\Pi}'_{n,p} \mathbf{V}_p$
- (b) $\mathbf{\Pi}_{n,p}(k) = \mathbf{\Pi}'_{n,p} + o(\delta^k)$, $k \rightarrow \infty$

where δ is given by (2.16)

- (c) *the variables \mathbf{X}_n and \mathbf{Y}_n corresponding to the general and aggregated systems respectively verify*

$$\begin{aligned} \mathbf{X}_{n+1} &= \mathbf{M}_n \mathbf{V}_n \mathbf{Y}_n + o(\delta^k), \quad k \rightarrow \infty \\ \mathbf{Y}_n &= \mathbf{U}_{n+1} \mathbf{X}_n + o(\delta^k), \quad k \rightarrow \infty. \end{aligned} \tag{2.17}$$

Proof. (a) We know that $\mathbf{\Pi}'_{n,p} = \mathbf{M}_{n-1} \bar{\mathbf{P}}_{n-1} \cdots \mathbf{M}_{p+1} \bar{\mathbf{P}}_{p+1} \mathbf{M}_p \bar{\mathbf{P}}_p$. Multiplying on the left by \mathbf{U}_n , on the right by \mathbf{V}_p and bearing in mind Lemma 1 we have

$$\begin{aligned} \mathbf{U}_n \mathbf{\Pi}'_{n,p} \mathbf{V}_p &= \mathbf{U}_n \mathbf{M}_{n-1} \mathbf{V}_{n-1} \mathbf{U}_{n-1} \cdots \mathbf{M}_{p+1} \mathbf{V}_{p+1} \mathbf{U}_{p+1} \mathbf{M}_p \mathbf{V}_p \mathbf{U}_p \mathbf{V}_p \\ &= \bar{\mathbf{M}}_{n-1} \cdots \bar{\mathbf{M}}_{p+1} \bar{\mathbf{M}}_p = \bar{\mathbf{\Pi}}_{n,p}, \end{aligned}$$

as we wanted to show. On the other hand, from $\bar{\mathbf{\Pi}}_{n,p} = \mathbf{U}_n \mathbf{\Pi}'_{n,p} \mathbf{V}_p$ we have, multiplying on the left by $\mathbf{M}_n \mathbf{V}_n$ and on the right by \mathbf{U}_p ,

$$\begin{aligned} \mathbf{M}_n \mathbf{V}_n \bar{\mathbf{\Pi}}_{n,p} \mathbf{V}_p \mathbf{U}_p &= \mathbf{M}_n \mathbf{V}_n \mathbf{U}_n \mathbf{\Pi}'_{n,p} \mathbf{V}_p \mathbf{U}_p = \mathbf{M}_n \bar{\mathbf{P}}_n \mathbf{\Pi}'_{n,p} \bar{\mathbf{P}}_p \\ &= \mathbf{M}_n \bar{\mathbf{P}}_n \mathbf{M}_{n-1} \bar{\mathbf{P}}_{n-1} \cdots \mathbf{M}_{p+1} \bar{\mathbf{P}}_{p+1} \mathbf{M}_p \bar{\mathbf{P}}_p \bar{\mathbf{P}}_p = \mathbf{\Pi}'_{n+1,p}. \end{aligned}$$

(b) Let n and p be fixed. Using Proposition 1 we have

$$\begin{aligned} \mathbf{\Pi}_{n,p}(k) &= \mathbf{M}_{n-1} \mathbf{P}_{n-1}^k \cdots \mathbf{M}_{p+1} \mathbf{P}_{p+1}^k \mathbf{M}_p \mathbf{P}_p^k \\ &= \mathbf{M}_{n-1} (\bar{\mathbf{P}}_{n-1} + o(\delta^k)) \cdots \mathbf{M}_{p+1} (\bar{\mathbf{P}}_{p+1} + o(\delta^k)) \mathbf{M}_p (\bar{\mathbf{P}}_p + o(\delta^k)) \\ &= \mathbf{\Pi}'_{n,p} + \mathbf{F}_{n,p}(k), \end{aligned}$$

where $\mathbf{F}_{n,p}(k)$ is a sum of $2^{n-p-1} - 1$ factors in which each of them is $o(\delta^k)$, so the result follows.

(c) Trivial consequence of (a) and (b) since for the original system,

$$\begin{aligned} \mathbf{X}_{n+1} &= \mathbf{\Pi}_{n+1,0}(k) \mathbf{X}_0 = (\mathbf{\Pi}'_{n+1,0} + o(\delta^k)) \mathbf{X}_0 = \mathbf{M}_n \mathbf{V}_n \bar{\mathbf{\Pi}}_{n,0} \mathbf{U}_0 \mathbf{X}_0 + o(\delta^k) \\ &= \mathbf{M}_n \mathbf{V}_n \bar{\mathbf{\Pi}}_{n,0} \mathbf{Y}_0 + o(\delta^k) = \mathbf{M}_n \mathbf{V}_n \mathbf{Y}_n + o(\delta^k). \end{aligned}$$

On the other hand,

$$\mathbf{Y}_n = \mathbf{U}_{n+1} \mathbf{\Pi}'_{n,0} \mathbf{X}_0 = \mathbf{U}_{n+1} (\mathbf{\Pi}_{n,0}(k) + o(\delta^k)) \mathbf{X}_0 = \mathbf{U}_{n+1} \mathbf{X}_n + o(\delta^k). \quad \square$$

For each time step, and if the separation between the two time scales is sufficiently large, the incidence matrices corresponding to the original and auxiliary systems are the same, as the next result shows.

Lemma 4. *There exists a positive integer k_0 such that for all $k \geq k_0$ we have $\bar{\mathbf{P}}_n \sim \mathbf{P}_n^k$ (and therefore $\mathbf{M}_n \bar{\mathbf{P}}_n \sim \mathbf{M}_n \mathbf{P}_n^k$) for all n .*

Proof. Let i be fixed. Since $\mathbf{P}_i(n)$ is primitive for all n we have $\mathbf{P}_i^k(n) > 0$ for all $k \geq N_i^2 - 2N_i + 2$.²⁰ Since $\bar{\mathbf{P}}_i(n)$ is a positive matrix, if we choose $k_0 = N_{\max}^2 - 2N_{\max} + 2$, where $N_{\max} = \max\{N_1, \dots, N_q\}$, it follows that $\bar{\mathbf{P}}_i(n) \sim \mathbf{P}_i^k(n)$ for all $k \geq k_0$, all i and all n . \square

2.4. Aggregation of a non-autonomous multiregional model

In this section we illustrate with some applications the aggregation procedure considered in the preceding sections. We will consider the case of non-autonomous multiregional models. We will show how, in some practical cases found in the literature, we can distinguish two time scales that make possible the use of aggregation in order to simplify the corresponding model.

Multiregional models consider the dynamics of an age structured population distributed among different spatial patches among which they can migrate. These models have been used with profusion in Ref. 32 among other authors for the study of human populations. A list of ecological applications can be found in Refs. 10 and 27.

In contrast with these references, that do not explicitly consider the existence of different time scales, some approaches^{6-8,12,34} have considered that, as is usual in many situations, migration is fast in comparison with the demographic process. In our first application we aggregate a multiregional model under this hypothesis.

2.4.1. Aggregation of a multiregional model with fast migration

We suppose that the population under study is divided into q age classes (corresponding to groups) and spread out in r spatial patches (subgroups) among which individuals may migrate. In this way, the population is structured in qr stages, each of them corresponding to an age class and a spatial location.

The demographic and migratory processes are responsible for the transference of individuals between the different stages. In this application we suppose that migration is a fast process in comparison with demography, and we choose as time step $\Delta_n = [n, n + 1)$ for the model the duration of each age class.

We will denote by x_n^{ij} the number of individuals of age i in the j th spatial patch at time n , with $i = 1, 2, \dots, q$ and $j = 1, 2, \dots, r$. We use vectors $\mathbf{x}_n^i = (x_n^{i1}, x_n^{i2}, \dots, x_n^{ir}) \in \mathbb{R}^r$ ($i = 1, 2, \dots, q$), to describe the spatial allocation of individuals in age class i . The population will be described by vector $\mathbf{X}_n = (\mathbf{x}_n^1, \mathbf{x}_n^2, \dots, \mathbf{x}_n^q)^T \in \mathbb{R}^{rq}$. For each i and each interval Δ_n , migration for individuals of age i is modeled by a matrix $\mathbf{P}_i(n) \in \mathbb{R}^{r \times r}$ which, since migration is a conservative process for the total number of individuals, is stochastic. Besides we suppose that $\mathbf{P}_i(n)$ is primitive for each i and each n (this is the case, for example, if the fast process corresponding to each Δ_n verifies (i) transition from any patch to any other, in a sufficient number of steps, is allowed and (ii) individuals of at least one patch are allowed to stay in that patch).

In this way, each $\mathbf{P}_i(n)$ is primitive and, if the duration of each age class is sufficiently long with respect to the projection interval of migration, the migratory process in each Δ_n will tend to an equilibrium. Let $\mathbf{v}_i(n)$ be the vector that provides the equilibrium structure of the population for group i , i.e. the positive eigenvector of $\mathbf{P}_i(n)$ associated to eigenvalue 1 and normalized so that the sum of its components is one. Notice that, since the $\mathbf{P}_i(n)$ are stochastic, the left eigenvectors associated to eigenvalue one and verifying (2.4) are independent of n and have the form $\mathbf{u}_i = (1, 1, \dots, 1)^T \in \mathbb{R}^r$. So we have $\mathbf{V}_n = \text{diag}(\mathbf{v}_1(n), \dots, \mathbf{v}_q(n))$; $\mathbf{U} = \mathbf{U}_n = \text{diag}(\mathbf{u}_1^T, \dots, \mathbf{u}_q^T)$. Migration for the whole of the population is given, for each Δ_n , by matrix $\mathbf{P}_n = \text{diag}(\mathbf{P}_1(n), \dots, \mathbf{P}_q(n))$.

