APPLICATION OF AGGREGATION OF VARIABLES METHODS TO A CLASS OF TWO-TIME REACTION-DIFFUSION-CHEMOTAXIS MODELS OF SPATIALLY STRUCTURED POPULATIONS WITH CONSTANT DIFFUSION

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Abstract. The main goal of this paper is to adapt a class of complexity reduction methods called aggregation of variables methods to the construction of reduced models of two-time reaction-diffusion-chemotaxis models of spatially structured populations and to provide an error bound of the approximate dynamics. Aggregation of variables methods are general techniques that allow reducing the dimension of a mathematical dynamical system. Here we reduce a system of Partial Differential Equations to a simpler Ordinary Differential Equation system, provided that the evolution processes occur at two different time scales: a slow one for the demography and a fast one for migrations and chemotaxis, with a ratio \( \varepsilon > 0 \) small enough. We give an approximation of the error between solutions of both original and reduced model for a generic function representing the demography. Finally, we provide an optimization of the error bound and validate numerically this result for a spatial inter-specific model with constant diffusion and population growth given by a logistic law in population dynamics.

2020 Mathematics Subject Classification. Primary: 37M99, 37N25; Secondary: 35K55.

Key words and phrases. Aggregation of variables, two time scales, approximate dynamics, spatially structured population dynamics, reaction-diffusion-chemotaxis equations.

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1. Introduction. During the last decades, there has been a lot of interest in spatial dynamics of ecological systems [11, 17, 23]. Continuous space has been introduced in mathematical models of population dynamics in order to give a more realistic description of ecological systems and to understand how living organisms interact with their environment changes, which usually leads to models formulated as a set of partial differential equations. Ecological modellers, supported by the fast development of computers, produce a new generation of ecological models with more complexity and details, leading to large dynamical systems involving lots of variables, and thus hard to handle analytically. Aggregation of variables methods allow reducing the complexity of such models and building approximate models that are easier to analyze. In general, the aggregation of variables methods consist in introducing a small number of new variables, called global variables, and to derive a new reduced model describing their dynamics. In ecological models based on the existence of different time scales, it is possible to use these time scales in order to reduce the complexity of the initial complete model and to construct a simplified model (called an aggregated model), describing the dynamics with fewer global variables. Those methods have been developed several classes of models including time continuous systems as well as discrete models [2]. A particular attention has been brought to the cases of Ordinary Differential Equations (ODE) [3, 5], Partial Differential Equations (PDE) [4, 20, 21], and Delayed Differential Equations (DDE) [22].

Sanchez et al. [20] introduced the aggregation of variables methods to define an aggregated model that simplifies a two-time scales semi-linear evolution equation defined on a Banach lattice, and applied it to two-time scales reaction-diffusion models with large diffusivity. Mathematical models of such processes are given by partial differential equations of reaction-diffusion type [12]. In addition to diffusion processes, the oriented migration of cells and organisms in response to chemical gradients, chemotaxis, has attracted significant interest due to its critical role in a wide range of biological phenomena, and is considered in many disciplines [7, 10, 17]. In this work, we extend the use of the aggregation of variables methods to a class of two-time reaction-diffusion-chemotaxis models of spatially structured populations with large constant diffusivity. We assume that the diffusion and chemotaxis processes take place at a faster time scale than the demography, with a ratio $\varepsilon > 0$ small enough. We show that taking advantage of the time scales, it is possible to derive a reduced ODE model. We illustrate the aggregation methods with applications to spatially structured populations.

This paper is organized as follows. In Section 2, we recall the general principle of aggregation of variables methods. In Section 3, we apply it to construct an aggregated model for a class of two-time reaction-diffusion-chemotaxis models and to provide an approximation result. The approximation error is evaluated in Theorem 3.2. However, the assumptions on that class of models are too general to determine a satisfying error bound. In section 4, we apply aggregation of variable methods to a spatial inter-specific model with constant diffusion and population growth given by a logistic law. In this case, we are able to provide an optimized error bound. Finally, we provide a comparison result between the numerical solution to the complete model and its aggregated one.
2. Aggregation of variables in a two-time semilinear evolution differential equation. Let us consider the following Cauchy problem for an abstract semilinear evolution differential equation defined on a Banach lattice \((X, \| \cdot \|_X)\):

\[
(CP)_\varepsilon \left\{ \begin{array}{ll}
    n_\varepsilon(t) = \frac{1}{\varepsilon} An_\varepsilon(t) + \mathcal{F}(n_\varepsilon(t)), & t > 0, \\
    n_\varepsilon(0) = n_0,
  \end{array} \right.
\]

where \(\varepsilon > 0\) is a small parameter, and \(A\) and \(\mathcal{F}\) are two operators that satisfy the following hypotheses:

- \((H1)\) : The operator \(A : D(A) \subset X \to X\) is an infinitesimal generator of a \(C_0\)-semigroup \(\{T_0(t)\}_{t \geq 0}\) defined on \(X\).
- \((H2)\) : The nonlinear operator \(\mathcal{F} : X \to X\) is locally Lipschitz continuous, that is, for each \(\gamma > 0\) there exists a constant \(C_\gamma > 0\) such that for each \(\psi_i \in X\) with \(\|\psi_i\|_X \leq \gamma\), \(i = 1, 2\), the following inequality holds:
\[
    \|\mathcal{F}(\psi_1) - \mathcal{F}(\psi_2)\|_X \leq C_\gamma \|\psi_1 - \psi_2\|_X.
\]

Using the aggregation of variables methods, as described in [20], one will proceed to reduce the abstract evolution equation to an ordinary differential equation whose solutions serve to approximate the asymptotic dynamics of the initial complex dynamics, for \(\varepsilon > 0\) small enough. We summarize the aggregation of variables methods in the rest of this section.

To deal with population dynamics models that involve several populations, the perturbed problem \((CP)_\varepsilon\) is set as a vector formulation. For this, we will assume that \(X := E^q, q \geq 1\), where \((E, \| \cdot \|_E)\) is a Banach lattice and \(X\) is endowed with the product norm. Moreover we also assume that \(A := \text{diag}(A_1, ..., A_q)\) where \(A_j : D(A_j) \subset E \to E\) is the infinitesimal generator of a \(C_0\)-semigroup \(\{T_0(t)\}_{t \geq 0}\) defined on \(E\), \(j = 1, ..., q\), so that \(T_0(t) := \text{diag}(T_{01}(t), ..., T_{0q}(t))\).

