

## TIME SCALES IN DENSITY DEPENDENT DISCRETE MODELS

RAFAEL BRAVO DE LA PARRA

*Departamento de Matemáticas, Universidad de Alcalá de Henares,  
28871 Alcalá de Henares, Madrid, Spain  
E-mail: mtbravo@alcala.es*

EVA SÁNCHEZ

*Departamento de Matemáticas, E.T.S.I. Industriales,  
Universidad Politécnica de Madrid, c/ José Gutiérrez Abascal, 2, 28006 Madrid, Spain  
E-mail: c0550005@ccupm.upm.es*

and

PIERRE AUGER

*UMR CNRS 5558, IASBSE,  
Université Claude Bernard-Lyon 1,  
43 Boul. 11 novembre 1918, 69622 Villeurbanne Cedex, France  
E-mail: pauger@biomserv-lyon1.fr*

Received 24 April 1996

### ABSTRACT

The aim of this work is to extend approximate aggregation methods for multi-time scale systems of nonlinear ordinary differential equations to time discrete models. Approximate aggregation consist on describing the dynamics of a general system involving many coupled variables by means of the dynamics of a reduced system with a few global variables. We present discrete time models with two different time scales, the fast one considered linear and the slow one generally nonlinear. We transform the system to make the global variables appear, and use a version of center manifold theory to build up the aggregated system. Simple forms of the aggregated system are enough for the local study of the asymptotic behaviour of the general system provided that it has certain stability under perturbations. The general method is applied to aggregate a multiregional density dependent Leslie model into a density dependent Leslie model in which the demographic rates are expressed in terms of the equilibrium proportions of individuals in the different patches.

*Keywords:* Approximate aggregation of variables, population dynamics, time scales, dynamical systems, center manifold.

### 1. Introduction

In ecological modelling we always have to deal with very complex systems. Any model is a compromise between generality and simplicity on the one hand and biological realism on the other. The more biological details are included in specifying a model, the more complicated and specialized it becomes. Models describing

ecological systems in detail involve a very large number of coupled variables, that avoid a fruitful analytical study. At the other extreme, very simple models, which are mathematically tractable, do not justify the assumptions to be made in order to obtain such simplicity.

Aggregation methods study the relationship between a large class of complex systems and their corresponding "aggregated" systems. The aim of aggregation methods is twofold. First of all, the simpler aggregated systems summarize the dynamics of the complex ones, allowing their analytical study, and secondly, the complex systems justify the form of the aggregated ones.

The property of complex systems that allows their aggregation is the existence of two or more different time scales. As a result we can think of a hierarchically structured system with a division into subsystems that are weakly coupled and simultaneously exhibit a strong internal dynamics, see [1]. The idea of aggregation is then to choose a global variable, sometimes called a macrovariable, for each subsystem and to build up a reduced system for these global variables.

The reduced system, or aggregated system, must reflect in a certain way both dynamics, the one corresponding to the fast time scale and the one corresponding to the slow time scale. The slow dynamics of the general system, the initial complex one, usually corresponds to the dynamics of the reduced system, meanwhile the fast dynamics of the general system is reflected in the coefficients of the reduced one in such a way that it is possible to study the influences between the different hierarchical levels, which seems meaningful from an ecological point of view.

The aggregation methods have already been developed in the case of continuous time systems, systems of ordinary differential equations with different time scales, see [1-4]. The authors have also studied the case of linear, density independent, time discrete systems, see [5,20]. In the latter works we aggregate a very general linear model and prove that the elements defining the asymptotic behaviour of the general and the aggregated systems are equal up to certain order. These results are applied to models of structured populations with subpopulations in each stage class associated to different spatial patches or individual activities, considering a fast time scale for patch or activity dynamics and a slow time scale for demographic processes.

The aggregation of discrete systems has a clear interest. Discrete time models are widely used in population dynamics and many ecological models involve necessarily discrete time. For example, the classical Leslie or Leftkovich models describe an age or stage, respectively, structured population evolving in discrete time, [15,16]. Discrete models are also very useful in addressing the population dynamics of organisms that have distinct breeding periods and life-cycle stages, notably insects and other arthropods, see [8,18]. A model that has received considerable attention from theoretical and experimental population biologists is that of the host-parasitoid system, in particular the Nicholson-Bailey model [19], see also [9].

Though there are some widely used linear models, for example the Leslie model, the nonlinear models are recognized to be more realistic, density dependence being a generally accepted characteristic of ecological systems. In this article, we develop aggregation methods in the case of nonlinear discrete models, we are considering systems with a linear fast dynamics but a general nonlinear slow dynamics.

The aim of Sec. 2 is to present as easily as possible the method we develop generally later on. We develop a simple example of a population structured in two age classes and subdivided geographically into two patches. We consider a fast migration process and a slow demographic process with density dependent survival rates.

In Sec. 3 we present a general model that distinguish two time scales, with a group of populations subdivided into subpopulations. The fast dynamics, apart from linear, is internal for each population and asymptotically leads each population to certain constant proportions among its subpopulations. The slow dynamics is as general as possible being represented by a smooth mapping. The global variables used in the aggregation are the total numbers of individuals in each population, which are constants of motion for the fast dynamics.

Section 4 is devoted to the general system transformation so as to make appear the global variables and the differences between original variables and the fast dynamics equilibrium values. The last ones tends to zero if close enough to the equilibrium while the global ones govern the dynamics of the system. A version of center manifold theorem for an invariant manifold of attractive equilibrium points is used to make precise statements. The same kind of general systems are studied translating perturbation methods from systems of ordinary differential equations [12], to yield results of boundary layer type, which is an alternative in the study of the general system, but not the appropriate tool to reach the aggregation.

Finally, Sec. 5 develops a general model of an age structured population divided in age classes and subdivided in geographical patches. In the fast time scale is the migration dynamics and in the slow time scale is the demographic dynamic. The aggregated system, whose variables are the total number of individuals in each age class, is a sort of density dependent Leslie model in a slow time scale. The general method of Sec. 4 is used to yield some asymptotic results for the general system from the density dependent Leslie matrix appeared in the aggregated system. The two patch two age-class model of Sec. 2 is worked out to yield the existence of an asymptotically stable equilibrium.

## 2. Aggregating a Two Patch Density Dependent Leslie Model

We consider a population with juveniles (age class 1) and adults (age class 2) in a two patch environment. Let  $x_n^{ij}$  be the density of the subpopulation aged  $i$  on patch  $j$  at time  $n$ . On each patch, the population grows according to a Leslie model. Individuals belonging to a given age class also move from patch to patch, see Fig. 1.