The demographic process is defined through the following coefficients:

Fertility coefficients: $F_i^j(n)$ = fertility rate for individuals of age i in patch j during interval Δ_n ; $i = 1, \dots, q$; $j = 1, \dots, r$.

Survival coefficients: $S_i^j(n)$ = fertility rate for individuals of age i in patch j during interval Δ_n ; $i = 1, \dots, q - 1$; $j = 1, \dots, r$.

We define matrices

$$\mathbf{F}_i(n) = \text{diag}(F_i^1(n), \dots, F_i^r(n)), \quad i = 1, \dots, q$$

and

$$\mathbf{S}_i(n) = \text{diag}(S_i^1(n), \dots, S_i^r(n)), \quad i = 1, \dots, q - 1,$$

and then demography for the whole of the population is characterized, for each Δ_n , by the following generalized Leslie matrix:

$$\mathbf{M}_n = \begin{pmatrix} \mathbf{F}_1(n) & \mathbf{F}_2(n) & \cdots & \mathbf{F}_{q-1}(n) & \mathbf{F}_q(n) \\ \mathbf{S}_1(n) & \mathbf{0} & \cdots & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{S}_2(n) & \cdots & \mathbf{0} & \mathbf{0} \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ \mathbf{0} & \mathbf{0} & \cdots & \mathbf{S}_{q-1}(n) & \mathbf{0} \end{pmatrix}. \tag{2.18}$$

The general system consists, then, of the following system of rq difference equations:

$$\mathbf{X}_{n+1} = \mathbf{M}_n \mathbf{P}_n^k \mathbf{X}_n, \tag{2.19}$$

where k can be interpreted as the ratio between the projection intervals corresponding to the demographic and migratory processes.

According to (2.9) we will have q global variables, each of them corresponding to an age class, given by

$$y_n^i = \mathbf{u}_i^T \mathbf{x}_n^{iT} = x_n^{i1} + x_n^{i2} + \cdots + x_n^{ir}, \quad i = 1, \dots, q,$$

i.e. for a given instant n , the global variable corresponding to each class i is the total population with that age.

The aggregated system has the form

$$\mathbf{Y}_{n+1} = \bar{\mathbf{M}}_n \mathbf{Y}_n, \tag{2.20}$$

where $\bar{\mathbf{M}}_n$ is a Leslie matrix with time varying vital rates given by

$$\bar{\mathbf{M}}_n = \begin{pmatrix} f_1(n) & f_2(n) & \cdots & f_{q-1}(n) & f_q(n) \\ s_1(n) & 0 & \cdots & 0 & 0 \\ 0 & s_2(n) & \cdots & 0 & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & \cdots & s_{q-1}(n) & 0 \end{pmatrix}. \tag{2.21}$$

The vital rates in (2.21) have the form

$$f_i(n) = \mathbf{u}_i^T \mathbf{F}_i(n) \mathbf{v}_i(n) = \sum_{j=1}^r v_i^j(n) F_i^j(n), \quad i = 1, \dots, q,$$

$$s_i(n) = \mathbf{u}_{i+1}^T \mathbf{S}_i(n) \mathbf{v}_i(n) = \sum_{j=1}^r v_i^j(n) S_i^j(n), \quad i = 1, \dots, q - 1,$$

i.e. each fertility rate $f_i(n)$ in the aggregated system is a weighted linear combination of the fertility rates in the general system corresponding to individuals of age class i and time n , the weights being the coefficients $v_i^j(n)$ of the equilibrium spatial distribution for the migratory process in Δ_n . Something analogous holds for the survival rates.

Notice that $f_i(n)$ is nonzero if and only if $\mathbf{F}_i(n)$ is. In the same way, $s_i(n)$ is nonzero if and only if $\mathbf{S}_i(n)$ is.

In order to illustrate the above discussions we will particularize them to a very simple case in which there are only two patches and two age classes. Then the matrices \mathbf{M}_n and \mathbf{P}_n that characterize demography and migration are given by

$$\mathbf{M}_n = \begin{pmatrix} F_1^1(n) & 0 & F_2^1(n) & 0 \\ 0 & F_1^2(n) & 0 & F_2^2(n) \\ S_1(n) & 0 & 0 & 0 \\ 0 & S_2(n) & 0 & 0 \end{pmatrix},$$

$$\mathbf{P}_n = \text{diag}(\mathbf{P}_1(n), \mathbf{P}_2(n)) = \begin{pmatrix} 1 - p_1(n) & q_1(n) & 0 & 0 \\ p_1(n) & 1 - q_1(n) & 0 & 0 \\ 0 & 0 & 1 - p_2(n) & q_2(n) \\ 0 & 0 & p_2(n) & 1 - q_2(n) \end{pmatrix},$$

where $p_1(n)$ and $p_2(n)$ denote migration rates at time n for individuals of age class 1 and 2, respectively, from patch 1 to patch 2, and $q_1(n)$ and $q_2(n)$ have an analogous meaning for the migration from patch 2 to patch 1. $S_1(n)$ and $S_2(n)$ denote survival rates for age class one in patches 1 and 2 respectively.

If we assume that all the migration rates are different from 0 and 1, then matrices $\mathbf{P}_1(n)$ and $\mathbf{P}_2(n)$ are positive and, consequently, primitive. Vectors $\mathbf{v}_i(n)$ and \mathbf{u}_i are given by

$$\mathbf{v}_i(n) = \left(\frac{q_i(n)}{p_i(n) + q_i(n)}, \frac{p_i(n)}{p_i(n) + q_i(n)} \right)^T, \quad i = 1, 2, \quad \mathbf{u}_1 = \mathbf{u}_2 = (1, 1)^T,$$

so that the general system has the expression

$$\begin{pmatrix} x_{n+1}^{11} \\ x_{n+1}^{12} \\ x_{n+1}^{21} \\ x_{n+1}^{22} \end{pmatrix} = \mathbf{M}_n \mathbf{P}_n^k \begin{pmatrix} x_n^{11} \\ x_n^{12} \\ x_n^{21} \\ x_n^{22} \end{pmatrix},$$

and the global variables are

$$y_n^1 = \mathbf{u}_1^T(x_n^{11}, x_n^{12})^T = x_n^{11} + x_n^{12},$$

$$y_n^2 = \mathbf{u}_2^T(x_n^{21}, x_n^{22})^T = x_n^{21} + x_n^{22}.$$

The aggregated model has the following form

$$\begin{pmatrix} y_{n+1}^1 \\ y_{n+1}^2 \end{pmatrix} = \begin{pmatrix} \frac{q_1(n)F_1^1(n) + p_1(n)F_1^2(n)}{p_1(n) + q_1(n)} & \frac{q_2(n)F_2^1(n) + p_2(n)F_2^2(n)}{p_2(n) + q_2(n)} \\ \frac{q_1(n)S^1(n) + p_1(n)S^2(n)}{p_1(n) + q_1(n)} & 0 \end{pmatrix} \begin{pmatrix} y_n^1 \\ y_n^2 \end{pmatrix}.$$

2.4.2. Aggregation of a multiregional model with fast demography

In some practical cases found in the literature, demography can be considered a fast process in relation to migration. Investigating the dynamics of the population of Canada and Great Britain, Refs. 25 and 26 have shown, both empirically and analytically, that the tendency of a multiregional population projection to a fixed asymptotic distribution takes place in two stages: First, a relatively rapid convergence to the stable age compositions in each region and, second, a gradual convergence towards a stable interregional allocation of the national population. This suggests, as Rogers points out in Refs. 31 and 32, the use of aggregation techniques (in which the role of the fast dynamics will be played by the demographic process) in order to simplify the multiregional system

Therefore, we will now consider a multiregional model with demographic and migratory coefficients depending on time and in which the demographic process is fast in comparison with migration. We will first setup the general situation and then we will particularize it to a very simple case that will illustrate the methodology used.

As in the application above, we suppose a population structured by age and patch living in an environment composed of q patches (which in this case correspond to the different groups) and divided in r discrete age classes (subgroups). We will denote by x_n^{ij} the number of individuals of age j living in patch i at time n , with $i = 1, \dots, q$ and $j = 1, \dots, r$. The variables corresponding to patch i are given by vector $\mathbf{x}_n^i = (x_n^{i1}, x_n^{i2}, \dots, x_n^{ir})$ and the whole population is described by vector $\mathbf{X}_n = (\mathbf{x}_n^1, \mathbf{x}_n^2, \dots, \mathbf{x}_n^q)^T$ which therefore has qr components. Notice that the notation for this application has a different meaning from the previous one. This is a consequence of the fact that now the fast and slow processes are interchanged with respect to those corresponding to the first application.

We choose as time step $\Delta_n = [n, n + 1)$ for the model, the one corresponding to the migratory process. The characteristics of migration between the different patches are given, for each Δ_n , by the following coefficients:

$m_{kl}^j(n)$ = rate of transference of individuals of age j from patch l to patch k , during interval Δ_n ; $k, l = 1, \dots, q$; $j = 1, \dots, r$.

These coefficients must satisfy the obvious restrictions $0 \leq m_{kl}^j(n)$ for all k, l and $\sum_{k=1}^q m_{kl}^j(n) = 1$ for all l, j and n . From the last expression we have $m_{ll}^j(n) = 1 - \sum_{k \neq l} m_{kl}^j(n)$ for all l, j and n , i.e. the qr rates that characterize the proportion of the population that does not leave the corresponding patch are determined by the remaining $(q - 1)qr$ migration rates.