The construction of an aggregated model is based on projecting the dynamics of \((CP)_\varepsilon\) onto \(\ker A\). We build \(q\) new variables, called global variables, by introducing strictly positive functionals of \(\ker A\), and \(\ker A_0^*\). \(\mu_j\) and \(\mu_j^*\) such that \(\langle \mu_j, \mu_j^* \rangle = 1\), where \(A_0^*\) is the adjoint operator of \(A_0\) and \((\cdot, \cdot)\) stands for the duality \((E^*, E)\). The new global variables are then defined by

\[
    N_\varepsilon^j(t) = \langle \mu_j^*, n_\varepsilon^j(t) \rangle, \quad j = 1, ..., q; \quad N_\varepsilon(t) = (N_\varepsilon^1(t), ..., N_\varepsilon^q(t))^T \in \mathbb{R}^q.
\]

The complex perturbed model \((CP)_\varepsilon\) is approximated by a system of coupled nonlinear ordinary differential equations in \(\mathbb{R}^q\), called the aggregated model (for more details see [20]):

\[
    (N^j)'(t) = \langle \mu_j^*, \mathcal{F}_j \left( (N^1(t)\mu_1, ..., N^q(t)\mu_q) \right) \rangle, \quad j = 1, ..., q,
\]

where we substitute \(n_\varepsilon(t)\) by its projection onto \(\ker A\): \(n_\varepsilon^j(t) \approx N^j(t)\mu_j, j = 1, ..., q\), completed with the initial value:

\[
    N^j(0) = \langle \mu_j^*, n_\varepsilon^j(0) \rangle = \langle \mu_j^*, n_0^j \rangle, \quad j = 1, ..., q.
\]

Then, the aggregated model can be written as

\[
    N'(t) = \langle \mu^*, \mathcal{F}(N(t)\mu) \rangle; \quad N(0) = \langle \mu^*, n_0 \rangle,
\]

where we use the notations:

\[
    N(t)\mu := (N^1(t)\mu_1, ..., N^q(t)\mu_q)^T; \quad \langle \mu^*, \psi \rangle := (\langle \mu_1^*, \psi_1 \rangle, ..., \langle \mu_q^*, \psi_q \rangle)^T.
\]
3. Two-time scales in reaction-diffusion-chemotaxis models of population dynamics. In this section we apply the general aggregation of variables methods to a reaction-diffusion-chemotaxis system, modelling the dynamics of several continuously spatially distributed populations whose evolution processes occur at two different time scales: a slow one for the demography and a fast one for dispersal and chemotaxis. Here we consider \( q (q \geq 1) \) populations living in a spatial region \( \Omega \subset \mathbb{R}^p \) (\( p \geq 1 \)) where \( \Omega \) is a non-empty bounded, open and connected set with smooth boundary \( \partial \Omega \subset C^k, k \geq 1 \). Let \( n^i_\varepsilon (x,t), i = 1, ..., q \), be their spatially structured population densities and set \( n_\varepsilon (x,t) := (n^1_\varepsilon (x,t), ..., n^q_\varepsilon (x,t))^T \).

We assume that the demography is given by a nonlinear reaction term \( f(x,n_\varepsilon) \) that satisfies the following regularity conditions:

**Hypothesis 1.** The function \( f : \overline{\Omega} \times \mathbb{R}^q \to \mathbb{R}^q, f = (f_1, ..., f_q) \), is continuous and there exists a real-valued continuous positive function \( h \) defined on \( \overline{\Omega} \times \mathbb{R}^q \times \mathbb{R}^q \) such that \( \forall x \in \overline{\Omega} \) and \( \forall u, v \in \mathbb{R}^q \):

\[
|f(x,u) - f(x,v)| \leq h(x,u,v) |u - v|.
\]

We also assume a constant diffusion process in \( \Omega \) for each population, with coefficient \( D_i > 0, i = 1, ..., q \), and a linear chemotaxis process in \( \Omega \) for each population, with velocity \( \chi_i n^i_\varepsilon \nabla K_i \) by which each population moves up to the gradient of the carrying capacity of the environment where \( \chi_i \) denotes their chemotactic sensitivity and \( K_i \in C^2(\overline{\Omega}) \), \( K_i(x) \geq k^*_i > 0, i = 1, ..., q \). Both processes occur at a fast time scale determined by a parameter \( \varepsilon > 0 \) small enough. The balance law leads to the following two-time reaction-diffusion-chemotaxis system for the population densities, with \( i = 1, ..., q \):

\[
\begin{cases}
\frac{\partial n^i_\varepsilon}{\partial t} = \frac{1}{\varepsilon} \text{div} (D_i \nabla n^i_\varepsilon - \chi_i n^i_\varepsilon \nabla K_i (x)) + f_i(x,n_\varepsilon), \quad x \in \Omega, \ t > 0, \\
D_i \frac{\partial n^i_\varepsilon}{\partial \nu} - \chi_i n^i_\varepsilon \frac{\partial K_i(x)}{\partial \nu} = 0, \quad x \in \partial \Omega, \ t > 0, \\
n^i_\varepsilon (x,0) = n_0^i (x), \quad x \in \Omega, \ n_0(x) = (n^1_0(x), ..., n^q_0(x))^T.
\end{cases}
\]

This problem is coupled with the Neumann boundary conditions to indicate that the spatial domain \( \Omega \) is isolated from the external environment.

The dynamics at a fast time scale is obtained as follows. We switch the time scale as \( t = \varepsilon \tau \) in Equation (3) and making \( \varepsilon \to 0_+ \), we get:

\[
\frac{\partial n_i(x,\tau)}{\partial \tau} = \text{div} (D_i \nabla n_i(x,\tau) - \chi_i n_i(x,\tau) \nabla K_i (x)) , \quad i = 1, ..., q,
\]

where \( n_i(x,\tau) := n^i_\varepsilon (x,t) \).

The total population \( \int_{\Omega} n_i(x,\tau) dx \), at this time scale, satisfies that

\[
\int_{\Omega} n_i(x,\tau) dx = \int_{\Omega} \text{div} (D_i \nabla n_i(x,\tau) - \chi_i n_i(x,\tau) \nabla K_i (x)) dx
\]

\[
= \int_{\partial \Omega} \left( D_i \frac{\partial n_i(x,\tau)}{\partial \nu} - \chi_i n_i(x,\tau) \frac{\partial K_i(x)}{\partial \nu} \right) d\sigma = 0,
\]

which translates that the total population is conserved under the dispersal and chemotaxis processes, without taking into account the demographic evolution. This conception allows constructing a reduced model to approximate the complex model (3), taking as new global variables the total populations:

\[
N^i_\varepsilon (t) := \int_{\Omega} n^i_\varepsilon (x,t) dx; \quad N_\varepsilon (t) := (N^1_\varepsilon (t), ..., N^q_\varepsilon (t))^T.
\]
Further calculations on both sides of Equation (3) lead to:

\[ (N_i^*)'(t) = \int_\Omega f_i(x, n_e(x, t))dx, \ i = 1, \ldots, q. \]  

(4)

Now, to avoid the presence of \(n_e(x, t)\) in the right-hand side of (4), we search for an approximation of \(n_e(x, t)\) in terms of the total populations \(N_e(t)\). To this end, the equilibria, if it exists, of the fast dynamics given by:

\[
\begin{align*}
\text{div} \left( D_i \nabla \lambda_i^*(x) - \chi_i \lambda_i^*(x) \nabla K_i(x) \right) &= 0, \ x \in \Omega, \\
D_i \frac{\partial \lambda_i^*(x)}{\partial \nu} - \chi_i \lambda_i^*(x) \frac{\partial K_i(x)}{\partial \nu} &= 0, \ x \in \partial \Omega,
\end{align*}
\]

(5)

will be the functions \(\lambda_i^*(x) = \beta_i e^{\frac{\psi}{\lambda_i^*} K_i(x)}\). Since the total population is conserved under the fast dynamics, the initial conditions in (3) determine the values of \(\beta_i\) for the equilibria of the fast dynamics. In fact,

\[ N_i^*(0) = \int_\Omega n_i^0(x)dx = \int_\Omega \lambda_i^*(x)dx, \ i = 1, \ldots, q, \]

implies that

\[ \beta_i = \frac{N_i(0)}{\int_\Omega e^{\frac{\psi}{\lambda_i^*} K_i(x)}dx}, \ i = 1, \ldots, q, \]

then,

\[ \lambda_i^*(x) = \frac{e^{\frac{\psi}{\lambda_i^*} K_i(x)}}{\int_\Omega e^{\frac{\psi}{\lambda_i^*} K_i(y)}dy} N_i^*(0), \ i = 1, \ldots, q. \]