Let  $S^j$  be the survival rate of juveniles on patch  $j$  and  $F_i^j$  the fertility rate of age class  $i$  on patch  $j$ . On each patch  $j$ , the growth of the subpopulation is described by the next Leslie matrix

$$\mathbf{L}^j = \begin{pmatrix} F_1^j & F_2^j \\ S^j & 0 \end{pmatrix},$$

where the survival and fertility rates can be density dependent. For example, we consider constant fertility rates and survival rates depending on juveniles density as follows:

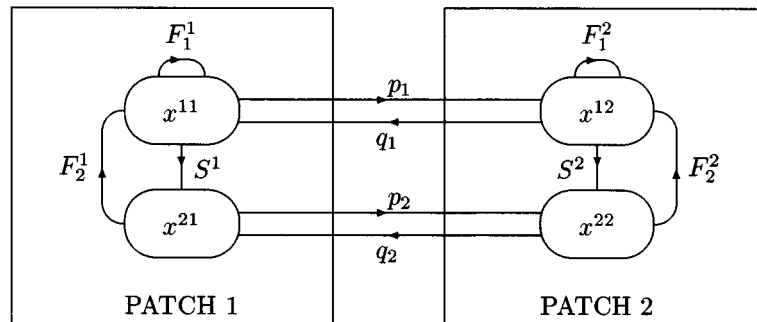
$$S^j(x^{1j}) = \frac{\mu_j}{1 + \alpha_j x^{1j}}.$$

This function is monotone decreasing, i.e., the survival rate of juveniles decreases as their density increases.

The migration of individuals of age  $i$  is described by the following migration matrix

$$\mathbf{P}_i = \begin{pmatrix} 1 - p_i & q_i \\ p_i & 1 - q_i \end{pmatrix},$$

where  $p_i$  (respectively  $q_i$ ) is the migration rate from patch 1 to patch 2 (respectively from patch 2 to patch 1) for individuals of age  $i$ .



**Fig. 1**

Furthermore, it is assumed that individuals frequently change patch. For example, individuals migrate several times per day while the age class duration is much larger.

The dynamics of the four variables  $x^{11}$ ,  $x^{12}$ ,  $x^{21}$  and  $x^{22}$  is thus described by a discrete system of four equations. The aim of this work is to take advantage of the two time scales in order to aggregate the system of four equations into a system of two equations governing the total numbers of individuals of age 1 and 2 (Fig. 2).

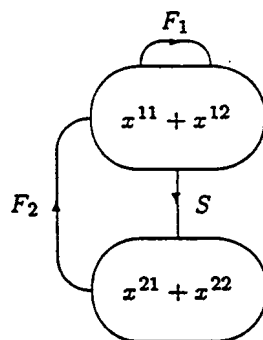


Fig. 2

In order to aggregate, we shall look for the fast equilibrium of migration and consequently eliminate the patches. For the sake of simplicity of the calculations it is convenient to describe the process as shown in Fig. 3, i.e., to group the patches per age class.

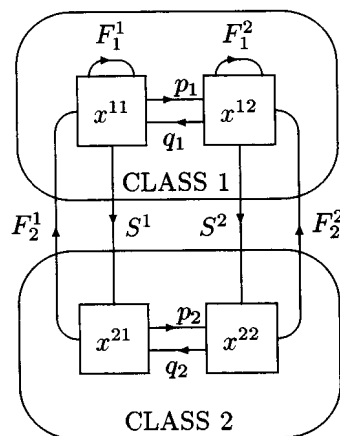


Fig. 3

We define a fertility matrix  $\mathbf{F}_i$  for each age class  $i$

$$\mathbf{F}_i = \begin{pmatrix} F_i^1 & 0 \\ 0 & F_i^2 \end{pmatrix},$$

we define a survival matrix  $\mathbf{S}$

$$\mathbf{S} = \begin{pmatrix} S^1 & 0 \\ 0 & S^2 \end{pmatrix},$$

and, finally, we obtain a generalized Leslie matrix  $\mathbf{L}$

$$\mathbf{L} = \begin{pmatrix} \mathbf{F}_1 & \mathbf{F}_2 \\ \mathbf{S} & \mathbf{0} \end{pmatrix}.$$

Neglecting fast migration the complete system is

$$\mathbf{X}_{n+1} = \mathbf{L} \mathbf{X}_n,$$

where  $\mathbf{X}_n = (x_n^{11}, x_n^{12}, x_n^{21}, x_n^{22})^\top$ . Now we consider a fast time scale in order to describe migrations. During a short time the variation due to demography is  $\varepsilon (\mathbf{L} \mathbf{X}_n - \mathbf{X}_n)$ , where  $\varepsilon$  is a small positive parameter. Consequently, after this short time interval, the system becomes

$$\mathbf{X}_{n+1} = \mathbf{X}_n + \varepsilon (\mathbf{L} \mathbf{X}_n - \mathbf{X}_n),$$

or else

$$\mathbf{X}_{n+1} = \mathbf{L}(\varepsilon) \mathbf{X}_n,$$

where  $\mathbf{L}(\varepsilon) = \mathbf{I} + \varepsilon (\mathbf{L} - \mathbf{I})$ .

To take into account the fast migration, we simply must multiply by the migration matrix  $\mathbf{P}$ ,

$$\mathbf{P} = \begin{pmatrix} \mathbf{P}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{P}_2 \end{pmatrix},$$

as follows

$$\mathbf{X}_{n+1} = \mathbf{L}(\varepsilon) \mathbf{P} \mathbf{X}_n,$$

which is the complete four dimensional model.

The aim of this work is to aggregate this initial model into a simpler system of two equations governing the total populations of each age class

$$\begin{pmatrix} s_{n+1}^1 \\ s_{n+1}^2 \end{pmatrix} = \begin{pmatrix} F_1 & F_2 \\ S & 0 \end{pmatrix} \begin{pmatrix} s_n^1 \\ s_n^2 \end{pmatrix},$$

where  $s^1 = x^{11} + x^{12}$  and  $s^2 = x^{21} + x^{22}$ .

In the next sections we present and justify the aggregation method in a general setting. In Sec. 5 we work out the above example.

### 3. General Model

We suppose in discrete time a general population classified into groups and each of these groups is divided into several subgroups. We consider a set of  $p$  populations (or groups) which are subdivided into subpopulations (or subgroups), with population  $i$  having  $N^i$  subpopulations,  $i = 1, \dots, p$ . Let  $x_n^{ij}$  be the density of subpopulation  $j$  of population  $i$  at time  $n$ ,  $j = 1, \dots, N^i$  and  $i = 1, \dots, p$ .  $N$  is the total number of variables, i.e. of subpopulations,  $N = N^1 + \dots + N^p$ . We use vector  $\mathbf{X}_n$  to

describe the total population at time  $n$ . This vector is a set of population vectors  $\mathbf{x}_n^i$  describing the internal structure of each subpopulations as follows:

$$\mathbf{X}_n = (\mathbf{x}_n^1, \dots, \mathbf{x}_n^p)^\top \quad \text{where} \quad \mathbf{x}_n^i = (x_n^{i1}, \dots, x_n^{iN^i})^\top$$

and  $^\top$  denotes transposition.

In the evolution of this population we distinguish between two different time scales, and so we will speak henceforth of two different dynamics, a slow one and a fast one. The fast dynamics is considered linear meanwhile the slow dynamics is generally nonlinear. We represent all this by means of the following system:

$$\mathbf{X}_{n+1} = \mathbf{P} \mathbf{X}_n + \varepsilon \mathbf{F}(\mathbf{X}_n) \quad (1)$$

where  $\mathbf{P}$  is an  $N \times N$  matrix and  $\mathbf{F}$  is a mapping from  $\mathbf{R}^N$  to  $\mathbf{R}^N$  that we will describe below, (2) and (6), and  $\varepsilon$  is a little positive parameter,  $\varepsilon \ll 1$ .