Therefore, migration for the whole population at time n is defined by the following matrix of dimensions $qr \times qr$.

$$\mathbf{M}_n = \begin{pmatrix} \mathbf{M}_{11}(n) & \mathbf{M}_{12}(n) & \cdots & \mathbf{M}_{1q}(n) \\ \mathbf{M}_{21}(n) & \mathbf{M}_{22}(n) & \cdots & \mathbf{M}_{2q}(n) \\ \vdots & \vdots & \ddots & \vdots \\ \mathbf{M}_{q1}(n) & \mathbf{M}_{q2}(n) & \cdots & \mathbf{M}_{qq}(n) \end{pmatrix},$$

where matrix $\mathbf{M}_{kl}(n) \in \mathbb{R}^{r \times r}$ characterizes the transference of individuals from patch l to patch k at time n , and is given by

$$\mathbf{M}_{kl}(n) = \text{diag}(m_{kl}^1(n), m_{kl}^2(n), \dots, m_{kl}^r(n)) \quad \text{for } k, l = 1, \dots, q.$$

Notice that, as it must be the case for a conservative process, each \mathbf{M}_n is a stochastic matrix.

Demography is an internal process for each patch. We assume that the fertility and survival coefficients are allowed to vary only with each time step corresponding to migration. Therefore, for each time step of the demographic process belonging to Δ_n , the demography for each patch i will be given by a Leslie matrix $\mathbf{P}_i(n)$ in the following way:

$$\mathbf{P}_i(n) = \begin{pmatrix} F_i^1(n) & F_i^2(n) & \dots & F_i^{r-1}(n) & F_i^r(n) \\ S_i^1(n) & 0 & \dots & 0 & 0 \\ 0 & S_i^2(n) & \dots & 0 & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & \dots & S_i^{r-1}(n) & 0 \end{pmatrix} \in \mathbb{R}^{r \times r}, \quad (2.22)$$

where the vital rates have the classical interpretation, i.e.

$$F_i^j(n) = \text{fertility rate of individuals of age } j \text{ in patch } i \text{ at time } n.$$

$$S_i^j(n) = \text{survival rate of individuals of age } j \text{ in patch } i \text{ at time } n.$$

We will assume that (i) all the survival rates are nonzero, i.e. $S_i^j(n) \neq 0$ for all i, j and n . (ii) for all patches and all times, the fertility coefficient of the last age class is nonzero, i.e. $F_i^r(n) \neq 0$ for all i and n . (iii) for all n , given any patch i , there is an age j such that $F_i^j(n) \neq 0$ and $\text{g.c.d.}(r, j) = 1$. These three conditions, which are usually met in most practical situations, guarantee that for all i and n matrices $\mathbf{P}_i(n)$ are primitive. Therefore, if Δ_n is large enough with respect to the projection interval corresponding to migration, the demographic process in all patches and all Δ_n tends to a steady structure. Besides, if we assume that, for all i and n , the dominant eigenvalue of $\mathbf{P}_i(n)$ is one, then the demography in each patch makes the individuals change age classes but does not make the total population of the patch grow indefinitely or decay to zero. This last assumption is reflected in the requirement that the vital rates of $\mathbf{P}_i(n)$ satisfy the following equality (see Ref. 10): For $i = 1, \dots, q$ and $n = 0, 1, \dots$,

$$F_i^1(n) + F_i^2(n)S_i^1(n) + \dots + F_i^r(n)S_i^1(n)S_i^2(n) \dots S_i^{r-1}(n) = 1.$$

We denote $\mathbf{v}_i(n)$ the vector expressing the equilibrium population structure corresponding to patch i in interval Δ_n , i.e. the positive probability normed eigenvector of $\mathbf{P}_i(n)$ associated to eigenvalue 1. We also define $\mathbf{u}_i(n)$ as the (positive) left eigenvector of $\mathbf{P}_i(n)$ associated to 1 and normalized so $\mathbf{u}_i^T(n)\mathbf{v}_i(n) = 1$; this vector characterizes the reproductive values of the individuals for the demographic process

in patch i and time Δ_n . For each j , $u_i^j(n)$ measures the relative contribution that individuals of patch i initially present in age j would have in the total equilibrium population of group i at the end of Δ_n if the system were controlled exclusively by demography and started to evolve at time n . The explicit expressions for vectors $\mathbf{u}_i(n)$ and $\mathbf{v}_i(n)$ in terms of the vital rates in patch i can be found in Ref. 10.

The demography for the whole population will be defined by matrix

$$\mathbf{P}_n = \text{diag}(\mathbf{P}_1(n), \mathbf{P}_2(n), \dots, \mathbf{P}_q(n)).$$

Following the general method described in previous sections we also define matrices $\mathbf{V}_n = \text{diag}(\mathbf{v}_1(n), \mathbf{v}_2(n), \dots, \mathbf{v}_q(n))$ and $\mathbf{U}_n = \text{diag}(\mathbf{u}_1^T(n), \mathbf{u}_2^T(n), \dots, \mathbf{u}_q^T(n))$.

In order to approximate the effect of demography over the time interval of the model, which is much longer than its own projection interval, we suppose that during each interval Δ_n matrix \mathbf{P}_n operates k times, where k is a large integer. Therefore, the proposed model will be the following system of qr difference equations

$$\mathbf{X}_{n+1} = \mathbf{M}_n \mathbf{P}_n^k \mathbf{X}_n.$$

Following the procedure proposed in Sec. 2.2 we will have q variables (global variables or macro variables), one for each of the patches, governing the aggregated system. These variables are given by:

$$y_n^i = \mathbf{u}_i^T(n) \mathbf{x}_n^{iT} = u_i^1(n)x_n^{i1} + u_i^2(n)x_n^{i2} + \dots + u_i^r(n)x_n^{ir}, \quad i = 1, \dots, q,$$

i.e. the global variable corresponding to patch i is a linear combination of the microvariables of patch i , the coefficient of each microvariable x_n^{ij} being proportional to the reproductive values of individuals of age j in that patch.

The aggregated system (2.10) has the form:

$$\mathbf{Y}_{n+1} = \bar{\mathbf{M}}_n \mathbf{Y}_n,$$

where matrix $\bar{\mathbf{M}}_n$ is given by (2.11):

$$\bar{\mathbf{M}}_n = \begin{pmatrix} \sum_{j=1}^r u_1^j(n+1)v_1^j(n)m_{11}^j(n) & \dots & \sum_{j=1}^r u_1^j(n+1)v_q^j(n)m_{1q}^j(n) \\ \vdots & \ddots & \vdots \\ \sum_{j=1}^r u_q^j(n+1)v_1^j(n)m_{q1}^j(n) & \dots & \sum_{j=1}^r u_q^j(n+1)v_q^j(n)m_{qq}^j(n) \end{pmatrix}.$$

As we can see, the entries of the matrix of the aggregated system are functions of the migration rates as well as the equilibrium characteristics of demography. We have collapsed the original system into the aggregated system in which the population is structured only by patch and in which each macro variable corresponds to one patch.

In order to illustrate the above discussions we will particularize them to a simple case in which there are only two spatial patches and two age classes. Under these

assumptions we have four microvariables $x_n^{11}, x_n^{12}, x_n^{21}, x_n^{22}$ and matrices \mathbf{M}_n and \mathbf{P}_n are given by

$$\mathbf{M}_n = \begin{pmatrix} 1 - p_1(n) & 0 & q_1(n) & 0 \\ 0 & 1 - p_2(n) & 0 & q_2(n) \\ p_1(n) & 0 & 1 - q_1(n) & 0 \\ 0 & p_2(n) & 0 & 1 - q_2(n) \end{pmatrix},$$

$$\mathbf{P}_n = \begin{pmatrix} F_1^1(n) & F_1^2(n) & 0 & 0 \\ S_1(n) & 0 & 0 & 0 \\ 0 & 0 & F_2^1(n) & F_2^2(n) \\ 0 & 0 & S_2(n) & 0 \end{pmatrix},$$

where the vital rates have the same meaning as in the previous application.

The restrictions on the vital rates so that matrices $\mathbf{P}_1(n)$ and $\mathbf{P}_2(n)$ have dominant eigenvalue 1 are $F_1^1(n) + F_1^2(n)S_1(n) = 1$ and $F_2^1(n) + F_2^2(n)S_2(n) = 1$. Besides, we will suppose that all the fertility and survival rates are always positive, which yields the primitivity of matrices $\mathbf{P}_1(n)$ and $\mathbf{P}_2(n)$. Vectors $\mathbf{v}_i(n)$ and $\mathbf{u}_i(n)$ are given by

$$\mathbf{v}_1(n) = \left(\frac{1}{1 + S_1(n)}, \frac{S_1(n)}{1 + S_1(n)} \right)^T, \quad \mathbf{v}_2(n) = \left(\frac{1}{1 + S_2(n)}, \frac{S_2(n)}{1 + S_2(n)} \right)^T,$$

$$\mathbf{u}_1(n) = \frac{1 + S_1(n)}{1 + F_1^2(n)S_1(n)}(1, F_1^2(n))^T, \quad \mathbf{u}_2(n) = \frac{1 + S_2(n)}{1 + F_2^2(n)S_2(n)}(1, F_2^2(n))^T.$$