In absence of demography, the equilibria of the fast dynamics is an inhomogeneous distribution on the spatial region. The above considerations provide an approximation of \(n_i^*(x, t)\) as follows:

\[ n_i^*(x, t) \approx \lambda_i(x) N_i^*(t), \ i = 1, \ldots, q, \]

where \(\lambda_i(x) = g_i(x)/\int_\Omega g_i(y)dy\) and \(g_i(x) = e^{\frac{\psi}{\lambda_i^*} K_i(x)}\), which yields the aggregated model of (3):

\[
\begin{align*}
\left\{ \begin{array}{l}
N'(t) = F(N(t)), \\
N(0) = N_0 = \int_\Omega n_0(x)dx,
\end{array} \right.
\end{align*}
\]

(6)

where \(F : \mathbb{R}^q \to \mathbb{R}^q\), \(F := (F_1, \ldots, F_q)\) is the function defined by:

\[ \forall u \in \mathbb{R}^q, \ F(u) = \int_\Omega f(x, \lambda(x)u)dx, \]

with:

\[ \lambda(x)u := (\lambda_1(x)u_1, \ldots, \lambda_q(x)u_q)^T. \]

We should notice that \(N(t)\), in (6), is an approximation of \(N_e(t)\) using aggregation of variables method.

To derive the comparison result between both models, we have to formulate (3) as an abstract evolution equation in the setting of the \(C_0\)-semigroup theory as described in [20]. To this end, we set as state space \(E := C(\Omega)\), the Banach space of continuous real-valued functions defined on \(\Omega\), endowed with the norm \(\|\psi\|_\infty := \sup_{x \in \Omega} |\psi(x)|\), so that \(X := [C(\Omega)]^q\) is endowed with the product norm.

Let us set the linear operator \(\hat{A}_i\) defined by

\[ \left( \hat{A}_i \psi \right)(x) := \text{div} \left( D_i \nabla \psi(x) - \chi_i \psi(x) \nabla K_i(x) \right) \text{ for all } x \in \Omega \]
with domain:

\[ D(\hat{A}_i) = \left\{ \psi \in C^2(\Omega) : \sup_{x,y \in \Omega, x \neq y} \frac{|D^m \psi(x) - D^m \psi(y)|}{\|x - y\|^n} < +\infty; \mathcal{H} \psi = 0 \text{ on } \partial \Omega \right\}, \]

where \( \mathcal{H} \psi := D_i \frac{\partial \psi}{\partial x_i} - \chi_i \psi \frac{\partial K_i}{\partial x_i}, \) \( 0 < \alpha < 1 \) and \( D^m \psi, \) \( m := (m_1, \ldots, m_N), \) represents the partial derivatives of \( \psi \) of order 2 = \( m_1 + \ldots + m_N. \)

Notice that \( \hat{A}_i \) is a strongly elliptic operator. Now, we have to verify that the linear diffusion-chemotaxis operator \( \hat{A}_i \) together with our boundary condition is the infinitesimal generator of a \( C_0 \)-semigroup on \( C(\Omega). \) We refer to [1, 13, 19] for the general theory which provides the results explained in the following proposition for the diffusion-chemotaxis operator \( \hat{A}_i. \) One can see similar results for the diffusion operator in Proposition 3 in [20]. For the diffusion-chemotaxis operator we have the following:

**Proposition 1.** The operator \( A_i \) defined as the closure in \( C(\Omega) \) of operator \( \hat{A}_i \) is the infinitesimal generator of an analytic and compact \( C_0 \)-semigroup \( \{T_{0i}(t)\}_{t \geq 0} \) on \( C(\Omega). \)

Moreover, the semigroup \( \{T_{0i}(t)\}_{t \geq 0} \) satisfies the following:

i) For all \( \psi \in C^2(\Omega) \) and \( x \in \Omega, \)

\[ (T_{0i}(t)\psi)(x) = g_i(x)S_{0i}(g_i(x)^{-1}t)(g_i(x)^{-1}\psi(x)), \quad t \geq 0 \]

where \( \{S_{0i}(s)\}_{s \geq 0} \) is the semigroup whose infinitesimal generator is the operator \( B_i \) defined as the closure in \( C(\Omega) \) of operator \( \hat{B}_i \) defined by

\[ (\hat{B}_i \psi)(x) = \text{div} (D_i g_i(x) \nabla \psi(x)); \quad x \in \Omega \]

with domain:

\[ D(\hat{B}_i) = \left\{ \psi \in C^2(\Omega) : \sup_{x,y \in \Omega, x \neq y} \frac{|D^m \psi(x) - D^m \psi(y)|}{\|x - y\|^n} < +\infty; \frac{\partial \psi}{\partial \nu} = 0 \text{ on } \partial \Omega \right\}. \]

ii) \( T_{0i}(t) \left( C_+^+(\Omega) \right) \subset C_+^+(\Omega), \) \( t \geq 0, \) where \( C_+^+(\Omega) \) is the subset of real-valued nonnegative continuous functions on \( \Omega. \)

iii) \( \{T_{0i}(t)\}_{t \geq 0} \) is an irreducible semigroup on \( C(\Omega). \)

**Proof.** It is clear that \( g_i \in C^2(\Omega). \) We define the multiplication operator:

\[ \mathcal{M}_{g_i} \psi := g_i \cdot \psi, \]

i.e.

\[ (\mathcal{M}_{g_i} \psi)(x) := g_i(x) \psi(x), \quad x \in \Omega. \]

It is easy to see that the diffusion-chemotaxis operator verifies

\[ \hat{A}_i = \mathcal{M}_{g_i}^{-1} \left( \mathcal{M}_{g_i} \hat{B}_i \mathcal{M}_{g_i}^{-1} \right). \]

According to [1], there is an easy way to obtain a semi-group \( \{T_{0i}(t)\}_{t \geq 0} \) having generator \( A_i \) of a given semigroup \( \{S_{0i}(t)\}_{t \geq 0} \) whose infinitesimal generator is the diffusion operator \( B_i \) (see [20]) with domain:

\[ D(\hat{A}_i) = \left\{ \psi \in C^2(\Omega) : \mathcal{M}_{g_i}^{-1} \psi \in D(\hat{B}_i) \right\}. \]
it follows that \( T_0(t) = M_{g_i} S_{0i}(t/g_i) M_{g_i}^{-1}, \ t \geq 0 \). To be precise, for all \( \psi \in C^2(\Omega) \) and \( x \in \Omega \),

\[
T_0(t)\psi(x) = g_i(x) S_{0i}(g_i(x)^{-1}t)(g_i(x)^{-1}\psi(x)), \ t \geq 0.
\]

The semigroup \( \{T_0(t)\}_{t \geq 0} \) is constructed as a multiplication semigroup of a similar one to \( \{S_{0i}(t)\}_{t \geq 0} \).

\( i \) and \( iii \) are direct consequences of \( i \) and Proposition 3 in \([20]\). \( \square \)

Now, we consider the operator \( F : X \to X \) defined by

\[
\forall \psi := (\psi_1, \ldots, \psi_q)^T \in X; \quad F(\psi)(x) := f(x, \psi(x)), \ x \in \Omega.
\]

Taking into account the operator \( A := \text{diag}(A_1, \ldots, A_q) \) and making the identification \( n_e(\cdot, t) := n_e(t)(\cdot) \) we can formulate (3) as the abstract Cauchy problem \((CP)\varepsilon\) of the previous section, on the Banach space \( X \). Using Hypothesis 1, it follows that the operator \( F \) satisfies Hypothesis \((H2)\) and an immediate consequence of Proposition 1 is that the operator \( A \) satisfies all the assumptions of Theorem 4 in \([20]\) and thus this theorem provides an approximation result for the behaviour of solutions to the initial two-time reaction-diffusion model through the solutions to the aggregated model.