The fast dynamics, represented by the term  $\mathbf{P} X$ , must verify some hypothesis so that the general system could be approximately aggregated. For every group  $i, i = 1, \dots, p$ , let fast dynamics be internal, conservative of the total number of individuals and with an asymptotically stable frequency distribution among the subgroups. These hypothesis are fulfilled if we let  $\mathbf{P}$  be a block diagonal matrix

$$\mathbf{P} = \text{diag}\{\mathbf{P}_1, \dots, \mathbf{P}_p\} \quad (2)$$

where  $\mathbf{P}_i$  is a regular stochastic matrix of dimensions  $N^i \times N^i$  that is the projection matrix associated to the fast dynamics for every group  $i$ .

Every matrix  $\mathbf{P}_i$  has an asymptotically stable probability distribution  $\boldsymbol{\nu}^i = (\nu^{i1}, \dots, \nu^{iN^i})^\top$  that verifies the following properties:

$$\mathbf{P}_i \boldsymbol{\nu}^i = \boldsymbol{\nu}^i; \quad \mathbf{P}_i^\top \mathbf{1}^i = \mathbf{1}^i$$

where  $\mathbf{1}^i = (1, \dots, 1)$ , and  $\mathbf{1}^i \boldsymbol{\nu}^i = 1$ . We define

$$\bar{\mathbf{P}}_i = \lim_{k \rightarrow \infty} \mathbf{P}_i^k = (\boldsymbol{\nu}^i | \dots | \boldsymbol{\nu}^i)$$

where  $\mathbf{P}_i^k$  is the  $k$ th power of the matrix  $\mathbf{P}_i$ .

We denote  $\text{diag}\{\bar{\mathbf{P}}_1, \dots, \bar{\mathbf{P}}_p\}$  by  $\bar{\mathbf{P}}$ , and so we have

$$\lim_{k \rightarrow \infty} \mathbf{P}^k = \bar{\mathbf{P}}. \quad (3)$$

The global variables whose dynamics is going to be approximated by the aggregated system are the total number of individuals in every population, and we shall denote it by  $s^i$

$$s^i = \sum_{j=1}^{N^i} x^{ij}, \quad i = 1, \dots, p$$

and they form the vector  $\mathbf{s} = (s^1, \dots, s^p)^\top$ . Vector  $\mathbf{s}$  is obtained from vector  $\mathbf{X}$  through the so called *aggregation matrix*  $\mathbf{U} = \text{diag}\{\mathbf{1}^1, \dots, \mathbf{1}^p\}$ ,

$$\mathbf{s} = \mathbf{U} \mathbf{X}. \quad (4)$$

In the next part we will also use matrix

$$\bar{\mathbf{P}}_c = \text{diag}\{\nu^1, \dots, \nu^p\}$$

which allows us to express all the equilibrium points of the fast dynamics from the global variables as

$$\bar{\mathbf{P}}_c \mathbf{s}$$

that is,  $\mathbf{X} = \bar{\mathbf{P}}_c \mathbf{s}$ ,  $\mathbf{s} \in R^p$ , are all the solutions of equation  $\mathbf{X} = \mathbf{P} \mathbf{X}$ .

We summarize the properties of matrices  $\mathbf{P}$ ,  $\bar{\mathbf{P}}$ ,  $\bar{\mathbf{P}}_c$  and  $\mathbf{U}$  that we will use below. We will henceforth denote by  $\mathbf{I}$  the identity matrix of the required dimension.

$$\bar{\mathbf{P}} \mathbf{P} = \mathbf{P} \bar{\mathbf{P}} = \bar{\mathbf{P}} \bar{\mathbf{P}} = \bar{\mathbf{P}}$$

$$\mathbf{P} \bar{\mathbf{P}}_c = \bar{\mathbf{P}} \bar{\mathbf{P}}_c = \bar{\mathbf{P}}_c \quad (5)$$

$$\mathbf{U} \bar{\mathbf{P}} = \mathbf{U}; \quad \mathbf{U} \bar{\mathbf{P}}_c = \mathbf{I}; \quad \bar{\mathbf{P}}_c \mathbf{U} = \bar{\mathbf{P}}.$$

From (5) we find that  $\mathbf{s}$  is invariant for fast dynamics

$$\mathbf{s}_{n+1} = \mathbf{U} \mathbf{X}_{n+1} = \mathbf{U} \mathbf{P} \mathbf{X}_n = \mathbf{U} \mathbf{X}_n = \mathbf{s}_n$$

and also the asymptotic property of fast dynamics: if we let  $\mathbf{X}_0$  be any initial condition and we make  $\mathbf{s}_0 = \mathbf{U} \mathbf{X}_0$ , then we obtain from (3) and (5)

$$\lim_{k \rightarrow \infty} \mathbf{P}^k \mathbf{X}_0 = \bar{\mathbf{P}} \mathbf{X}_0 = \bar{\mathbf{P}}_c \mathbf{U} \mathbf{X}_0 = \mathbf{P}_c \mathbf{s}_0.$$

The slow dynamics is represented by the term  $\varepsilon \mathbf{F}(X)$ , where  $\mathbf{F} \in C^\infty(\mathbf{R}^N)$ , and following the same notation as for vector  $\mathbf{X}$ , we have

$$\mathbf{F}(X) = (\mathbf{f}^1(\mathbf{X}), \dots, \mathbf{f}^p(\mathbf{X}))^\top \quad \text{and} \quad \mathbf{f}^i(\mathbf{X}) = (f^{i1}(\mathbf{X}), \dots, f^{iN^i}(\mathbf{X}))^\top. \quad (6)$$

We suppose that  $\mathbf{f}^i(\mathbf{X}) = O(|\mathbf{x}^i|)$ ,  $i = 1, \dots, p$ . From this we see that when for nonnegative values of variables  $x^{ij}$  we have

$$\mathbf{f}^i(\mathbf{X}) = O(s^i), \quad i = 1, \dots, p. \quad (7)$$

which implies, in particular, that slow dynamics do not produce any variations if the total number of individuals of a population  $i$  is zero.

#### 4. Aggregated Model

In this section we propose an aggregated model for the system (1). For this we make a change of variables and use the center manifold theorem developed in the



appendix. The result will be a system for the  $p$  global variables  $s^i$  whose dynamics will reflect that of the general system.

#### 4.1. Change of Variables

For every  $i = 1, \dots, p$  we substitute the variable  $x^{iN^i}$  by global variable  $s^i$  and the other  $N^i - 1$  variables in group  $i$  by the new variables  $q^{ij} = x^{ij} - \nu^{ij} s^i$ ,  $j = 1, \dots, N^i - 1$ , that is, we change each variable, except the last in every group, by itself minus the corresponding value in the fast dynamics equilibrium, and the last ones are changed by the global variables.