The microsystem has the form

$$\begin{pmatrix} x_{n+1}^{11} \\ x_{n+1}^{12} \\ x_{n+1}^{21} \\ x_{n+1}^{22} \end{pmatrix} = \mathbf{M}_n \mathbf{P}_n^k \begin{pmatrix} x_n^{11} \\ x_n^{12} \\ x_n^{21} \\ x_n^{22} \end{pmatrix},$$

and the global variables y_n^1 and y_n^2 corresponding, respectively, to patches 1 and 2 are defined by

$$y_n^1 = \mathbf{u}_1^T(n)(x_n^{11}, x_n^{12})^T = \frac{1}{1 + F_1^2(n)S_1(n)}(x_n^{11} + F_1^2(n)x_n^{12})$$

$$y_n^2 = \mathbf{u}_2^T(n)(x_n^{21}, x_n^{22})^T = \frac{1}{1 + F_2^2(n)S_2(n)}(x_n^{21} + F_2^2(n)x_n^{22}),$$

while the aggregated system reads as

$$\begin{pmatrix} y_{n+1}^1 \\ y_{n+1}^2 \end{pmatrix} = \bar{\mathbf{M}} \begin{pmatrix} y_n^1 \\ y_n^2 \end{pmatrix},$$

with

$$\bar{\mathbf{M}} = \begin{pmatrix} \frac{(1+S_1(n+1))p'_1(n)+F_1^2(n+1)S_1(n)p'_2(n)}{1+S_1(n)} & \frac{(1+S_1(n+1))(q_1(n)+F_1^2(n+1)S_1(n)q_2(n))}{(1+S_2(n))(1+F_1^2(n+1)S_1(n+1))} \\ \frac{(1+S_2(n+1))(p_1(n)+F_2^2(n+1)S_1(n)p_2(n))}{(1+S_1(n))(1+F_2^2(n+1)S_2(n+1))} & \frac{1+S_2(n+1)}{1+S_2(n)} \frac{q'_1(n)+F_2^2(n+1)S_2(n)q'_2(n)}{1+F_2^2(n+1)S_2(n+1)} \end{pmatrix},$$

where, for the sake of compactness, we have denoted $p'(n) = 1 - p(n)$ and $q'(n) = 1 - q(n)$.

3. Non-Autonomous Systems and Weak Ergodicity

Let us consider a generic linear time discrete model for a stage-structured population with N stages, in which the conditions of the environment are changing through time. We will therefore deal with a system of difference equations with non-constant coefficients of the kind (2.13), where $\mathbf{z}_n \in \mathbb{R}^N$ and $\mathbf{A}_n \in \mathbb{R}^{N \times N}$ ($n = 0, 1, \dots$), are non-negative matrices which represent the vital rates of the population in the different environmental conditions. Let us denote by $\| * \|$ the 1-norm in \mathbb{R}^N , i.e. if $\mathbf{z} = (z_1, z_2, \dots, z_N)^T$ we have $\|\mathbf{z}\| = |z_1| + |z_2| + \dots + |z_N|$. Then, the total population of system (2.13) at time n is $\|\mathbf{z}_n\|$ and the population structure at time n will be given by $\mathbf{z}_n/\|\mathbf{z}_n\|$. Given any initial condition $\mathbf{z}_0 \neq \mathbf{0}$, the population vector for any time $n \geq 0$ is $\mathbf{z}_n = \mathbf{T}_n \mathbf{z}_0$, where

$$\mathbf{T}_n = \mathbf{A}_{n-1} \cdots \mathbf{A}_1 \mathbf{A}_0,$$

and so the population structure at time n will be defined by $\mathbf{T}_n \mathbf{z}_0 / \|\mathbf{T}_n \mathbf{z}_0\|$.

The type of study we are interested in for a system of the kind (2.13) depends on the pattern of environmental variation. A typical case is the one corresponding to periodical variation, i.e. $\mathbf{A}_{n+T} = \mathbf{A}_n$ for all n . The population eventually grows exponentially and typically the asymptotic population structure oscillates among T vectors.¹⁰

Another interesting situation appears when the environment tends to stabilization, i.e. there exists a matrix \mathbf{A} which represents the environment at equilibrium, such that $\lim_{n \rightarrow \infty} \mathbf{A}_n = \mathbf{A}$. In that case it can be shown (see Ref. 34) that under some very general conditions, the system behaves asymptotically as if the environment were constant and defined by matrix \mathbf{A} . In particular, the population grows asymptotically in an exponential fashion and the population structure converges to a certain vector which is independent of initial conditions, i.e. for all $\mathbf{z}_0 \neq 0$, $\mathbf{z}_0 \geq 0$, it follows $\lim_{n \rightarrow \infty} \mathbf{z}_n / \|\mathbf{z}_n\| = \mathbf{v}$ for a certain \mathbf{v} . This property of the system, by which there is a convergence of the population structure to a fixed vector independent of the initial conditions, is known as “strong ergodicity”. It implies that the system “forgets its past” in the sense that, for sufficiently high times, the population structure tends to a fixed vector independent of the initial condition. In Ref. 34 the authors have investigated the relationships between the original and the aggregated systems in the cases in which the environment varies in a periodic fashion or tends to stabilization.

In the case in which the environment changes with time in a general fashion,³⁰ it is not possible to expect that the population grows exponentially or that population structure converges to a certain vector. However, under quite general circumstances, the population structure also “forgets its past” in the sense that two different initial populations, subjected to the same sequence of environmental variation, have structures that become more and more alike (even though they do not necessarily converge). In other words, system (2.13) is weakly ergodic when, for any nonzero initial conditions \mathbf{z}_0 and \mathbf{z}'_0 we have

$$\lim_{n \rightarrow \infty} \left\| \frac{\mathbf{T}_n \mathbf{z}_0}{\|\mathbf{T}_n \mathbf{z}_0\|} - \frac{\mathbf{T}_n \mathbf{z}'_0}{\|\mathbf{T}_n \mathbf{z}'_0\|} \right\| = 0, \quad (3.23)$$

and therefore the structure of the population vector asymptotically becomes independent of the nonzero initial conditions.

When this property, denoted “weak ergodicity”, holds, the population structure for sufficiently high times will be determined by the recent history of vital rates. The importance of weak ergodicity lies in the fact that, in the absence of some kind of ergodic result, the explanation of population structure at a given time would require an explanation of the initial population, i.e. we would need to know its prior age structures indefinitely into the past.¹⁷ The rest of this paper is devoted to establishing relationships between this property of weak ergodicity for the original and aggregated systems.

The weak ergodicity of certain age structured populations was first demonstrated in Ref. 28 and has been extended to general time discrete systems using the so-called “contractive property” of multiplication by positive matrices.^{16,19,37} More recently, some results have been proved concerning weak ergodicity for certain systems in continuous time.^{21,38} In Ref. 23 an experimental study of weak ergodicity in human populations is considered in which it is shown that, in several practical situations, the knowledge of (approximately) 75 years prior to a given instant completely determine, at practical effects, the population structure at that time. Weak ergodicity also plays an important role in the study of stochastic systems^{15,17} in which it has to do with the capacity of the probability distribution of the population structure to become independent of initial conditions.

In our approach, and in other works in the field of population dynamics^{17,18,23,28} weak ergodicity has to do with the capacity of the system to become independent of conditions at time 0. Most of the mathematical approaches to weak ergodicity^{16,19,37} are slightly different in the sense that in them weak ergodicity means the capacity of the system to become independent of the conditions of the system at any time and not only of initial conditions

In order to study the weak ergodicity of a system, it is customary to use a mathematical tool called “projective distance”.^{18,37} This is a pseudometric that measures the distance between positive vectors attending to their relative composition, i.e. it is independent of their size and only depends on the structure of the vectors under consideration. Related to the projective distance is the “ergodicity coefficient” of a

non-negative matrix, that loosely speaking measures the capacity of the matrices to act contractively in this metric.

For the interested reader, the Appendix contains some mathematical details and references about these matters. Most of the mathematical theory involved in the study of weak ergodicity can be found in the work of E. Seneta.³⁷

In order to study the ergodicity of a system using the projective distance and the ergodicity coefficient as a tool, it is usual to slightly modify the definition given by (3.23). In particular, the attention is restricted to systems in which the \mathbf{A}_n are allowable matrices. We adopt as definition of weak ergodicity the following one^{19,37}:

Definition 1. Let \mathbf{A}_n be a sequence of $N \times N$ allowable matrices. The products $\mathbf{T}_n = [t_n^{ij}]$ are weakly ergodic or, equivalently, system (2.13) is weakly ergodic, when there exists a sequence of $N \times N$ positive matrices of rank one $\mathbf{S}_n = [s_n^{ij}]$ such that

$$\lim_{n \rightarrow \infty} \frac{t_n^{ij}}{s_n^{ij}} = 1 \quad \text{for all } i, j = 1, 2, \dots, N. \tag{3.24}$$

It is straightforward to check that condition (3.24), which can be paraphrased saying that the columns of \mathbf{T}_n asymptotically become positive and proportional, implies (3.23). Notice that a necessary condition for the weak ergodicity of system (2.13) is that the products \mathbf{T}_n become positive for large enough n .

Necessary and sufficient conditions on the matrices \mathbf{A}_n for weak ergodicity to hold are not known. The following theorem, essentially E. Seneta’s Theorem 3.3 in Ref. 37, gives very general sufficient conditions for weak ergodicity which hold in many practical situations for populations and are easy to check in practice. Besides, those sufficient conditions guarantee that the system forgets its past in a “geometric fashion”, concept that is made clear in the Appendix.

We will adopt the notation $\min^+(\mathbf{A})$ and $\max(\mathbf{A})$ to denote, respectively, the smallest positive element and the largest element of \mathbf{A} .

Theorem 1. *Let \mathbf{A}_n be a sequence of matrices such that:*

- (a) *the \mathbf{A}_n are allowable.*
- (b) *the positive entries of the \mathbf{A}_n are bounded away from zero and infinity, i.e. there exist positive constants $c \leq d$ such that $\min^+(\mathbf{A}_n) \geq c$ and $\max(\mathbf{A}_n) \leq d$ for all n .*

Then, if there exists a positive integer t such that for all $m = 0, 1, 2, \dots$ we have

$$\mathbf{A}_{(m+1)t-1} \cdots \mathbf{A}_{mt+1} \mathbf{A}_{mt} > 0$$

(in the sequel condition (D)), it follows weak ergodicity for system (2.13).