3.1. Approximation result for positive solutions to the two-time reaction-diffusion-chemotaxis models. In this subsection we will make a comparison result between the solutions to (3) with the solutions to the aggregated model (6) when \( \varepsilon \to 0^+ \), without assuming the existence of equilibria for the aggregated model. We will proceed to study the nonnegativity of solutions, their global existence, and the existence of suitable bounds using some additional smoothness assumption on the reaction term. For the sake of simplicity, we consider a scalar formulation of the problem:

\[
\begin{cases}
\frac{\partial n_e}{\partial t} = \frac{1}{\varepsilon} \text{div} (D \nabla n_e - \chi n_e \nabla K(x)) + f(x, n_e), & x \in \Omega, \ t > 0, \\
D \frac{\partial n_e}{\partial \nu} - \chi n_e \frac{\partial K(x)}{\partial \nu} = 0, & x \in \partial \Omega, \ t > 0, \\
n_e(x, 0) = n_0(x), & x \in \Omega,
\end{cases}
\]

and assume a standard condition to eliminate blow-up of positive solutions to (3):

**Hypothesis 2.** The function \( f : \Omega \times \mathbb{R} \to \mathbb{R} \) satisfies the following:

\( i \) \( f(x, 0) = 0, \ \forall x \in \Omega. \)

\( ii \) There exists a constant \( C > 0 \) such that \( \forall x \in \Omega \) and \( \forall u \in \mathbb{R} \) with \( |u| \geq C \), we have \( f(x, u) \leq 0 \).

The ecological significance of these hypotheses lies in two considerations: the first is that there is no spontaneous generation of individuals, and the second is that the population grows nowhere indefinitely, their growth is limited for example by the finite amount of food available in the environment.

3.1.1. Main features of both problems. We proceed to show that positive solutions are defined on \([0, +\infty)\) and are globally bounded by some constant depending on the initial data as shown in the following lemma:

**Lemma 3.1.** Under Hypotheses 1 and 2, for each initial data \( N_0 > 0 \), the corresponding solution \( N(t) \) to (6) is positive and defined on \([0, +\infty)\). Furthermore there exists a constant \( K(N_0) > 0 \) such that \( 0 < N(t) < K(N_0) \) for all \( t \in [0, +\infty) \).
Proof. The uniqueness of solutions together with $F(0) = 0$ ensures positivity of solutions to (6), that is, if $N_0 > 0$, then there exists a non-negative real $t_{\text{max}}$ such that $N(t) > 0$ for all $t \in [0, t_{\text{max}})$.

To prove that positive solutions are defined on $[0, +\infty)$ and are globally bounded, we follow the same techniques as used in the proof of Lemma 1 in [20] with taking $C^* = C[1/\lambda(x)]$ instead of $C^* = C\Omega$. Choosing $K(N_0) := \max(N_0, C^*) > 0$ allows to complete the proof of the lemma. 

Focusing on nonnegative solutions to $(CP)_e$, we will give global existence and a monotonicity result of nonnegative solutions. The following proposition holds:

**Proposition 2.** If the initial data $n_0 \in C(\overline{\Omega})$ is nonnegative, then there exists a non-negative real $T_{\text{max}}$ such that the corresponding maximal solution $n_e$ satisfies $n_e(x, t) \geq 0$, $\forall x \in \Omega$, $\forall t \in [0, T_{\text{max}})$.

Proof. We introduce the notation:

for all $\psi \in C(\overline{\Omega})$, $\psi^+(x) := \max(\psi(x), 0)$ and $\psi^-(x) := \max(-\psi(x), 0)$.

Multiply both sides of $(CP)_e$ by $g_i(x)^{-1}n_e(x, t)$ and integrating on $\Omega$, we have

$$
\int_\Omega \frac{\partial n_e}{\partial t} n_e^+ g(x)^{-1} dx = \frac{D}{\varepsilon} \int_\Omega \text{div} \left( g\nabla (n_e g(x)^{-1}) \right) n_e^- g(x)^{-1} dx + \int_\Omega f(x, n_e) n_e^- g(x)^{-1} dx,
$$

where $g(x) = e^{\frac{K(x)}{\varepsilon}}$.

After applying a Green formula and taking into account the Neumann boundary condition, we obtain that $\forall \psi \in D(A)$:

$$
\int_\Omega \text{div} \left( g(x)\nabla \psi(x) \right) \psi^-(x) dx = - \int_\Omega g(x) \nabla \psi(x) \nabla \psi^-(x) dx = \int_\Omega g(x) \|\nabla \psi^-(x)\|^2 dx \geq 0. \tag{8}
$$

Taking into account that $n_e(x, t) = n_e^+(x, t) - n_e^-(x, t)$ and the estimation (8), we have

$$
\frac{1}{2} \frac{d}{dt} \int_\Omega \left[ n_e^+ \right]^2 g(x)^{-1} dx \leq - \int_\Omega f(x, n_e) n_e^- g(x)^{-1} dx \leq \int_\Omega |f(x, n_e)| n_e^- |g(x)^{-1}| dx.
$$

Fixing $T \in (0, T_{\text{max}})$, $T < +\infty$, we have $\forall t \in [0, T]$:

$$
|n_e(x, t)| \leq \sup_{t \in [0, T]} \|n_e(\cdot, t)\|_\infty := \gamma(T) < +\infty.
$$

This estimation together with Hypotheses 1 and 2-(i) yield, $\forall t \in [0, T]$, $\forall u \in \overline{\Omega}$:

$$
|f(x, n_e)| = |f(x, n_e(x, t))| = |f(x, n_e(x, t)) - f(x, 0)| \leq h(x, n_e(x, t), 0)|n_e(x, t)| \leq R(T)|n_e(x, t)|
$$

for some constant $R(T) > 0$,

$$
R(T) = \sup \{h(x, u, 0); (x, u) \in \text{the compact } \overline{\Omega} \times [-\gamma(T), \gamma(T)]\}.
$$

To simplify we set $v(t) := \int_\Omega \left[ n_e^-(x, t) \right]^2 g(x)^{-1} dx$. Then we have for $t \in [0, T]$:

$$
\frac{1}{2} v'(t) \leq R(T) \int_\Omega \left[ n_e(x, t) \right] |n_e^-(x, t)| g(x)^{-1} dx = R(T)v(t).
$$
Grönwall’s lemma leads to $0 \leq v(t) \leq v(0)e^{2R(T)t}$. The nonnegativity of the initial data $n_0$ assures that $v(0) = 0$, which implies that $n_\varepsilon(x, t) = 0$, $\forall t \in [0, T]$. This equality holds for all $T \in (0, T_{\max})$. Then we deduce that $n_\varepsilon(x, t) \geq 0$, $\forall (x, t) \in \Omega \times [0, T_{\max})$. That completes the proof.