We will use the following notation,

$$\mathbf{q}^i = (q^{i1}, \dots, q^{iN^i-1})^\top \quad \text{and} \quad \mathbf{q} = (\mathbf{q}^1, \dots, \mathbf{q}^p)$$

and so we have

$$x^{ij} = q^{ij} + \nu^{ij} s^i, \quad j = 1, \dots, N^i - 1$$

$$x^{iN^i} = s^i - \sum_{j=1}^{N^i-1} x^{ij} = s^i - \sum_{j=1}^{N^i-1} (q^{ij} + \nu^{ij} s^i) = \nu^{iN^i} s^i - \mathbf{1} q^i$$

where  $\mathbf{1}$  means a row vector with every component equal to 1 and the required dimension for the expression to make sense. Henceforth, we will use this convention unless stated otherwise.

The last equalities allow us to write

$$\mathbf{x}^i = s^i \boldsymbol{\nu}^i + (\mathbf{q}^i, -\mathbf{1} q^i)^\top$$

and denoting by  $\mathbf{D}_i$  the  $N^i \times (N^i - 1)$  matrix

$$\mathbf{D}_i = \begin{pmatrix} \mathbf{I} \\ -\mathbf{1} \end{pmatrix} \quad \text{and} \quad \mathbf{D} = \text{diag}\{\mathbf{D}_1, \dots, \mathbf{D}_p\}$$

we obtain vector  $\mathbf{X}$  from vectors  $\mathbf{s}$  and  $\mathbf{q}$  in the following equation

$$\mathbf{X} = \bar{\mathbf{P}}_c \mathbf{s} + \mathbf{D} \mathbf{q}. \quad (8)$$

On the other side we already know (4) that  $\mathbf{s} = \mathbf{U} \mathbf{X}$  and denoting by  $\mathbf{A}$  the projector

$$[(\mathbf{x}_a^1, x^{1N^1}), \dots, (\mathbf{x}_a^p, x^{pN^p})] \xrightarrow{\mathbf{A}} (\mathbf{x}_a^1, \dots, \mathbf{x}_a^p)$$

where  $\mathbf{x}_a^i = (x^{i1}, \dots, x^{iN^i-1})$ ,  $i = 1, \dots, p$ , we obtain

$$\mathbf{q} = \mathbf{A} (\mathbf{X} - \bar{\mathbf{P}}_c \mathbf{s}) = \mathbf{A} (\mathbf{I} - \bar{\mathbf{P}}) \mathbf{X}. \quad (9)$$

We now transform system (1) by using the change of variables described by (4,8,9) and the equalities (5)

$$\mathbf{s}_{n+1} = \mathbf{U} \mathbf{X}_{n+1} = \mathbf{U} \mathbf{P} \mathbf{X}_n + \varepsilon \mathbf{U} \mathbf{F}(\mathbf{X}_n) = \mathbf{s}_n + \varepsilon \mathbf{U} \mathbf{F}(\bar{\mathbf{P}}_c \mathbf{s}_n + \mathbf{D} \mathbf{q}_n)$$

and

$$\begin{aligned}\mathbf{q}_{n+1} &= \mathbf{A} (\mathbf{X}_{n+1} - \bar{\mathbf{P}}_c \mathbf{s}_{n+1}) = \mathbf{A} [\mathbf{P} \mathbf{X}_n + \varepsilon \mathbf{F}(\mathbf{X}_n) - \bar{\mathbf{P}}_c (\mathbf{s}_n + \varepsilon \mathbf{U} \mathbf{F}(\mathbf{X}_n))] \\ &= \mathbf{A} \mathbf{P} (\bar{\mathbf{P}}_c \mathbf{s}_n + \mathbf{D} \mathbf{q}_n) - \mathbf{A} \bar{\mathbf{P}}_c \mathbf{s}_n + \varepsilon \mathbf{A} (\mathbf{I} - \bar{\mathbf{P}}_c) \mathbf{U} \mathbf{F}(\bar{\mathbf{P}}_c \mathbf{s}_n + \mathbf{D} \mathbf{q}_n) \\ &= \mathbf{A} \mathbf{P} \mathbf{D} \mathbf{q}_n + \varepsilon \mathbf{A} (\mathbf{I} - \bar{\mathbf{P}}) \mathbf{F}(\bar{\mathbf{P}}_c \mathbf{s}_n + \mathbf{D} \mathbf{q}_n).\end{aligned}$$

If we consider  $\mathbf{A} \mathbf{P} \mathbf{D}$  as an  $(N-p) \times (N-p)$  matrix that we denote by  $\mathbf{Q}$ , we can prove that this matrix is block-diagonal,  $\mathbf{Q} = \text{diag}\{\mathbf{Q}_1, \dots, \mathbf{Q}_p\}$ , and that the eigenvalues of  $\mathbf{Q}_i$ ,  $i = 1, \dots, p$ , are those of  $\mathbf{P}_i$  except 1 (see Appendix I), which implies that the spectral radius of  $\mathbf{Q}$  is less than one,  $\rho(\mathbf{Q}) < 1$ . Moreover, denoting by  $\mathbf{f}$  the mapping from  $\mathbf{R}^N$  to  $\mathbf{R}^p$

$$\mathbf{f}(s, \mathbf{q}) = \mathbf{U} \mathbf{F}(\bar{\mathbf{P}}_c \mathbf{s} + \mathbf{D} \mathbf{q}) \quad (10)$$

and by  $\mathbf{g}$  the mapping from  $\mathbf{R}^N$  to  $\mathbf{R}^{N-p}$

$$\mathbf{g}(s, \mathbf{q}) = \mathbf{A}(\mathbf{I} - \bar{\mathbf{P}}) \mathbf{F}(\bar{\mathbf{P}}_c \mathbf{s} + \mathbf{D} \mathbf{q}) \quad (11)$$

the general system (1) is transformed into the following one

$$\begin{aligned}\mathbf{s}_{n+1} &= \mathbf{s}_n + \varepsilon \mathbf{f}(s_n, \mathbf{q}_n) \\ \mathbf{q}_{n+1} &= \mathbf{Q} \mathbf{q}_n + \varepsilon \mathbf{g}(s_n, \mathbf{q}_n)\end{aligned} \quad (12)$$

where  $\mathbf{f}$  and  $\mathbf{g}$  are  $C^\infty$  mappings that satisfy  $\mathbf{f}(\mathbf{0}, \mathbf{0}) = \mathbf{0}$  and  $\mathbf{g}(\mathbf{0}, \mathbf{0}) = \mathbf{0}$ .

#### 4.2. Aggregated System

The system (12) verifies the hypothesis of the center manifold theorem developed in Appendix II. So, for every  $M > 0$ , there exists  $\delta > 0$  and a mapping  $\mathbf{q} = \mathbf{h}(\mathbf{s}, \varepsilon)$  defined for  $|\mathbf{s}| < M$  and  $|\varepsilon| < \delta$ , whose graph,  $W_\varepsilon$ , for a fixed  $\varepsilon$  is locally attractive invariant manifold that allows us to study the dynamics of system (12) by means of its restriction to  $W_\varepsilon$ .