Proof. This theorem is essentially Seneta’s Theorem 3.3 in Ref. 37. In our case the definition of weak ergodicity corresponds to that of the “backwards products” of Seneta making $p = 0$. Seneta’s condition (ii) follows trivially if our condition

(b) is met, and Seneta’s condition (i) for $p = 0$ is our condition (D). The same reasoning as Seneta’s shows that there exists $\delta < 1$ such that for all m we have $\tau(\mathbf{A}_{(m+1)t-1} \cdots \mathbf{A}_{mt+1} \mathbf{A}_{mt}) < \delta$ and therefore $0 \leq \lim_{n \rightarrow \infty} \tau(\mathbf{A}_n \mathbf{A}_{n-1} \cdots \mathbf{A}_0) \leq \lim_{n \rightarrow \infty} \delta^{[n/t]} = 0$ ($[*]$ denotes integer part) as we wanted to show. \square

Condition (a) can be interpreted by saying that in system (2.13) the following two conditions hold: For all n , if the population is nonzero at time n , it will be nonzero at time $n + 1$, and if at time n there are individuals in all stages (z_n is positive), the same thing happens at time $n + 1$.

Condition (D), which gives (a) and (b) guarantees the weak ergodicity of the system, can be interpreted in the following way: There exists a positive integer t such that any individual initially present in the population is allowed to be in any stage by time t . In the same way, any of these individuals present at time t are allowed to be in any stage by time $2t$, and so on.

Notice that, in particular, condition (D) is satisfied if matrices \mathbf{A}_n are bounded between two primitive matrices, i.e. there exist primitive matrices \mathbf{C} and \mathbf{D} such that

$$\mathbf{C} \leq \mathbf{A}_n \leq \mathbf{D} \quad \text{for all } n. \tag{3.25}$$

In the rest of this work we will use the term “ergodicity” to denote weak ergodicity.

4. Weak Ergodicity for the Original and Aggregated Systems

In this section we obtain results that relate the ergodicity property of the original system (2.3) to that of the aggregated system (2.10). We will prove that in very general situations, the sufficient conditions for ergodicity established by Theorem 1 hold simultaneously for the general and aggregated systems assuming that the separation between the two time scales is sufficiently high. More precisely, we will show that, given properties (a) and (b) of Theorem 1 hold for both systems, then condition (D) regarding the “positivity of the product of a consecutive number of matrices” is satisfied simultaneously for both systems.

We will impose the following two starting hypotheses on our system:

H1. The nonzero entries of matrices \mathbf{M}_n and \mathbf{P}_n are bounded away from zero and infinity, i.e. there exist positive constants $\varepsilon, K, \varepsilon'$ and K' such that for all n we have

$$\begin{aligned} \min^+(\mathbf{M}_n) &\geq \varepsilon, & \min^+(\mathbf{P}_n) &\geq \varepsilon' \\ \max(\mathbf{M}_n) &\leq K, & \max(\mathbf{P}_n) &\leq K'. \end{aligned}$$

H2. For each n , \mathbf{M}_n is row allowable and “blockwise column allowable”.

We say that \mathbf{M}_n is “blockwise column allowable” when for all $j = 1, \dots, q$ there exists $i = i(j)$ such that $\mathbf{M}_{ij}(n) \neq \mathbf{0}$. Notice that H2 can be interpreted by saying

that for all n the slow process verifies: (a) for all $i = 1, 2, \dots, q$ and $j = 1, 2, \dots, N_i$, there exists at least one allowed transition towards subgroup j of group i and (b) for all $j = 1, \dots, q$ there is at least one allowed transition from group j to any other group (possibly also group j).

The next proposition shows that under condition $H1$, the positive entries corresponding to the general and aggregated systems are bounded away from zero and infinity (condition (b) of Theorem 1). It is also shown that condition $H2$ is necessary and sufficient for the matrices of the original and aggregated systems to be allowable (condition (a) of Theorem 1) for a separation of time scales sufficiently high.

Proposition 3. (a) *Assume $H1$ holds and k is fixed. Then there exist positive constants a, b, c and d such that for all n we have*

$$\begin{aligned} \min^+(\mathbf{M}_n \mathbf{P}_n^k) &\geq a, & \min^+(\bar{\mathbf{M}}_n) &\geq c, \\ \max(\mathbf{M}_n \mathbf{P}_n^k) &\leq b, & \max(\bar{\mathbf{M}}_n) &\leq d. \end{aligned}$$

(b) *Let n be fixed. Matrices $\bar{\mathbf{M}}_n$ and $\mathbf{M}_n \mathbf{P}_n^k$ are allowable for k large enough if and only if \mathbf{M}_n is row allowable and blockwise column allowable.*

Proof. (1) First, we will prove that the set of right and left eigenvectors for the $\mathbf{P}_i(n)$ defined by conditions (2.4) has entries bounded away from zero and infinity. Let $\eta, \phi > 0$ and let \mathcal{A} be the set constituted by the primitive matrices of size $r \times r$, with spectral radius equal to one and such that for all $\mathbf{A} \in \mathcal{A}$ is $\min^+(\mathbf{A}) \geq \eta$ and $\max(\mathbf{A}) \leq \phi$ (*). In order to demonstrate that \mathcal{A} is a compact set, it is sufficient to show that it is closed, for it is obviously bounded. If (\mathbf{A}_n) is a Cauchy sequence of matrices belonging to \mathcal{A} , it converges in $\mathbb{R}_+^{r \times r}$ to a certain matrix \mathbf{A} . Because of the continuity of eigenvalues as functions of the entries of the corresponding matrix, it must be $\rho(\mathbf{A}) = 1$. Besides, \mathbf{A} must verify conditions (*). Next, conditions (*) and the convergence of \mathbf{A}_n imply that, from a certain n_0 on, $\mathbf{A}_n \sim \mathbf{A}$, so \mathbf{A} must be primitive. In conclusion, \mathcal{A} is a compact set.

We define the mapping $f : \mathcal{A} \rightarrow \mathbb{R}$ in the following way: $f(\mathbf{A}) = \max(\mathbf{v})$, where \mathbf{v} is the positive eigenvector of \mathbf{A} associated to one and normalized so that it is unitary in norm one. This is a continuous mapping, for normalized eigenvectors associated to simple eigenvalues are continuous functions of the entries of the matrix and the mapping $\max(\mathbf{v})$ is continuous. Since f is continuous in a compact set it reaches its maximum and minimum in that set, so there exists ρ such that if $\mathbf{A} \in \mathcal{A}$, then $\max(\mathbf{v}) \leq \rho$. A similar reasoning for the mapping $g(\mathbf{A}) = \min(\mathbf{v})$ leads to the conclusion that there exists a positive ρ' such that $\min(\mathbf{v}) \geq \rho'$ for $\mathbf{A} \in \mathcal{A}$. Proceeding in a similar way we can guarantee that the largest and smallest entries for the left eigenvalues of matrices from \mathcal{A} associated to one and verifying any normalization condition are bounded away from zero and infinity. Since all matrices $\mathbf{P}_i(n)$ belong to \mathcal{A} , for $i = 1, \dots, q$ and $n = 0, 1, \dots$, then $H1$ guarantees that vectors $\mathbf{v}_i(n)$ and $\mathbf{u}_i(n)$ verify the desired boundedness conditions. As a consequence, the nonzero elements of \mathbf{V}_n and \mathbf{U}_n are bounded away from zero and infinity.

It is straightforward to check the validity of the following result: If $\mathbf{A} \in \mathbb{R}^{t \times r}$ and $\mathbf{B} \in \mathbb{R}^{r \times l}$ are non-negative and $\mathbf{AB} \neq \mathbf{0}$, then $\min^+(\mathbf{AB}) \geq \min^+(\mathbf{A}) \min^+(\mathbf{B})$ and $\max(\mathbf{AB}) \leq r \max(\mathbf{A}) \max(\mathbf{B})$. So, if matrices \mathbf{A} and \mathbf{B} belong to a set \mathcal{T} for which there exist positive constants a and b such that $\min^+(\mathbf{A}) \geq a$ and $\max(\mathbf{A}) \leq b$ for $\mathbf{A} \in \mathcal{T}$, then $\min^+(\mathbf{AB}) \geq a^2$ and $\max(\mathbf{A}) \leq rb^2$ for all $\mathbf{A}, \mathbf{B} \in \mathcal{T}$. The results follow then as a consequence of *H1* just taking into account that k is fixed, that $\bar{\mathbf{P}}_n = \mathbf{V}_n \mathbf{U}_n$ and that the nonzero elements of \mathbf{V}_n and \mathbf{U}_n are bounded away from zero and infinity.