Now, we give the following monotonicity result:

**Corollary 1.** Let $n_\varepsilon$ and $v_\varepsilon$ be two continuous solutions to $(CP)_\varepsilon$ both defined on an interval $[0, T]$, $T > 0$, with respective initial conditions $n_0$, $v_0 \in C(\Omega)$ such that $n_0(x) \geq v_0(x)$, $x \in \Omega$. Then,

$$\forall x \in \Omega, \forall t \in [0, T], \ n_\varepsilon(x, t) \geq v_\varepsilon(x, t).$$

**Proof.** Similar arguments to those in the proof of Corollary 2 in [20] lead to the monotonicity result.

The following result concerns the existence of global solutions to $(CP)_\varepsilon$:

**Proposition 3.** The continuous solutions to $(CP)_\varepsilon$, corresponding to nonnegative continuous initial data are defined on $[0, +\infty)$ and are uniformly bounded on $t$ and on $\varepsilon > 0$.

**Proof.** Let $n_\varepsilon(., t)$ be the nonnegative maximal solution defined on $[0, T_{\max})$, corresponding to initial data $n_0 \in C(\Omega)$, $n_0 \geq 0$.

Setting $w_\varepsilon(x, t) := g(x)^{-1}n_\varepsilon(x, t)$ in $(CP)_\varepsilon$, we get:

$$\frac{\partial w_\varepsilon}{\partial t} = \frac{D}{\varepsilon}\text{div}(g\nabla w_\varepsilon) + f(x, gw_\varepsilon), \ x \in \Omega, \ t > 0,$$

completed with Neumann boundary conditions: $\partial w_\varepsilon/\partial \nu = 0$, $x \in \partial \Omega$, $t > 0$, plus initial conditions: $w_0(x, 0) = g(x)^{-1}n_0(x)$, $x \in \Omega$.

By introducing the notation $C_0(n_0) = \max(C, ||n_0||_\infty)$, where $C > 0$ is the constant mentioned in Hypothesis 2-(ii), we multiply both sides of Equation (9) by $(w_\varepsilon(., t) - C_0(w_0))^+$, $C_0(w_0) = ||1/g||_\infty C_0(n_0)$, and integrating on $\Omega$, similar calculations to those in the proof of Proposition 2 lead to

$$\frac{1}{2} \frac{d}{dt} \int_\Omega [(w_\varepsilon(x, t) - C_0(w_0))^+]^2 g(x)dx \leq \int_\Omega f(x, gw_\varepsilon(x, t))(w_\varepsilon(x, t) - C_0(w_0))^+ dx.$$

If $0 \leq w_\varepsilon \leq C_0(w_0)$, we have $(w_\varepsilon(x, t) - C_0(w_0))^+ = 0$, and if $w_\varepsilon \geq C_0(w_0)$, this inequality implies $f(x, gw_\varepsilon(x, t)) \leq 0$. In both cases, we conclude that

$$\frac{1}{2} \frac{d}{dt} \int_\Omega [(w_\varepsilon(x, t) - C_0(w_0))^+]^2 g(x)dx \leq 0,$$

which gives $(w_\varepsilon(x, t) - C_0(w_0))^+ = 0$ and then

$$\forall (x, t) \in \Omega \times [0, T_{\max}), \ 0 \leq w_\varepsilon(x, t) \leq C_0(w_0).$$

This means that

$$\forall (x, t) \in \Omega \times [0, T_{\max}), \ 0 \leq n_\varepsilon(x, t) \leq C_1(n_0).$$

This implies that $T_{\max} = +\infty$ and $\sup_{t \geq 0} ||n_\varepsilon(., t)||_\infty \leq C_1(n_0).$
3.1.2. Comparison result between both models. In this subsection, we will give an approximation result for the solutions to the perturbed model in terms of that of the aggregated model, for \( \varepsilon > 0 \) small enough. This approximation result is established in the following theorem:

**Theorem 3.2.** For each nonnegative initial data \( n_0 \in C(\Omega) \), the two time scales reaction-diffusion model (3) has a unique classical nonnegative global solution \( n_\varepsilon(x,t) \) which can be written as:

\[
\forall x \in \Omega, \forall t > 0, \ n_\varepsilon(x,t) = \lambda(x)N(t) + r_\varepsilon(x,t),
\]

where \( N(t) \) is the solution to the aggregated model (6) corresponding to the initial data \( N(0) = \int_\Omega n_0(x)dx \) and

\[
\sup_{x \in \Omega} |r_\varepsilon(x,t)| \leq c_1 \varepsilon e^{c_2 t} + c_3 \varepsilon^{-\alpha^* t/\varepsilon}; \ t > 0, \ \varepsilon > 0,
\]

where \( c_1, c_2, \) and \( c_3 \) are positive constants depending on the initial value \( n_0 \) and the equilibria of the fast dynamics of the population \( \lambda \), and \( \alpha^* > 0 \) is the constant mentioned in Theorem 2 in [20].

**Proof.** We follow the same arguments as in [20]. Let us consider a solution to Problem (CP)\( _\varepsilon \), \( n_\varepsilon(t) := \lambda N_\varepsilon(t) + \rho_\varepsilon(t) \), corresponding to a nonnegative initial data \( n_0 = \lambda N_0 + \rho_0 \in C(\Omega) \).

Using the fact that \( n_\varepsilon \) is non-negative, defined on \([0, +\infty)\) and uniformly bounded with respect to \( t \) and \( \varepsilon \), we can introduce the bound:

\[
\|F_S(n_\varepsilon(\sigma))\|_\infty \leq C_1 \|F(n_\varepsilon(\sigma)) - F(0)\|_\infty
\]

\[
\leq C_2(n_0) \|n_\varepsilon(\sigma)\|_\infty \leq C_3(n_0).
\]

The previous bound together with the following variation of constants formula:

\[
\rho_\varepsilon(t) = T_S(t/\varepsilon)\rho_0 + \int_0^t T_S((t - \sigma)/\varepsilon) (F_S(N_\varepsilon(\sigma)\lambda + \rho_\varepsilon(\sigma))) d\sigma,
\]

where \( T_S(t/\varepsilon) \) and \( F_S \) represent respectively the restriction of \( T_0(t/\varepsilon) \) and \( F \) to \( S = \text{Im} A \), provide the following estimation, valid for \( t \geq 0, \ \varepsilon > 0 \):

\[
\|\rho_\varepsilon(t)\|_\infty \leq C_1 e^{-\alpha^* t/\varepsilon} \|\rho_0\|_\infty + C_2(n_0)\varepsilon.
\]

Now, we will proceed to estimate \( y_\varepsilon(t) = N_\varepsilon(t) - N(t) \).

Bearing in mind the bounds:

\[
\forall x \in \Omega, \forall t \geq 0, \ |N(t)| \leq K(N_0) \text{ and } |n_\varepsilon(x,t)| \leq K_0(n_0),
\]

and the local Lipschitz continuity of operator \( F \) we have, for \( t > 0 \):

\[
|y_\varepsilon(t)| \leq \int_0^t \left( \int_\Omega f(x, \lambda(x)N_\varepsilon(\sigma) + \rho_\varepsilon(\sigma) - f(x, \lambda(x)N(\sigma)) \right) d\sigma
\]

\[
\leq H_0(n_0, \lambda) \left[ \int_0^t |y_\varepsilon(\sigma)| d\sigma + \int_0^t \left( \int_\Omega |\rho_\varepsilon(\sigma)(x)| dx \right) d\sigma \right]
\]

for some constant \( H_0(n_0, \lambda) > 0 \).