The system restricted to  $W_\varepsilon$  is what we call the *aggregated system* and from (23) has the form

$$\mathbf{s}_{n+1} = \mathbf{s}_n + \varepsilon \mathbf{f}(\mathbf{s}_n, \mathbf{h}(s_n, \varepsilon))$$

or using (24)

$$\mathbf{s}_{n+1} = \mathbf{s}_n + \varepsilon \mathbf{f}(s_n, \varepsilon(\mathbf{I} - \mathbf{Q})^{-1} \mathbf{g}(s_n, \mathbf{0}) + O(\varepsilon^2))$$

where (11) implies that  $\mathbf{g}(s, \mathbf{0}) = \mathbf{A}(\mathbf{I} - \bar{\mathbf{P}}) \mathbf{F}(\bar{\mathbf{P}}_c \mathbf{s})$ . It is also possible to express the aggregated system in the simpler form

$$\mathbf{s}_{n+1} = \mathbf{s}_n + \varepsilon \mathbf{f}(s_n, \mathbf{0}) + O(\varepsilon^2)$$

that yields, using (10),

$$\mathbf{s}_{n+1} = \mathbf{s}_n + \varepsilon \mathbf{U} \mathbf{F}(\bar{\mathbf{P}}_c \mathbf{s}_n) + O(\varepsilon^2) \quad (13)$$

## 5. Multiregional Density Dependent Leslie Model with Different Time Scales

In this section we are going to apply the above general aggregation method to the case of an age-structured population located in a multipatch environment. These kinds of models have been frequently treated in the literature, to have an introduction and a list of references see [7,17]. In contrast with these two references, we propose a model where the migration and the demography processes develop in different time scales, migration being a fast process in comparison with demography. We will also allow demography to be density dependent.

We suppose a population divided into  $p$  age-classes and living in an environment composed of  $m$  patches. We follow the notation of Sec. 2, being

$$x_n^{ij} = \text{number of individuals of age class } i \text{ in patch } j \text{ at time } n,$$

$$i=1, \dots, p, j=1, \dots, m,$$

$$\mathbf{X}_n = (\mathbf{x}_n^1, \dots, \mathbf{x}_n^p)^\top \quad \text{where} \quad \mathbf{x}_n^i = (x_n^{i1}, \dots, x_n^{im})^\top,$$

$$s_n^i = \sum_{j=1}^m x_n^{ij} \quad i = 1, \dots, p, \quad \text{and} \quad \mathbf{s}_n = (s_n^1, \dots, s_n^p)^\top.$$

We suppose that the changes between different patches of individuals of age  $i$  are represented by a regular stochastic matrix  $\mathbf{P}_i$  of order  $m \times m$ . So matrix  $\mathbf{P} = \text{diag}\{\mathbf{P}_1, \dots, \mathbf{P}_p\}$  represents the migration process of whole population.

The demography is defined by means of two kinds of transference coefficients as in the classical Leslie model:

Fertility rates

$$F_i^j = \text{fertility rate of age class } i \text{ in patch } j, \quad i = 1, \dots, p, \quad j = 1, \dots, m.$$

Survival rates

$$S_i^j = \text{survival rate of age class } i \text{ in patch } j, \quad i = 1, \dots, p-1, \quad j = 1, \dots, m.$$

These coefficients satisfy the usual constraints of Leslie model.

We define matrices  $\mathbf{F}_i = \text{diag}\{F_i^1, \dots, F_i^m\}$ ,  $i = 1, \dots, p$ ,  $\mathbf{S}_i = \text{diag}\{S_i^1, \dots, S_i^m\}$ ,  $i = 1, \dots, p-1$ . And finally we get a generalized Leslie matrix

$$\mathbf{L} = \begin{pmatrix} \mathbf{F}_1 & \mathbf{F}_2 & \dots & \mathbf{F}_{p-1} & \mathbf{F}_p \\ \mathbf{S}_1 & \mathbf{0} & \dots & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{S}_2 & \dots & \mathbf{0} & \mathbf{0} \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ \mathbf{0} & \mathbf{0} & \dots & \mathbf{S}_i & \mathbf{0} \end{pmatrix},$$

where  $\mathbf{L}$  is considered density dependent, so  $\mathbf{L} = \mathbf{L}(\mathbf{X})$  in a general way, or if we want to reflect that dependence is on total population in every patch we will have  $\mathbf{L} = \mathbf{L}(s)$ .

In order to distinguish between the two different time scales, those associated to  $\mathbf{P}$  and  $\mathbf{L}$ , respectively, we chose as unit time the projection interval corresponding to  $\mathbf{P}$  and approximate the effect of  $\mathbf{L}$  over that interval, which is much shorter than its own projection interval, using the following matrix

$$\mathbf{L}_\varepsilon = \varepsilon\mathbf{L} + (1 - \varepsilon)\mathbf{I}, \quad 0 < \varepsilon \ll 1.$$

Finally we propose the following multipatch density dependent Leslie model

$$\mathbf{X}_{n+1} = \mathbf{L}_\varepsilon(\mathbf{X}_n) \mathbf{P} \mathbf{X}_n$$

or in the form of general system (1)

$$\mathbf{X}_{n+1} = \mathbf{P} \mathbf{X}_n + \varepsilon(\mathbf{L}(\mathbf{X}_n) - \mathbf{I}) \mathbf{P} \mathbf{X}_n \quad (14)$$

so  $\mathbf{F}(\mathbf{X}) = (\mathbf{L}(\mathbf{X}) - \mathbf{I}) \mathbf{P} \mathbf{X}$  and Eq. (13) becomes in this case

$$s_{n+1} = s_n + \varepsilon \mathbf{U} (\mathbf{L}(\bar{\mathbf{P}}_c s_n) - \mathbf{I}) \mathbf{P} \bar{\mathbf{P}}_c s_n + O(\varepsilon^2)$$

and using (5) we obtain

$$s_{n+1} = s_n + \varepsilon (\mathbf{U} \mathbf{L}(\bar{\mathbf{P}}_c s_n) \bar{\mathbf{P}}_c - \mathbf{I}) s_n + O(\varepsilon^2) \quad (15)$$

where  $\mathbf{U} \mathbf{L}(\bar{\mathbf{P}}_c s) \bar{\mathbf{P}}_c$  is a general density dependent Leslie matrix of order  $p$ , denoted by  $\bar{\mathbf{L}}(\bar{\mathbf{P}}_c s)$ , whose entries are

$$\begin{aligned} f_i &= \mathbf{1} \mathbf{F}_i(\bar{\mathbf{P}}_c s) \nu^i, \quad i = 1, \dots, p && \text{(fertility rates)} \\ s_i &= \mathbf{1} \mathbf{S}_i(\bar{\mathbf{P}}_c s) \nu^i, \quad i = 1, \dots, p-1 && \text{(survival rates)} \end{aligned}$$

Here we can notice the way the aggregated system (15) takes account of the fast dynamics, meanwhile it defines a slow dynamics for the global variables. From matrix  $\bar{\mathbf{L}}(\bar{\mathbf{P}}_c s)$  we can get information about the dynamics of system (14). To give a simple example, it is easy to prove that if  $s^*$  is an equilibrium point of the system

$$s_{n+1} = \bar{\mathbf{L}}(\bar{\mathbf{P}}_c s_n) s_n$$

and the spectral radius of the linearization of the system at this point is less than 1, the same asymptotic property is verified by the system

$$s_{n+1} = s_n + \varepsilon (\mathbf{U} \mathbf{L}(\bar{\mathbf{P}}_c s_n) \bar{\mathbf{P}}_c - \mathbf{I}) s_n$$

that implies the existence of an equilibrium point of the form  $s^* + O(\varepsilon)$  with the same stability property for system (15) and analogously an equilibrium point  $\bar{\mathbf{P}}_c s^* + O(\varepsilon)$  for system (14).