(2) Let n be fixed. (a) First, we will show that \mathbf{M}_n is row allowable if and only if $\mathbf{M}_n \bar{\mathbf{P}}_n$ also is. If \mathbf{M}_n is row allowable, then for all $i = 1, \dots, q$ and $l = 1, \dots, N_i$ there exists $j = j(i, l) \in \{1, \dots, q\}$ and $m = m(i, l) \in \{1, \dots, N_j\}$ such that element (l, m) of $\mathbf{M}_{ij}(n)$ is nonzero. Bearing in mind (2.8) and the fact of matrices $\bar{\mathbf{P}}_j(n)$ being positive, row l of $\mathbf{M}_{ij}(n) \bar{\mathbf{P}}_j(n)$ is positive and therefore $\mathbf{M}_n \bar{\mathbf{P}}_n$ is row allowable. Reciprocally, if $\mathbf{M}_n \bar{\mathbf{P}}_n$ is row allowable then for $i = 1, \dots, q$ and $l = 1, \dots, N_i$ there exists $j = j(i, l) \in \{1, \dots, q\}$ and $m = m(i, l) \in \{1, \dots, N_j\}$ such that the element (l, m) of $\mathbf{M}_{ij}(n) \bar{\mathbf{P}}_j(n)$ is nonzero which implies that row l of $\mathbf{M}_{ij}(n)$ must be nonzero. So \mathbf{M}_n is row allowable. (b) Lemma 3 guarantees that $\bar{\mathbf{M}}_n$ is row allowable if \mathbf{M}_n is.

(c) We will now show that $\mathbf{M}_n \bar{\mathbf{P}}_n$ is column allowable if and only if \mathbf{M}_n is blockwise column allowable. If for all $j = 1, \dots, q$ there exists $i = i(j)$ such that $\mathbf{M}_{ij}(n) \neq \mathbf{0}$ then, since $\bar{\mathbf{P}}_j(n)$ is positive, $\mathbf{M}_{ij}(n) \bar{\mathbf{P}}_j(n)$ is column allowable. Therefore $\mathbf{M}_n \bar{\mathbf{P}}_n$ is column allowable. Reciprocally, if all $\mathbf{M}_{ij}(n)$ were zero for some j , then it would be $\mathbf{M}_{ij}(n) \bar{\mathbf{P}}_j(n) = \mathbf{0}$ for all j and then $\mathbf{M}_n \bar{\mathbf{P}}_n$ would not be column allowable. (d) Lemma 3 guarantees that $\bar{\mathbf{M}}_n$ is column allowable if and only if \mathbf{M}_n is blockwise column allowable. The result now follows just taking into account Proposition 4, since $\bar{\mathbf{P}}_n \sim \mathbf{P}_n^k$ for k large enough. \square

Therefore, Theorem 1 guarantees that, given *H1* and *H2*, property (D) for the original (aggregated) system is sufficient for the ergodicity of the original (aggregated) system. The next proposition relates the ergodicity of systems (2.3) to that of (2.10) and is based on the fact that under conditions *H1* and *H2*, property (D) verifies simultaneously for both systems.

Proposition 4. *Assume hypotheses H1 and H2 hold. Then:*

- (1) *The aggregated system verifies condition (D) if and only if the original system verifies property (D) for k large enough.*
- (2) *As a consequence, property (D) for the aggregated system implies that both the aggregated and general systems (for k large enough) are weakly ergodic (in a geometric fashion, see the Appendix).*

Proof. Assume *H2* holds. First, we will prove two preliminary results:

- (i) if $\mathbf{\Pi}_{p+t,p}(k) > 0$ for some t, p and k large enough, then $\bar{\mathbf{\Pi}}_{p+t,p} > 0$. Indeed, since $\bar{\mathbf{\Pi}}_{p+t,p} = \mathbf{U}_{p+t} \mathbf{\Pi}'_{p+t,p} \mathbf{V}_p$, the result follows taking into account that the \mathbf{U}_n and \mathbf{V}_n are allowable and using Lemma 4.
- (ii) if $\bar{\mathbf{\Pi}}_{p+t,p} > 0$ for some t and p , then $\mathbf{\Pi}_{p+t+1,p}(k) > 0$ for k large enough. Indeed, we have (Proposition 2) $\mathbf{\Pi}'_{p+t+1,p} = \mathbf{M}_{p+t} \mathbf{V}_{p+t} \bar{\mathbf{\Pi}}_{p+t,p} \mathbf{U}_p$. Since the \mathbf{M}_n and the \mathbf{V}_n are row allowable, so is their product. Therefore $\mathbf{M}_{p+t} \mathbf{V}_{p+t} \bar{\mathbf{\Pi}}_{p+t,p} > 0$ and since \mathbf{U}_p is column allowable, $\mathbf{\Pi}'_{p+t+1,p} > 0$. The desired result now follows from Lemma 4.

(1) Now, let us suppose that system (2.3) verifies condition (D), i.e. there exists t such that for k large enough, $\mathbf{\Pi}_{(m+1)t,mt}(k) > 0$ for all m . Then using (i), $\bar{\mathbf{\Pi}}_{(m+1)t,mt} > 0$ for all m and therefore system (2.10) meets condition (D).

Conversely, let us assume that system (2.10) meets condition (D), i.e. there exists t such that $\bar{\mathbf{\Pi}}_{(l+1)t,lt} > 0$ for all $l = 0, 1, \dots$

- (iii) we will show that system (2.3) verifies condition (D) for products with $2t$ factors. Indeed, using the notation $\mathbf{A}_n(k) = \mathbf{M}_n \mathbf{P}_n^k$ we have

$$\mathbf{\Pi}_{(m+1)2t,2mt}(k) = \mathbf{A}_{2mt+2t-1}(k) \cdots \mathbf{A}_{2mt+t+2}(k) \mathbf{A}_{2mt+t+1}(k) \mathbf{\Pi}_{(2m+1)t+1,2mt}(k).$$

Now, using (iii) with $l = 2m$ we have that, for k large enough, $\mathbf{\Pi}_{(2m+1)t+1,2mt}(k) > 0$ and besides the $\mathbf{A}_n(k)$ are allowable, so $\mathbf{\Pi}_{(2m+1)t+1,2mt}(k) > 0$ for all m as we wanted to show.

(2) immediate from (1), Proposition 3 and Theorem 1. □

4.1. Common incidence matrix

In many practical situations, the matrices that define a discrete non-autonomous system of the kind (2.13) share the same incidence matrix, i.e. $\mathbf{A}_n \sim \mathbf{A}_{n'}$ for all n and n' . In this way the vital rates that characterize the population may vary with time but in such a way that if a parameter is zero (nonzero) at some time, it will be zero (nonzero) for all times.

In the sequel we study the relationships between the weak ergodicity for macro- and microsystem under the hypothesis that all matrices that characterize the latter have the same incidence matrix. Stronger results than the one corresponding to the general case are obtained.

The next hypothesis guarantees that both the general system (for k large enough) and the aggregated system verify the equality of incidence matrices mentioned above.

H3. All matrices \mathbf{M}_n share a same incidence matrix.

Notice that Lemma 4 guarantees that *H3* implies that $\bar{\mathbf{M}}_n \sim \bar{\mathbf{M}}_{n'}$ and $\mathbf{M}_n \mathbf{P}_n^k \sim \mathbf{M}_{n'} \mathbf{P}_{n'}^k$, for all n and n' independently of the incidence matrices of the \mathbf{P}_n .

The following proposition gives necessary and sufficient conditions for the ergodicity property of both systems to hold.

Proposition 5. *Assume hypotheses H1, H2 and H3 hold and let $i(\bar{\mathbf{M}})$ be the incidence matrix of the $\bar{\mathbf{M}}_n$. Then:
the microsystem is weakly ergodic for k large enough if and only if the aggregated system is weakly ergodic if and only if $i(\bar{\mathbf{M}})$ is primitive.*

Proof. Particular case of Proposition 7 with $T = 1$ and $\mathbf{C} = i(\bar{\mathbf{M}})$. □

4.2. Cyclical sequence of incidence matrices

Now we will address the problem of studying the weak ergodicity of a generic system of the kind (2.13) under the hypothesis that the incidence matrices of the \mathbf{A}_n vary in a cyclic fashion, i.e. in such a way that there exists a positive integer T such that $i(\mathbf{A}_n) = i(\mathbf{A}_{n+T})$ for all n . Notice that this situation is a generalization of the periodic case, i.e. $\mathbf{A}_n = \mathbf{A}_{n+T}$ for all n . The setting we propose corresponds to the practical situation in which a population lives in a periodic environment with T seasons; the vital rates may vary in a nonperiodic way but subjected to the following restriction: If a vital rate is zero (nonzero) at a given time n corresponding, say, to season j , then it will always be zero (nonzero) as long as the environmental conditions correspond to season j , i.e. at times $n + T, n + 2T, \dots$. This situation arises in those models in which one accepts that the environmental conditions for each season are not constant (for example, two springs are never the same with respect to temperature, rain, etc.) but the vital rates which are zero or nonzero are always the same.

As an illustrative example, we can think of a population living in an environment with seasonal variation (say, summer and winter) with dynamics characterized by a Leslie model with variable coefficients in the following way: The fertility rates vary with time, but if an age class has zero (nonzero) fertility rate in summer (or winter), then it will also be zero (nonzero) the following summer (or winter) and so on. Something analogous holds for the survival coefficients.

Under these conditions, and given hypotheses similar to those considered in Sec. 4, we will obtain necessary and sufficient conditions for a system of the kind (2.13) to be weakly ergodic.

In the first place, let us define the different incidence matrices for system (2.13) by $\mathbf{B}_n = i(\mathbf{A}_n)$; $n = 0, 1, \dots, T - 1$. The following proposition, which is an adaptation of Theorem 1 for this situation, characterizes the ergodicity of system (2.13).

Proposition 6. *If the following conditions hold:*

- (a) *there exists an integer T such that $i(\mathbf{A}_n) = i(\mathbf{A}_{n+T})$ for all n ,*
- (b) *matrices \mathbf{A}_n are allowable,*
- (c) *there exist positive constants $c \leq d$ such that $\min^+(\mathbf{A}_n) \geq c$ and $\max(\mathbf{A}_n) \leq d$ for all n .*

Then, system (2.13) is weakly ergodic if and only if matrix $\mathbf{C} = \mathbf{B}_{T-1} \cdots \mathbf{B}_1 \mathbf{B}_0$ is primitive.