On the other hand, we have

\[
\int_0^t \left( \int_\Omega |\rho_\varepsilon(\sigma)(x)| dx \right) d\sigma \leq |\Omega| \int_0^t \left[ C_1 e^{-\alpha^* \varepsilon/\varepsilon} \|\rho_0\|_\infty + C_2(n_0)\varepsilon \right] d\sigma
\]

\[
\leq C_1^*(n_0)\varepsilon(1 + t)
\]

for some constant \( C_1^*(n_0) > 0 \), depending on the initial value \( \|\rho_0\|_\infty \).
Therefore:

$$|y_\varepsilon(t)| \leq H_0(n_0, \lambda) \left( \int_0^t |y_\varepsilon(\sigma)| \, d\sigma + C^*_1(n_0) \varepsilon(1 + t) \right).$$

The Gronwall inequality provides, for $t > 0$:

$$|y_\varepsilon(t)| \leq C^*_2(n_0, \lambda) \varepsilon(1 + t)e^{H_0(n_0, \lambda)t}$$

for some constant $C^*_2(n_0, \lambda) > 0$.

This completes the proof, together with

$$r_\varepsilon(x, t) = n_\varepsilon(x, t) - \lambda(x)N(t) = \lambda(x) (N_\varepsilon(t) - N(t)) + \rho_\varepsilon(x, t).$$

We have shown that the behavior of solutions to the two-time reaction-diffusion model can be given through the solutions to the aggregated model, which makes easier the study of the asymptotic behavior of the perturbed problem. This approximation result means that $n_\varepsilon(x, t)$ tends when $\varepsilon \to 0_+$ and $t > 0$ fixed, to an inhomogeneous spatial distribution given by the solution to the aggregated model and the fast equilibria. Moreover, this convergence is uniform with respect to $x$ in $\Omega$ and with respect to $t$ on each compact interval $[t_0, T]$ with $0 < t_0 < T < +\infty$.

4. Application to a spatially distributed population growing logistically with fast diffusion and chemotaxis. We have seen that it is difficult to find a good approximation of the error: Theorem 3.2 only gives that the error is lower than a function that is growing exponentially with time for fixed $\varepsilon$. Obtaining a better approximation of the error is a very difficult task when considering generic functions. To this end, in the following section, we will optimize the error bound and validate numerically the above studies to a spatially distributed population model with fast diffusion and chemotaxis.

4.1. Presentation of a spatially distributed population growing logistically with fast diffusion and chemotaxis. In ecology, the ideal free distribution (IFD) predicts that animals distribute themselves among several patches of resources in a way that is proportional to the amount of resources available in each patch. In meta-population models, the space is represented as a discrete network of patches connected by migrations. In such models, the local resource availability is represented by local carrying capacities, noted $K_i$ for patch $i$. It can be shown that if one assumes that migration rates from patch $i$ to any patch $k$ are inversely proportional to the departure patch carrying capacity $K_i$, the migration process leads to an equilibrium spatial distribution of animals among patches that is precisely the IFD. Such an example for fishery models can be found in [6] where fishes distribute in different fishing regions proportionally to the resource available in each of them.

However, in the present paper, the environment is represented as a continuous space. In that case, the carrying capacity becomes a continuous function of the space, i.e. a function $K(x)$ with space variable $x$. In this type of spatial continuous models, animal movement can be represented by the use of chemotaxic terms in reaction-diffusion models. The chemotaxis is the movement of an animal in response to resource gradients. Therefore, animals are assumed to move in the direction of higher gradients of food leading to spatial distributions that are similar to IFD in the discrete case.
The model reads as follows:

\[
\begin{cases}
\frac{\partial n_\varepsilon}{\partial t} = \frac{1}{\varepsilon} \text{div} \left( D n_\varepsilon - \chi n_\varepsilon \nabla K \right) + r n_\varepsilon \left( 1 - \frac{n_\varepsilon}{K} \right), & x \in \Omega, \ t \in (0, T), \\
D \frac{\partial n_\varepsilon}{\partial \nu} - \chi n_\varepsilon \frac{\partial K}{\partial \nu} (x) = 0, & x \in \partial \Omega, \ t \in (0, T), \\
n_\varepsilon(x, 0) = n_0(x), & x \in \Omega,
\end{cases}
\] (11)

where \(n_\varepsilon(x, t)\) represents the population density at position \(x\) in time \(t\). The function representing the population growth defined by

\[f(x, n_\varepsilon(x, t)) = r n_\varepsilon(x, t) \left( 1 - \frac{n_\varepsilon(x, t)}{K(x)} \right),\]

where \(r > 0\) is the growth rate, satisfies Hypotheses 1 and 2, thus aggregation of variables methods can be applied. The aggregated model of (11) is

\[
\begin{cases}
N'(t) = \int_\Omega f(x, \lambda(x) N(t)) \, dx = r N(t) \left( 1 - \frac{N(t)}{K^*} \right), \\
N(0) = N_0 = \int_\Omega n_0(x) \, dx,
\end{cases}
\] (12)

where the global variable \(N(t)\) is the total population and

\[K^* = \left( \int_\Omega g(x) \, dx \right)^2 \left( \int_\Omega \frac{g(x)^2}{K(x)} \, dx \right)^{-1}\]

is the new homogeneous carrying capacity for the aggregated model, where we use \(g(x) = e^{\chi K(x)/D}\).

We notice that the new homogeneous carrying capacity \(K^*\) for the aggregated model (12) satisfies

\[K^* \leq K_T := \int_\Omega K(x) \, dx.\]

In fact,

\[
\begin{align*}
K^* &= \left( \int_\Omega g(x) \, dx \right)^2 \left( \int_\Omega \frac{g(x)^2}{K(x)} \, dx \right)^{-1} \\
&\leq \int_\Omega K(x) \, dx \int_\Omega \frac{g(x)^2}{K(x)} \, dx \left( \int_\Omega \frac{g(x)^2}{K(x)} \, dx \right)^{-1} \\
&\leq K_T.
\end{align*}
\]

4.2. Optimization of the error bound. In this subsection, we are providing a better approximation of the error bound mentioned in Theorem 3.2, between the solution to a population dynamics model and its aggregated one. Comparison result between the solutions to the two-time reaction-diffusion model (11) and the solutions to the aggregated model is given by the following theorem:

**Theorem 4.1.** For each nonnegative initial data \(n_0 \in C(\Omega)\), the two time scales reaction-diffusion-chemotaxis model (11) has a unique classical nonnegative global solution \(n_\varepsilon(x, t)\) which can be written as:

\[\forall x \in \Omega, \forall t > 0, \ n_\varepsilon(x, t) = \lambda(x) N(t) + r_\varepsilon(x, t),\]

where \(N(t)\) is the solution to the aggregated model (12) corresponding to the initial data \(N(0) = \int_\Omega n_0(x) \, dx\). Furthermore, there exists \(\varepsilon_0 > 0\) and \(t_0(\varepsilon_0) \geq 0\) such that

\[\|r_\varepsilon(\cdot, t)\|_\infty \leq c_1 (\sqrt{\varepsilon} + \varepsilon + \varepsilon e^{-\varepsilon t}) + c_3 e^{-\alpha^* t/\varepsilon}; \ t > t_0(\varepsilon_0), \ \varepsilon < \varepsilon_0,\]
where $c_1$, $c_2$, and $c_3$ are positive constants depending on the initial value $n_0$ and the equilibria of the fast dynamics of the population $\lambda$, and $\alpha^*>0$ is the constant mentioned in Theorem 2 in [20].