To illustrate the usefulness of the process of aggregation we treat the example developed in Sec. 2. We suppose a population divided in 2 age-classes and living in an environment composed of 2 patches, with the migration changes performed in a much faster time scale than the demographic changes, and with a survival rate in the young class depending on the density of young individuals.

The migration process is represented by matrix

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

and so the equilibrium frequencies of fast dynamics are included in

$$\bar{\mathbf{P}}_c = \text{diag}\{\nu^1, \nu^2\} = \begin{pmatrix} \frac{q_1}{p_1+q_1} & 0 \\ \frac{p_1}{p_1+q_1} & 0 \\ 0 & \frac{q_2}{p_2+q_2} \\ 0 & \frac{p_2}{p_2+q_2} \end{pmatrix}.$$

The demography is defined by means of the matrix

$$\mathbf{L} = \begin{pmatrix} \mathbf{F}_1 & \mathbf{F}_2 \\ \mathbf{S} & \mathbf{0} \end{pmatrix},$$

where

$$\mathbf{F}_i = \begin{pmatrix} F_i^1 & 0 \\ 0 & F_i^2 \end{pmatrix}, \quad i = 1, 2, \quad \text{and} \quad \mathbf{S} = \begin{pmatrix} \frac{\mu_1}{1+\alpha_1 x^{11}} & 0 \\ 0 & \frac{\mu_2}{1+\alpha_2 x^{12}} \end{pmatrix},$$

where  $\mu_i$  and  $\alpha_i$  are positive parameters.

The general system (14) is

$$\mathbf{X}_{n+1} = \mathbf{P} \mathbf{X}_n + \varepsilon \begin{pmatrix} F_1^1 - 1 & 0 & F_2^1 & 0 \\ 0 & F_1^2 - 1 & 0 & F_2^2 \\ \frac{\mu_1}{1+\alpha_1 x_n^{11}} & 0 & -1 & 0 \\ 0 & \frac{\mu_2}{1+\alpha_2 x_n^{12}} & 0 & -1 \end{pmatrix} \mathbf{P} \mathbf{X}_n. \quad (16)$$

The aggregated system (15) can be expressed in the form

$$\begin{pmatrix} s_{n+1}^1 \\ s_{n+1}^2 \end{pmatrix} = \begin{pmatrix} s_n^1 \\ s_n^2 \end{pmatrix} + \varepsilon \left[ \begin{pmatrix} F_1 & F_2 \\ S(s_n^1) & 0 \end{pmatrix} - \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix} \right] \begin{pmatrix} s_n^1 \\ s_n^2 \end{pmatrix} + O(\varepsilon^2), \quad (17)$$

where

$$F_i = \frac{F_i^1 q_i + F_i^2 p_i}{p_i + q_i}, \quad i = 1, 2,$$

and

$$\begin{aligned} S(s^1) &= \frac{q_1}{p_1 + q_1} \frac{\mu_1}{1 + \alpha_1 \frac{q_1}{p_1 + q_1} s^1} + \frac{p_1}{p_1 + q_1} \frac{\mu_2}{1 + \alpha_2 \frac{p_1}{p_1 + q_1} s^1} \\ &= \frac{q_1 \mu_1}{p_1 + q_1 + \alpha_1 q_1 s^1} + \frac{p_1 \mu_2}{p_1 + q_1 + \alpha_2 p_1 s^1}. \end{aligned}$$

We now try to find under which conditions system (16) has an asymptotically stable equilibrium. For that, we start studying the same problem for system

$$\mathbf{s}_{n+1} = \mathbf{s}_n + \varepsilon (\bar{\mathbf{L}}(s_n^1) - \mathbf{I}) \mathbf{s}_n \quad (18)$$

that is, the aggregated system neglecting the  $O(\varepsilon^2)$  term. The system (18) has an equilibrium  $\mathbf{s}^* = (s^{1*}, s^{2*})^\top$  if  $s^{1*}$  satisfies

$$0 = \det(\bar{\mathbf{L}}(s^1) - \mathbf{I}) = 1 - F_1 - F_2 \left( \frac{q_1 \mu_1}{p_1 + q_1 + \alpha_1 q_1 s^1} + \frac{p_1 \mu_2}{p_1 + q_1 + \alpha_2 p_1 s^1} \right) \quad (19)$$

and that happens, for  $s^{1*} > 0$ , if and only if  $F_1 < 1 < F_1 + F_2 \left( \frac{q_1 \mu_1 + p_1 \mu_2}{p_1 + q_1} \right)$ , that is

$$\frac{F_1^1 q_1 + F_1^2 p_1}{p_1 + q_1} < 1 < \frac{F_1^1 q_1 + F_1^2 p_1}{p_1 + q_1} + \left( \frac{F_2^1 q_2 + F_2^2 p_2}{p_2 + q_2} \right) \left( \frac{q_1 \mu_1 + p_1 \mu_2}{p_1 + q_1} \right). \quad (20)$$

In this case there is a unique value  $s^{1*}$  which satisfies (19) and the corresponding  $s^{2*}$  is  $\frac{1-F_1}{F_2} s^{1*}$ . We are proving that  $\mathbf{s}^*$  is always asymptotically stable for small  $\varepsilon$ .

If we call  $\mathbf{F}$  to the map associated to system (18)

$$\mathbf{F}(s) = \mathbf{s} + \varepsilon (\bar{\mathbf{L}}(s^1) - \mathbf{I}) \mathbf{s}$$

its Jacobian matrix at  $\mathbf{s}^*$  is

$$J\mathbf{F}(s^*) = \begin{pmatrix} 1 - \varepsilon + \varepsilon F^1 & \varepsilon F^2 \\ \varepsilon c(s^{1*}) & 1 - \varepsilon \end{pmatrix}$$

where

$$c(s^{1*}) = \frac{q_1 \mu_1}{p_1 + q_1 + \alpha_1 q_1 s^{1*}} + \frac{p_1 \mu_2}{p_1 + q_1 + \alpha_2 p_1 s^{1*}} - \gamma,$$

where  $\gamma > 0$  is

$$\gamma = s^{1*} \left( \frac{q_1 \mu_1 \alpha_1 q_1}{(p_1 + q_1 + \alpha_1 q_1 s^{1*})^2} + \frac{p_1 \mu_2 \alpha_2 p_1}{(p_1 + q_1 + \alpha_2 p_1 s^{1*})^2} \right)$$

and using that  $s^{1*}$  satisfies (19)

$$c(\mathbf{s}^{1*}) = \frac{1 - F_1}{F_2} - \gamma$$

which implies that

$$\text{Tr}(\mathbf{J}\mathbf{F}(s^*)) = 2(1 - \varepsilon) + \varepsilon F_1 = 2 + \varepsilon(F_1 - 2)$$

and

$$\begin{aligned} \det(\mathbf{J}\mathbf{F}(s^*)) &= (1 - \varepsilon + \varepsilon F_1)(1 - \varepsilon) - \varepsilon^2 F_2 c(\mathbf{s}^{1*}) \\ &= 1 + \varepsilon(F_1 - 2) + \varepsilon^2 F_2 \gamma. \end{aligned}$$

For small  $\varepsilon$  we have

$$|\text{Tr}(\mathbf{J}\mathbf{F}(s^*))| < 1 + \det(\mathbf{J}\mathbf{F}(s^*)) < 2$$

and this yields  $\rho(\mathbf{J}\mathbf{F}(s^*)) < 1$ .