Proof. Let us assume that system (2.13) is weakly ergodic. Then there exists n_0 such that for all $n \geq n_0$, $\mathbf{T}_n > 0$. Then, choosing $n \geq n_0$ with $n = mT$ and using (a) we have $\mathbf{T}_n \sim \mathbf{C}^m > 0$ and so \mathbf{C} must be primitive. Conversely, if \mathbf{C} is primitive then there exists s such that $\mathbf{C}^s > 0$. For all m we have, using (a), $\mathbf{A}_{(m+1)Ts-1} \cdots \mathbf{A}_{mTs+1} \mathbf{A}_{mTs} \sim \mathbf{C}^s$ and therefore condition (D) of Theorem 1 is met for $t = sT$. Since the rest of the hypotheses of the theorem are trivially satisfied, weak ergodicity for system (2.13) follows. \square

Now we address the study of the weak ergodicity of the original and aggregated systems in the assumption that the incidence matrices in each of them varies in a periodic fashion. In the first place, we establish a sufficient condition for the above-mentioned periodicity of incidence matrices to hold.

H4. The incidence matrices of the \mathbf{M}_n vary in a periodic way, i.e. there exists a positive integer T such that $i(\mathbf{M}_{n+T}) = i(\mathbf{M}_n)$ for all n .

Notice that Lemma 4 implies that for all n and n' and for k large enough, we have $\bar{\mathbf{M}}_{n+T} \sim \bar{\mathbf{M}}_n$, $\mathbf{M}_{n+T} \bar{\mathbf{P}}_{n+T} \sim \mathbf{M}_n \bar{\mathbf{P}}_n$ and $\mathbf{M}_{n+T} \mathbf{P}_{n+T}^k \sim \mathbf{M}_n \mathbf{P}_n^k$ independently of the incidence matrices of the \mathbf{P}_n .

Let us define matrices $\mathbf{B}_j = i(\bar{\mathbf{M}}_j)$. Then:

Proposition 7. *Given conditions H1, H2 and H4 hold, then: the original system is weakly ergodic for k large enough if and only if the aggregated system is weakly ergodic if and only if matrix $\mathbf{C} = \mathbf{B}_{T-1} \cdots \mathbf{B}_1 \mathbf{B}_0$ is primitive.*

Proof. Let $\mathbf{C}(k) = i(\mathbf{M}_{T-1} \mathbf{P}_{T-1}^k) \cdots i(\mathbf{M}_0 \mathbf{P}_0^k)$. In the first place we will show that \mathbf{C} is primitive if and only $\mathbf{C}(k)$ is primitive (for k large enough). (a) From H4 we have $\bar{\mathbf{\Pi}}_{mT,0} \sim \mathbf{C}^m$ and therefore \mathbf{C} is primitive if and only if $\bar{\mathbf{\Pi}}_{mT,0} > 0$ for large enough m (*). From (ii) in the proof of Proposition 4 we find that $\bar{\mathbf{\Pi}}_{mT,0} > 0$ implies $\mathbf{\Pi}_{mT+1,0}(k) > 0$ for k large enough, and since matrices $\mathbf{M}_n \mathbf{P}_n^k$ are allowable, it follows that $\mathbf{\Pi}_{(m+1)T,0}(k) > 0$ for k large enough. From H4 we have $\mathbf{\Pi}_{(m+1)T,0}(k) \sim \mathbf{C}(k)^{m+1}$ (**) and, since the left-hand side is positive, it must be $\mathbf{C}(k)$ primitive for k large enough. (b) From (**) it follows that, if $\mathbf{C}(k)$ is primitive for k large enough, then $\mathbf{\Pi}_{mT,0}(k) > 0$ for k and m large enough. Taking into account (i) in the proof of Proposition 4 we have $\bar{\mathbf{\Pi}}_{mT,0} > 0$ for m large enough, and from (*) \mathbf{C} must be primitive. From H1, H2 and H4, the original and aggregated systems verify conditions (a), (b) and (c) of Proposition 6, and therefore the desired result follows. \square

4.3. Weak ergodicity in a multiregional model with fast migration

In this section we illustrate the preceding results applying them to the study of the weak ergodicity of the multiregional model with fast migration (2.19) and its aggregated system (2.20) proposed in Sec. 2.4.1.

Application 1. Let us assume the multiregional model of Sec. 2.4.1 with the following additional hypotheses:

- (a) at every instant, the survival coefficients for all patches and age classes are nonzero, i.e. $S_l^i(n) \neq 0$ for all n, i and l .
- (b) At all times, the fertility coefficient corresponding to the last age class is nonzero in all the patches, i.e. $F_l^q(n) \neq 0$ for all l and n . Besides, there is at least another age class i such that i and q are mutually prime and such that for all times that class is fertile in at least one patch, i.e. there exists i with $\text{g.c.d.}(i, q) = 1$ such that $\mathbf{F}_i(n) \neq \mathbf{0}$ for all n .
- (c) The nonzero entries of matrices \mathbf{M}_n and \mathbf{P}_n corresponding, respectively, to demography and migration, are bounded away from zero and infinity. In other words, as far as demography is concerned: (1) both the nonzero fertility rates and the nonzero survival rates cannot descend below a certain positive threshold and (2) the fertility rates are bounded above. Regarding migration, the nonzero migration coefficients cannot be lower than a certain positive value.

It is clear from the previous results that $H1$ and $H2$ are met. Besides, as we will show, condition (3.25) (and consequently condition (D)) is also met for the aggregated multiregional model. Therefore, Proposition 4 guarantees that both the original and the aggregated models are weakly ergodic for a sufficiently high separation of time scales between the migratory and the demographic processes. Indeed, let us consider c and d from Proposition 3. Then we have

$$c\mathbf{L} \leq \bar{\mathbf{M}}_n \leq d\mathbf{1}\mathbf{1}^T,$$

where $\mathbf{L} \in \mathbb{R}^{q \times q}$ is the incidence matrix of a primitive Leslie matrix and $\mathbf{1} = (1, 1, \dots, 1)^T$ and so condition (3.25) is met.

Application 2: Cyclical sequence of incidence matrices for demography

In this occasion, we consider the multiregional model and assume that the incidence matrices for demography have a periodic variation with period T . To simplify the exposition, let us consider the multiregional model of Sec. 2.4.1 in the case that the population has three age classes (i.e. $q = 3$) and it is distributed among r regions. Moreover, let us assume $T = 2$, which may correspond to a typical seasonal model with two seasons (say summer and winter) and incidence matrix for demography constant for instants corresponding to the same season. In such a case, matrices \mathbf{M}_n and \mathbf{P}_n have dimensions $3r \times 3r$ and matrices $\bar{\mathbf{M}}_n$ dimensions 3×3 .

As an example, let us assume that demography verifies:

- (a) At any time, the survival coefficients for all patches and age classes are nonzero, i.e. $S_l^i(n) \neq 0$ for all n, i and l .
- (b) At any time, the fertility coefficients for the third age class in all regions are nonzero, i.e. $F_l^3(n) \neq 0$ for all n and l .
- (c) For all $n = 0, 2, 4, \dots$ there is at least one nonzero fertility coefficient for the second age class. Besides, all the fertility rates for the first age class are zero.

- For all $n = 1, 3, 5, \dots$ there is at least one nonzero fertility coefficient for the first age class, meanwhile all the fertility rates for the second age class are zero.
- (d) The nonzero entries of the matrices that characterize demography and migration are bounded away from zero and infinity (condition $H1$).

Then we have that the incidence matrices for the aggregated system verify:

$$i(\bar{\mathbf{M}}_n) = \begin{cases} \mathbf{B}_0 & \text{if } n = 0, 2, 4, \dots \\ \mathbf{B}_1 & \text{if } n = 1, 3, 5, \dots \end{cases}$$

where

$$\mathbf{B}_0 = \begin{pmatrix} 0 & + & + \\ + & 0 & 0 \\ 0 & + & 0 \end{pmatrix}, \quad \mathbf{B}_1 = \begin{pmatrix} + & 0 & + \\ + & 0 & 0 \\ 0 & + & 0 \end{pmatrix},$$

and the symbol $+$ denotes nonzero elements.

The product $\mathbf{B}_1\mathbf{B}_0 = \begin{pmatrix} 0 & + & + \\ 0 & + & + \\ + & 0 & 0 \end{pmatrix}$ is primitive, and therefore Proposition 7 guarantees that the aggregated system is ergodic and so is the general system for k large enough.

5. Conclusion

The method developed here allows one to aggregate a time varying complex system with two time scales to obtain a reduced time varying aggregated system. The variables which govern the aggregated system are certain linear combinations of the state variables of the original system, the coefficients being dependent on the characteristics of the fast process. The parameters of the aggregated system can be easily expressed as functions of the slow dynamics and of the equilibrium proportions of individuals corresponding to the fast process. In this way, it is possible to study how changes in the fast dynamics affect the dynamics of the aggregated system.

The variables corresponding to the original and reduced systems can be related easily, therefore allowing one to study the dynamics of the former through that of the latter. Besides, in a very general framework, the weak ergodicity of the original system can be related to that of the reduced one.

In future contributions the authors plan to generalize the original system presented here to include the more realistic possibility of dealing with a fast dynamics which can vary within the characteristic time corresponding to the slow process.

In Ref. 36, the authors have partially addressed the study of aggregation techniques in systems with environmental stochasticity, relating the variables and the moments of the population vector of the original system to those of the aggregated system. Another line of research will be directed towards investigating possible relationships concerning weak and strong stochastic ergodicity for these systems.