Before introducing the proof of this theorem, we need the following lemma:

**Lemma 4.2.** Under the assumptions of Theorem 4.1. For $\theta \in [0,1/2)$, there exist $\varepsilon_0>0$ and $t_0(\varepsilon_0)\geq 0$ such that

$$\forall t > t_0(\varepsilon_0), \quad \left(1 - \frac{N_\varepsilon(t) + N(t)}{K^*}\right) < -\theta,$$

for fixed $\varepsilon < \varepsilon_0$.

**Proof.** Let $\theta \in [0,1/2)$. We will proceed to ensure the existence of $\varepsilon_0$ and $t_0(\varepsilon_0)$ such that

$$\forall t > t_0(\varepsilon_0), \quad N(t) + N_\varepsilon(t) > K^*(1 + \theta).$$

for fixed $\varepsilon < \varepsilon_0$.

First, the total population $N_\varepsilon(t) = \int_\Omega n_\varepsilon(x,t)dx$ of the global model (11) satisfies the following

$$N_\varepsilon'(t) = \int_\Omega r n_\varepsilon(x,t) \left(1 - \frac{n_\varepsilon(x,t)}{K(x)}\right) dx \quad (13)$$

with $N_\varepsilon(0) = N_0 = \int_\Omega n_0(x)dx$.

Multiplying both sides of Equation (13) by $N_\varepsilon(t) - K^*$, we get

$$\frac{1}{2} \left( (N_\varepsilon(t) - K^*)^2 \right)' = r (N_\varepsilon(t) - K^*) \int_\Omega n_\varepsilon(x,t) \left(1 - \frac{n_\varepsilon(x,t)}{K(x)}\right) dx. \quad (14)$$

Bearing in mind that $\int_\Omega \lambda(x)dx = 1$, $1/K^* = \int_\Omega \lambda(x)^2/K(x)dx$, and $n_\varepsilon = \lambda N_\varepsilon + \rho_\varepsilon$, Equation (14) yields

$$\frac{1}{2} \left( (N_\varepsilon(t) - K^*)^2 \right)' \leq \frac{-r N_\varepsilon(t)}{K^*} (N_\varepsilon(t) - K^*)^2 + 2r N_\varepsilon(t)||1/K||_\infty |N_\varepsilon(t) - K^*| ||\rho_\varepsilon(.,t)||_\infty.$$

Using the inequality $ab \leq (a^2/\gamma + \beta^2)/2$, the previous inequality becomes,

$$\frac{1}{2} \left( (N_\varepsilon(t) - K^*)^2 \right)' \leq \frac{-r N_\varepsilon(t)}{2K^*} (N_\varepsilon(t) - K^*)^2 + 2r N_\varepsilon(t) K^* ||1/K||_\infty^2 ||\rho_\varepsilon(.,t)||_\infty^2,$$

this gives, using the non-neagativity and boundedness of $n_\varepsilon$,

$$\left( (N_\varepsilon(t) - K^*)^2 \right)' \leq -\beta (N_\varepsilon(t) - K^*)^2 + C_3(n_0)||\rho_\varepsilon(.,t)||_\infty^2,$$

where $0 < \beta := r \inf\{N_\varepsilon(t), \ t \geq 0\}/K^*, \inf\{N_\varepsilon(t), \ t \geq 0\} > 0$.

The Gronwall inequality provides, for $t > 0$:

$$(N_\varepsilon(t) - K^*)^2 \leq (N_\varepsilon(0) - K^*)^2 e^{-\beta t} + C_3(n_0) \int_0^t e^{\beta(s-t)} ||\rho_\varepsilon(.,s)||_\infty^2 ds. \quad (15)$$

On the other hand, we have

$$\int_0^t e^{\beta(s-t)} ||\rho_\varepsilon(.,s)||_\infty^2 ds \leq e^{-\beta t} \int_0^t 2C_1 e^{(\beta - 2\alpha^*/\varepsilon)^s ||\rho_0||_\infty + 2C_2(n_0)\varepsilon^2 e^{\beta s} ds$$

$$\leq C(\rho_0) e^{-\beta t} \int_0^t e^{(\beta - 2\alpha^*/\varepsilon)s} ds + C(n_0)\varepsilon^2.$$
Proof of Theorem 4.1. We use in this proof the same notations and arguments introduced in the proof of Theorem 3.2. The equation for the error \(\varepsilon < \varepsilon\) is written as

\[
\int_0^t e^{\beta(s-t)} ||\rho_x(., s)||^2_\infty ds \leq C(\rho_0)(te^{-\beta t} + \varepsilon^2),
\]

otherwise we have

\[
\int_0^t e^{\beta(s-t)} ||\rho_x(., s)||^2_\infty ds \leq C(\rho_0) \frac{\varepsilon}{\varepsilon_\beta - 2\alpha^*} \left(e^{-2\alpha^*/\varepsilon} - e^{-\beta t}\right) + C(n_0)\varepsilon^2.
\]

In both cases, using the previous bounds in (15), we get \(|N_\varepsilon(t) - K^*|\) tends to \(C^*\varepsilon\) as \(t \to +\infty\), for fixed \(\varepsilon\).

In addition, we notice that the solution to the aggregated model (12) is given by

\[
N(t) = \frac{K^*N_0}{(K^* - N_0)e^{-rt} + N_0},
\]

and \(N(t)\) tends to \(K^*\) when \(t \to +\infty\).

The fact that \(|N_\varepsilon(t) - K^*| + N(t) - K^*\) tends to \(C^*\varepsilon\) as \(t \to +\infty\) yields, for all \(\alpha > 0\), there exists \(t_0 \geq 0\) such that for all \(t > t_0\) we have

\[
2K^* - \alpha - C^*\varepsilon < N(t) + N_\varepsilon(t) < 2K^* + \alpha + C^*\varepsilon.
\]

Setting \(\varepsilon_0\) such as \(0 < \varepsilon_0 = K^*(1 - \theta)/C^*.\) For \(\varepsilon < \varepsilon_0\), we have

\[
2K^* - \alpha - C^*\varepsilon_0 < N(t) + N_\varepsilon(t) < 2K^* + \alpha + C^*\varepsilon_0.
\]

We choose \(\alpha = K^*(1 - \theta) - C^*\varepsilon_0\), then, there exists \(t_0(\varepsilon_0) \geq 0\) such that for all \(t > t_0(\varepsilon_0)\) and \(\varepsilon < \varepsilon_0\) we have

\[
N(t) + N_\varepsilon(t) > 2K^* - \alpha - C^*\varepsilon_0 = K^*(1 + \theta).
\]

As we wanted to prove.

\[\square\]

Proof of Theorem 4.1. We use in this proof the same notations and arguments introduced in the proof of Theorem 3.2. The equation for the error \(y_\varepsilon(t) := N_\varepsilon(t) - N(t)\) is written as

\[
y_\varepsilon(t) = \int_\Omega \left[f(x, \lambda(x)N_\varepsilon(t) + \rho_x(x, t)) - f(x, \lambda(x)N(t))\right] dx
\]

\[
= \int_\Omega \left[f(x, \lambda(x)N_\varepsilon(t) + \rho_x(x, t)) - f(x, \lambda(x)N_\varepsilon(t))\right] dx
\]

\[
+ \int_\Omega \left[f(x, \lambda(x)N_\varepsilon(t)) - f(x, \lambda(x)N(t))\right] dx.
\]

Multiplying both sides of this equation by \(y_\varepsilon(t)\) and using Hypothesis 1, we get

\[
\frac{1}{2} (y_\varepsilon^2(t))' \leq C_1(n_0)||\rho_x(., t)||_\infty|y_\varepsilon(t)| + k(t)y_\varepsilon^2(t),
\]

for some constant \(C_1(n_0) > 0\), where we introduced the notation

\[
k(t) := r \left(1 - \frac{N_\varepsilon(t) + N(t)}{K^*}\right).
\]

Let \(\theta \in ]0, 1/2\) then, using Lemma 4.2, there exist \(\varepsilon_0 > 0\) and \(t_0(\varepsilon_0) \geq 0\) such that

\[
\forall t > t_0(\varepsilon_0),\ 1 - \frac{N_\varepsilon(t) + N(t)}{K^*} < -\theta,
\]

for \(\varepsilon < \varepsilon_0\).
Using $ab \leq (a^2/\nu + \nu b^2)/2$, the inequality (16) becomes,

$$(y^2(t))' \leq \frac{C^2(n_0)}{\nu}||\rho_\varepsilon(., t)||^2_{\infty} - \nu y^2(t).$$

with $\nu = r\theta$.