The previous study of system (18) gives the following information about systems (17) and (16). If condition (20) is verified then there exists a unique equilibrium, that is asymptotically stable for small  $\varepsilon$ , of the form  $\mathbf{s}^* + O(\varepsilon)$  for system (17) and of the form  $\bar{\mathbf{P}}_c \mathbf{s}^* + O(\varepsilon)$  for system (16),  $\mathbf{s}^*$  being the unique equilibrium of system (18).

## 6. Conclusion

Our method allows to aggregate a complex system with two time scales, obtaining a simplified model and also the relationships between the parameters of the latter system and the parameters which control the fast dynamics of the former system. For example, in the patch and age structured population, the aggregated model is density dependent Leslie model where the fecundity and survival rates are expressed in terms of the spatial distributions of individuals on the different patches. Thus, a change in the spatial distribution has an effect on the aggregated Leslie matrix that can be calculated.

Our general results allow to make different applications. In the present work we have only introduced a model of an age structured population in a multipatch environment, but it is possible to study, for example, the influence of spatial heterogeneity on the stability of ecological communities. Spatial heterogeneity can play a very important role with regard to the stability of ecological communities. We plan to model a patch structured host-parasitoid community. It would be interesting to compare the results of our model and of those of the cell automaton spatial model based on the Nicholson-Bailey model [10].

We also intend to apply our result to the case of the tse tse fly. In the paper by Jarry *et al.* [14] a detailed Leslie type model of the *Glossina* life-cycle has been given. A two patch Leslie model, incorporating capture and the influence of different

types of density dependent migrations will yield some insights about the growth of the tse tse fly populations.

### Acknowledgements

This work has been partially supported by *Acción Integrada Hispano-Francesa 111B (1994)*.

### Appendix I

We follow the notations of section 4.1. If we write down the matrix representation of  $\mathbf{A}$  and call it also  $\mathbf{A}$  we have  $\mathbf{A} = \text{diag}\{\mathbf{A}_1, \dots, \mathbf{A}_p\}$ , where  $\mathbf{A}_i$  is an  $(N^i-1) \times N^i$  matrix of the form  $(: \mathbf{I} : | \mathbf{0})$ ,  $i = 1, \dots, p$ , with  $\mathbf{0}$  being a column vector zero. So matrix  $\mathbf{Q} = \mathbf{A} \mathbf{P} \mathbf{D}$  has the form  $\mathbf{Q} = \text{diag}\{\mathbf{Q}_1, \dots, \mathbf{Q}_p\}$ , where  $\mathbf{Q}_i = \mathbf{A}_i \mathbf{P}_i \mathbf{D}_i$ ,  $i = 1, \dots, p$ .

For every  $i = 1, \dots, p$ , matrix  $\mathbf{P}_i$  is a regular stochastic matrix of order  $N^i$ , which implies that it has a simple eigenvalue equal to 1 and the rest of the spectrum lies in the open unit disk. We are proving that  $\mathbf{Q}_i$  is a matrix of order  $N^i-1$  whose eigenvalues are those of  $\mathbf{P}_i$  different from 1.

We decompose  $\mathbf{P}_i$  into blocks in the following way

$$\left( \begin{array}{c|c} \mathbf{P}_i^{11} & \mathbf{p}_i^{12} \\ \hline \mathbf{p}_i^{21} & p_i^{22} \end{array} \right)$$

where  $\mathbf{P}_i^{11}$  is a submatrix of dimensions  $(N^i-1) \times (N^i-1)$ ,  $\mathbf{p}_i^{12}$  is  $(N^i-1) \times 1$ ,  $\mathbf{p}_i^{21}$  is  $1 \times (N^i-1)$  and  $p_i^{22}$  is  $1 \times 1$ . So we have

$$\mathbf{Q}_i = (: \mathbf{I} : | \mathbf{0}) \left( \begin{array}{c|c} \mathbf{P}_i^{11} & \mathbf{p}_i^{12} \\ \hline \mathbf{p}_i^{21} & p_i^{22} \end{array} \right) \begin{pmatrix} \mathbf{I} \\ -\mathbf{I} \end{pmatrix} = \mathbf{P}_i^{11} - \mathbf{p}_i^{12} \mathbf{1}$$

and we can prove the relationship between the characteristic polynomials of matrices  $\mathbf{P}_i$  and  $\mathbf{Q}_i$ ,  $\Pi_{\mathbf{P}_i}(\lambda)$  and  $\Pi_{\mathbf{Q}_i}(\lambda)$  respectively. Using that columns of  $\mathbf{P}_i$  sum up to one we get

$$\begin{aligned} \Pi_{\mathbf{P}_i}(\lambda) &= \det \left( \begin{array}{c|c} \mathbf{P}_i^{11} - \lambda \mathbf{I} & \mathbf{p}_i^{12} \\ \hline \mathbf{p}_i^{21} & p_i^{22} - \lambda \end{array} \right) = \det \left( \begin{array}{c|c} \mathbf{P}_i^{11} - \lambda \mathbf{I} & \mathbf{p}_i^{12} \\ \hline (1-\lambda)\mathbf{1} & 1-\lambda \end{array} \right) \\ &= \det \left( \begin{array}{c|c} \mathbf{P}_i^{11} - \mathbf{p}_i^{12} \mathbf{1} - \lambda \mathbf{I} & \mathbf{p}_i^{12} \\ \hline \mathbf{0} & 1-\lambda \end{array} \right) = (1-\lambda) \Pi_{\mathbf{Q}_i}(\lambda). \end{aligned}$$

### Appendix II

To obtain the aggregated system we use center manifold theory. The classical center manifold theorem is valid in a neighbourhood of an equilibrium point of a dynamical



system and tells us that it is possible to study the general dynamics of the system by means of its restriction to a certain invariant manifold, the center manifold that corresponds to the nonhyperbolic part of the equilibrium, see [6]. There are much more general settings where this kind of results applies, see for instance Hirsch *et al.* [11], where the equilibrium point is allowed to be a general invariant manifold.

In this work, we need a center manifold not only for an equilibrium point, but rather for a simple manifold of equilibrium points, which represents a small generalization of the classical result. To be specific let us state the theorem.