Appendix A

If \mathbf{x} and \mathbf{y} are positive vectors of the same dimension, their projective distance is defined by

$$d(\mathbf{x}, \mathbf{y}) = \ln \left[\frac{\max_i \left(\frac{x_i}{y_i} \right)}{\min_i \left(\frac{x_i}{y_i} \right)} \right] = \max_{i,j} \ln \left(\frac{x_i y_j}{x_j y_i} \right).$$

This mapping has the properties of a metric except the following: $d(\mathbf{x}, \mathbf{y}) = 0 \Leftrightarrow \mathbf{x} = \lambda \mathbf{y}$ for any $\lambda > 0$. Besides, $d(\mathbf{x}, \mathbf{y}) = d(\lambda \mathbf{x}, \mu \mathbf{y})$ for λ and $\mu > 0$, which makes it appropriate for measuring distances between the structure of population vectors.

The use of the projective distance in the studies of weak ergodicity is based on the property by which multiplication by non-negative matrices acts as a contraction in this metric (see Ref. 37 for details in all this section). If $\mathbf{A} \geq 0$ is row allowable and $\mathbf{x}, \mathbf{y} > 0$, then $d(\mathbf{Ax}, \mathbf{Ay}) \leq d(\mathbf{x}, \mathbf{y})$ (we require that \mathbf{A} is row allowable in order to guarantee that \mathbf{Ax} is positive if \mathbf{x} is, so that $d(\mathbf{Ax}, \mathbf{Ay})$ is defined). Besides, if \mathbf{A} is strictly positive, the inequality is strict. In order to quantify the contraction produced when multiplying by a certain non-negative matrix it is useful to define the “ergodicity coefficient” or “contraction coefficient” of a row allowable matrix \mathbf{A} by

$$\tau(\mathbf{A}) = \sup_{\mathbf{x}, \mathbf{y} > 0, \mathbf{x} \neq \lambda \mathbf{y}} \frac{d(\mathbf{Ax}, \mathbf{Ay})}{d(\mathbf{x}, \mathbf{y})} \tag{A.1}$$

from where $\tau(\mathbf{A}) \leq 1$ follows immediately. In order to simplify the study of the contraction coefficient, most works in this field deal exclusively with allowable matrices^{19,37} (a notable exception is Ref. 16). If \mathbf{A} is allowable we have: (a) $\tau(\mathbf{A}) < 1$ if and only if \mathbf{A} is positive, and (b) $\tau(\mathbf{A}) = 0$ if and only if \mathbf{A} is positive and has rank one, i.e. it maps any two positive vectors into proportional ones. Besides, it is easy to evaluate this coefficient in terms of the entries of the matrix.

Definition (1) corresponds to Seneta’s definition of ergodicity in Ref. 37 if $p = 0$ is fixed. As it is shown in this reference, it can be stated in terms of the contraction coefficient in the following way: Let \mathbf{A}_n be a sequence of allowable matrices. The products \mathbf{T}_n are weakly ergodic if and only if $\lim_{n \rightarrow \infty} \tau(\mathbf{T}_n) = 0$.

If the hypotheses to Theorem 1 are met, the weak ergodicity of the system is said to be geometric, i.e. the decay to zero of $\tau(\mathbf{T}_n)$ is geometric. More precisely, there exists σ (depending on b, c and t) belonging to $(0, 1)$ such that for each n

$$\tau(\mathbf{T}_n) \leq \sigma^{\lceil n/t \rceil}.$$

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References

1. P. Auger, **Dynamics and Thermodynamics in Hierarchically Organized Systems, Applications in Physics, Biology and Economics** (Pergamon, 1989).

2. P. Auger and E. Benoit, *A prey-predator model in a multipatch environment with different time scales*, *J. Biol. Sys.* **1** (1993) 187–197.
3. P. Auger and J. C. Poggiale, *Emergence of population growth models: Fast migration and slow growth*, *J. Theor. Biol.* **182** (1996) 99–108.
4. P. Auger and J. C. Poggiale, *Aggregation and emergence in hierarchically organized systems: Population dynamics*, *Acta Biotheor.* **44** (1996) 301–316.
5. P. Auger and J. C. Poggiale, *Aggregation and emergence in systems of ordinary differential equations*, *Math. Comput. Modelling* **27** (1998) 1–21.
6. R. Bravo de la Parra, P. Auger and E. Sánchez, *Aggregation methods in discrete models*, *J. Biol. Sys.* **3** (1995) 603–612.
7. R. Bravo de la Parra, E. Sánchez and P. Auger, *Time scales in density dependent discrete models*, *J. Biol. Sys.* **5** (1997) 111–129.
8. R. Bravo de la Parra and E. Sánchez, *Aggregation methods in population dynamics discrete models*, *Math. Comput. Modelling* **4** (1998) 23–39.
9. R. Bravo de la Parra, E. Sánchez, O. Arino and P. Auger, *A discrete model with density dependent fast migration*, *Math. Biosci.* **157** (1999) 91–109.
10. H. Caswell, **Matrix Population Models** (Sinauer Associates Inc., 1989).
11. H. Caswell, *Matrix methods for population analysis*, in **Structured-Population Models in Marine, Terrestrial and Freshwater Systems**, eds. S. Tuljapurkar and H. Caswell (Chapman and Hall, 1997), pp. 19–58.
12. S. Charles, R. Bravo de la Parra, J. P. Mallet, H. Persat and P. Auger, *Population dynamics modelling in an hierarchical arborescent river network: An attempt with *Salmo trutta**, *Acta Biot.* **46** (1998) 223–234.
13. S. Charles, R. Bravo de la Parra, J. P. Mallet, H. Persat and P. Auger, *Density dependent model describing *Salmo trutta* population dynamics in an hierarchical arborescent river network: effects of dams and channeling*, *C.R. Acad. Fci. Paris, sciences de la vie* **321** (1998) 979–990.
14. S. Charles, R. Bravo de la Parra, J. P. Mallet, H. Persat and P. Auger, *Annual spawning migrations in modelling brown trout population dynamics inside an arborescent river network*, *Ecological Modelling* **133** (2000) 15–31.
15. J. E. Cohen, *Ergodicity of age structure in populations with Markovian vital rates, II. General states*, *Adv. Appl. Probab.* **9** (1977) 18–37.
16. J. E. Cohen, *Contractive inhomogeneous products of non-negative matrices*, *Math. Proc. Cambridge Philosophical Soc.* **86** (1979) 351–364.
17. J. E. Cohen, *Ergodics theorems of demography*, *Bull. Am. Math. Soc. N.S.* **1** (1979) 275–295.
18. M. Golubitsky, E. B. Keeler and M. Rothschild, *Convergence of the age structure: applications of the projective metric*, *Theor. Pop. Biol.* **7** (1975) 84–93.
19. J. Hajnal, *On products of non-negative matrices*, *Math. Proc. Cambridge Philosophical Soc.* **79** (1976) 521–530.
20. R. A. Horn and C. A. Johnson, **Matrix Analysis** (Cambridge Univ. Press, 1985).
21. H. Inaba, *Weak ergodicity of population evolution processes*, *Math. Biosci.* **96** (1989) 195–219.
22. Y. Iwasa, V. Andreasen and S. A. Levin, *Aggregation in model ecosystems. (I) Perfect Aggregation*, *Ecol. Modelling* **37** (1987) 287–302.
23. Y. K. Kim and Z. M. Sykes, *An experimental study of weak ergodicity in human populations*, *Theor. Popul. Biol.* **10** (1976) 150–172.
24. L. P. Leftkovich, *The study of population growth in organisms grouped by stages*, *Biometrics* **21** (1965) 1–18.
25. K. L. Liaw, *Multistate dynamics: the convergence of an age-by-region population system*, *Environment and Planning* **A12** (1980) 589–613.

26. K. L. Liaw, *Spatial Population Dynamics*, in **Migration and Settlement: A Multiregional Comparative Study**, eds. A. Rogers and F. Willekens (D. Reidel, 1986), pp. 419–455.
27. D. O. Logofet, **Matrices and Graphs. Stability Problems in Mathematical Ecology** (CRC Press, 1993).
28. A. Lopez, **Problems in Stable Population Theory** (Princeton Univ. Press, 1961).
29. J. C. Poggiale and P. Auger, *Fast oscillating migration in a prey-predator model*, *Math. Models Methods Appl. Sci.* **6** (1995) 217–226.
30. T. J. Quinn, *The use of Leslie-type age-structure models for the Pacific halibut population*, in **Quantitative Population Dynamics**, eds. D. G. Chapman and F. Galluci (1981), pp. 217–242.
31. A. Rogers, *Shrinking large-scale population projection models by aggregation and decomposition*, *Environment and Planning* **A8** (1976) 515–541.
32. A. Rogers, **Multiregional Demography** (Chichester, 1995).
33. E. Sánchez, R. Bravo de la Parra and P. Auger, *Linear discrete models with different time scales*, *Acta Biotheor.* **43** (1995) 465–479.
34. L. Sanz and R. Bravo de la Parra, *Variables aggregation in time varying discrete systems*, *Acta Biotheor.* **46** (1998) 273–297.
35. L. Sanz and R. Bravo de la Parra, *Variables aggregation in a time discrete linear model*, *Math. Biosc.* **157** (1999) 111–146.
36. L. Sanz and R. Bravo de la Parra, *Time scales in stochastic multiregional models*, *Non Linear Analysis: Real World Applications* **1** (2000) 89–122.
37. E. Seneta, **Non-Negative Matrices and Markov Chains** (Springer-Verlag, 1981).
38. S. Tuljapurkar, *Population dynamics in variable environments. IV. Weak ergodicity in the Lotka equation*, *J. Math. Biol.* **14** (1982) 221–230.
39. S. Tuljapurkar, **Population Dynamics in Variable Environments** (Springer-Verlag, 1990).