The Gronwall inequality provides, for $t > t_0$:

$$y^2(t) \leq y^2(t_0)e^{-\nu(t-t_0)} + C_2(n_0) \int_{t_0}^{t} e^{\nu(\sigma-t)}||\rho_\varepsilon(., \sigma)||^2_{\infty} d\sigma.$$

On the other hand, we recall that

$$\int_{t_0}^{t} e^{\nu(\sigma-t)}||\rho_\varepsilon(., \sigma)||^2_{\infty} d\sigma \leq \int_{0}^{t} e^{\nu(\sigma-t)}||\rho_\varepsilon(., \sigma)||^2_{\infty} d\sigma \leq \int_{0}^{t} e^{\nu(\sigma-t)} \left[C_1 e^{-2\alpha^*\sigma/\varepsilon} \|\rho_0\|_{\infty} + C_3(n_0)\varepsilon^2 \right] d\sigma \leq C_4(n_0)(\varepsilon + \varepsilon^2)$$

for some constant $C_4(n_0) > 0$.

Using the bound (10) in the proof of Theorem 3.2, we can get $y^2(t_0) = C_5(n_0, t_0)\varepsilon^2$. Finally, we have

$$y^2(t) \leq C_0(n_0, t_0)(\varepsilon^2 e^{-\nu t} + \varepsilon + \varepsilon^2).$$

This completes the proof. 

4.3. **Comparison of the numerical solution of a global model with its aggregated one.** We are providing in this subsection a comparison result between the numerical solution to the model (11) and its aggregated one (12), when the parameter $\varepsilon > 0$ is small enough. To this end, we begin with the resolution of (11) using finite volume method (see [8, 14, 24], among others). The choice of this method for our problem is due to the conservative aspect that is suitable to the conservation law of Problem (11). We use a semi-implicit finite volume scheme, triangular mesh of $\Omega = (0, 1) \times (0, 1)$ with maximum edge length $h = 0.05$, and a time step $\Delta t = 10^{-3}$ to compute numerical solutions to (11). We perform the numerical experiments with the following data $D = 3, \chi = 0.1, r = 0.2$, and $K(x_1, x_2) = x_1^2 + x_1 x_2^2 + 1$. The simulation results for the perturbed model (11) and its aggregated model (12) are shown in Figures 1 and 2, for $\varepsilon = 1e - 1$, corresponding to initial data $n_0(x_1, x_2) = x_1 x_2 + 0.4$.

An approximate solution to the model (11) based on aggregation of variables methods is given by the solution to the aggregated model (12) which is a nonlinear ordinary differential equation whose exact solution is given by

$$N(t) = \frac{K^* N_0}{(K^* - N_0) e^{-rt} + N_0}$$

we recall that $K^* = (\int_{\Omega} g(x) dx)^2 / \int_{\Omega} g(x)^2 / K(x) dx$ and $g(x) = e^{\chi K(x)}$. Finally, the approximate solution to the model (11) based on aggregation of variables methods is $\lambda(x) N(t)$. Now, we proceed to give numerical simulation of the approximate solution by considering the same triangulation of $\Omega = (0, 1) \times (0, 1)$ used in the above finite volume scheme, as given in Figure 1.

Figures 1 and 2 represent the numerical solution of the perturbed (11) and aggregated (12) models, and show that the dynamics of the two models get closer with time. One can notice that there is a large difference in spatial distribution between the two models at the beginning of the simulation ($t = 0.2$) in Figure 1: in the
aggregated model, the spatial distribution is calculated as the fast equilibrium, and not obtained from the differential equations. Figure 2 illustrates that the dynamics of total populations are very close for $\varepsilon$ small enough.

According to Figure 3, it is clear that the norm of the error $\|n_\varepsilon(.,t) - \lambda(.)N(t)\|\infty$ between the numerical solution to the model (11) and its aggregated one (12), increases sharply and arrives to a peak at the beginning, after that it decreases dramatically and stabilizes near 0 after some time, for all values of $\varepsilon$. Likewise, the error gradually decreases when $\varepsilon$ tends to 0 and $t$ fixed. In conclusion, we have validated numerically that the asymptotic dynamics of both perturbed and aggregated models are qualitatively the same, and that the error tends towards 0 when $\varepsilon$ decreases.

**Conclusion.** This work provides an application of aggregation of variables methods to a class of two-time reaction-diffusion-chemotaxis models of spatially structured populations with constant diffusion assuming that the evolution processes occur at two different time scales: a slow one for the demography and a fast one for
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Figure 2. Plot of total population of the global model and its approximate solution using aggregation of variables methods for for \( \varepsilon = 1e-1 \). \( K_T := \int_{\Omega} K(x) dx \) stands for the total carrying capacity of the environment and \( K^* \) for the new homogeneous one.

Figure 3. Plot of errors, \( |N_\varepsilon(t) - N(t)| \), (A), and \( \|n_\varepsilon(.,t) - \lambda(.)N(t)\|_\infty \) with \( t \geq 1 \), (B), with respect to time \( t \) for different values of \( \varepsilon; \varepsilon = 1e-1, \varepsilon = 1e-2, \varepsilon = 1e-3 \), and \( \varepsilon = 1e-4 \).

migrations and chemotaxis, with a ratio \( \varepsilon > 0 \) small enough. Such methods allow constructing an aggregated model to approximate their dynamics, which makes easier the study of the asymptotic behavior of the problem. Furthermore, we give an error bound between solutions of both complete and aggregated model for a generic function representing the demography. Optimizing the error bound is a very difficult task when considering generic reaction functions and without assuming
additional hypothesis on the reaction term. To this end, we gave an optimization of the error bound and validated numerically this result for a spatial inter-specific model with constant diffusion and population growth given by a logistic law, in population dynamics.

One should notice that such methods focus on asymptotic dynamics and provide very inaccurate results for the transient part. They should be used only when the modeler needs mainly information on the asymptotic dynamics; it is frequent in ecology, for example, when one wants to know about the persistence of populations on the long term.

The methods described in this paper are intended to be used in many applications, especially in ecology. For example, many previous works used aggregation of variables methods in spatial models of fisheries [6, 16, 18] or conservation ecology [15]. Animals or fish movements are fast compared to demography and economic dynamics, hence slow-fast aggregation methods are very useful to analyze such models. However, the environment has been represented in those articles as a network of discrete patches connected by fast dispersal. The work presented here allows now to extend such studies to the more realistic case of continuous space: chemotaxis is a natural process in the context of ecology since animals move along gradients of resources. The results presented in this paper allow us to revisit the works on Marine Protected Areas, bio-economics of fisheries or wildlife management in the near future.

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