**Center Manifold Theorem.** *Let the system*

$$\begin{aligned} \mathbf{x}_{n+1} &= \mathbf{B} \mathbf{x}_n + \varepsilon \mathbf{F}(\mathbf{x}_n, \mathbf{y}_n) \\ \mathbf{y}_{n+1} &= \mathbf{C} \mathbf{y}_n + \varepsilon \mathbf{G}(\mathbf{x}_n, \mathbf{y}_n) \end{aligned} \quad (21)$$

be such that  $\mathbf{x} \in \mathbf{R}^k$ ,  $\mathbf{y} \in \mathbf{R}^m$  and  $\varepsilon \in \mathbf{R}$ ,  $\mathbf{B}$  is an  $k \times k$  matrix whose eigenvalues have modulus equal to 1 and  $\mathbf{C}$  is an  $m \times m$  matrix of eigenvalues lying in the open unit disk, and  $\mathbf{F}$  and  $\mathbf{G}$  are  $C^\infty$  mappings from  $\mathbf{R}^{k+m}$  to  $\mathbf{R}^k$  and  $\mathbf{R}^m$ , respectively, with  $\mathbf{F}(\mathbf{0}, \mathbf{0}) = \mathbf{0}$  and  $\mathbf{G}(\mathbf{0}, \mathbf{0}) = \mathbf{0}$ . For every  $M > 0$  there exists  $\delta > 0$  and a  $C^\infty$  mapping  $\mathbf{h}(\mathbf{x}, \varepsilon)$  defined for every  $|\mathbf{x}| < M$  and  $|\varepsilon| < \delta$  with range in  $\mathbf{R}^m$  that satisfies:

- i.  $|\mathbf{h}(\mathbf{x}, \varepsilon)| < K|\varepsilon|$ , with  $K$  constant.
- ii. For every  $\varepsilon$ ,  $|\varepsilon| < \delta$ , the graph of  $\mathbf{h}(\cdot, \varepsilon)$ ,  $W_\varepsilon$ , is a locally invariant manifold, that is, for  $|\mathbf{x}| < M$

$$\mathbf{h}(\mathbf{x} + \varepsilon \mathbf{F}(\mathbf{x}, \mathbf{h}(\mathbf{x}, \varepsilon))) = \mathbf{C} \mathbf{h}(\mathbf{x}, \varepsilon) + \varepsilon \mathbf{G}(\mathbf{x}, \mathbf{h}(\mathbf{x}, \varepsilon)). \quad (22)$$

- iii. The dynamics of system (21) restricted to  $W_\varepsilon$  is defined by the equation,

$$\mathbf{u}_{n+1} = \mathbf{B} \mathbf{u}_n + \varepsilon \mathbf{F}(\mathbf{u}_n, \mathbf{h}(\mathbf{u}_n, \varepsilon)), \quad \mathbf{u} \in \mathbf{R}^k. \quad (23)$$

- iv.  $W_\varepsilon$  is locally attractive, that is, if  $\{(\mathbf{x}_k, \mathbf{y}_k)\}$  is a solution of system (21) with  $|\mathbf{x}_0| < M$  and  $\mathbf{y}_0$  small enough, then there exists  $\{\mathbf{u}_k\}$  solution of Eq. (23) such that

$$|\mathbf{x}_k - \mathbf{u}_k| \leq K\beta^k \quad \text{and} \quad |\mathbf{y}_k - \mathbf{h}(\mathbf{u}_k, \varepsilon)| \leq K\beta^k$$

where  $K$  and  $\beta$  are positive constants, with  $\beta < 1$ .

**Proof.** We follow the proof of Center Manifold Theorem in [13] (pp. 146–153) using the functional space

$$\mathbf{A}_0 = \{\varphi : \mathbf{R}^k \times \mathbf{R} \rightarrow \mathbf{R}^m : \varphi \in C^0, |\varphi|_\infty \leq 1, \varphi(\mathbf{x}, 0) = \mathbf{0}$$

$$\text{and } |\varphi(\mathbf{x}, \varepsilon) - \varphi(\mathbf{x}', \varepsilon)| \leq |\mathbf{x} - \mathbf{x}'|\}$$

and the mapping  $\mathcal{F}$  from  $\mathbf{A}_0$  to  $\mathbf{A}_0$  defined by

$$(\mathcal{F}\varphi)(\tilde{\mathbf{x}}, \varepsilon) = \mathbf{C}\varphi(\mathbf{x}, \varepsilon) + \varepsilon\mathbf{G}(\mathbf{x}, \varphi(\mathbf{x}, \varepsilon))$$

where  $\tilde{\mathbf{x}} = \Phi_{\varphi, \varepsilon}(\mathbf{x}) = \mathbf{x} + \varepsilon\mathbf{F}(\mathbf{x}, \varphi(\mathbf{x}, \varepsilon))$ .

In the system (12) we have  $\mathbf{B} = \mathbf{I}$ , and the points of the form  $(\mathbf{s}, \mathbf{0})$  represent the manifold of equilibrium points for  $\varepsilon = 0$ . Though, in general, it is not possible to find out explicitly  $\mathbf{h}(\mathbf{x}, \varepsilon)$ , and even the center manifold is not unique, we know that the coefficients of its Taylor series are unique, and therefore we could use the equality (22) to calculate its expansion in  $\varepsilon$  powers. If we make  $\mathbf{h}(\mathbf{x}, \varepsilon) = \varepsilon\mathbf{h}_1(\mathbf{x}) + O(\varepsilon^2)$ , then (22) yields

$$\begin{aligned} \varepsilon\mathbf{h}_1[\mathbf{x} + \varepsilon\mathbf{F}(\mathbf{x}, \varepsilon\mathbf{h}_1(\mathbf{x}) + O(\varepsilon^2))] + O(\varepsilon^2) = \\ \mathbf{C}(\varepsilon\mathbf{h}_1(\mathbf{x}) + O(\varepsilon^2)) + \varepsilon\mathbf{G}(\mathbf{x}, \varepsilon\mathbf{h}_1(\mathbf{x}) + O(\varepsilon^2)) \end{aligned}$$

and identifying the terms in  $\varepsilon$  we obtain

$$\mathbf{h}_1(\mathbf{x}) = \mathbf{C}\mathbf{h}_1\mathbf{x} + \mathbf{G}(\mathbf{x}, \mathbf{0}) \quad \text{and} \quad \mathbf{h}_1(\mathbf{x}) = (\mathbf{I} - \mathbf{C})^{-1}\mathbf{G}(\mathbf{x}, \mathbf{0})$$

and so

$$\mathbf{h}(\mathbf{x}, \varepsilon) = \varepsilon(\mathbf{I} - \mathbf{C})^{-1}\mathbf{G}(\mathbf{x}, \mathbf{0}) + O(\varepsilon^2)$$

and Eq. (23) admits the form

$$\mathbf{u}_{n+1} = \mathbf{u}_n + \varepsilon\mathbf{F}(\mathbf{u}_n, \varepsilon(\mathbf{I} - \mathbf{C})^{-1}\mathbf{G}(\mathbf{u}_n, \mathbf{0}) + O(\varepsilon^2)). \quad (24)$$

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