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The Chapman–Enskog procedure for an age-structured population model: initial, boundary and corner layer corrections

Meri Lisi [a], Silvia Totaro [b,*]

[a] *Dipartimento di Matematica Ulisse Dini, Viale Morgagni 67a, 50134 Firenze, Italy*
[b] *Dipartimento di Scienze Matematiche ed Informatiche Roberto Magari, Pian dei Mantellini 44, 53100 Siena, Italy*

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Abstract

We consider a mathematical model of an age-structured population of some fisheries (for example, anchovies, sardines or soles). Two time scales are involved in the problem: the fast time scale for the migration dynamics and the slow time scale for the demographic process. At a first step, we study the so called 'aggregated' system by means of the semigroups theory. Then, we study the asymptotic behaviour of the model by using the Chapman–Enskog procedure. In particular, we study initial, boundary and corner layer effects in order to obtain the exact initial and boundary conditions the approximated solution has to satisfy.

Keywords: Population model; Semigroup theory; Aggregation method; Singular perturbation methods; Chapman–Enskog procedure; Initial, boundary and corner layers

1. Introduction

Several researches concern vertical migrations related to the movement of larvae of fish or early juvenile fish. This is because many fish (for example, anchovies and sardines), but especially

* Corresponding author. Tel.: +39 0577 233740; fax: +39 0577 233730.
E-mail addresses: lisi@math.unifi.it (M. Lisi), totaro@unisi.it (S. Totaro).

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flatfish (like soles), spawn offshore but early juveniles migrate inshore. These migrations towards the sea bed occurs during the day, while the lack of light induces migrations towards the surface. Thus, the process of vertical migration is performed daily, which is a fast time scale compared with that of the demographics process.

In cases of natural events which happen at different time scales, it is common practice to consider those events which happen at the fastest time scale as being instantaneous with respect to the slower ones, in order to use a smaller number of variables or parameters to describe the evolution of the system.

A following matter is to determine how far the results obtained from the reduced system are from the real ones. Many mathematical methods have been developed to study this kind of problems: the best known are averaging methods, singular perturbation methods and aggregation methods.

In the case of the common sole, Solea solea, we have active vertical migrations only during the larval stage, [1]. The study of this stage is interesting also because only one egg over 1–2 millions eggs becomes adult. Moreover, presently, catches of common sole are the greatest one among other commercial fish in Europe.

The model we present takes account of the main characteristics of the dynamics of a sole larval population of the Bay of Biscay, a region of the North Atlantic, along the West Coast of France, extending from the Brittany peninsula in the north, to Spain in the south and which covers an area of approximately 223 000 km^2.

The life of the sole of Bay of Biscay has been intensively studied in the field as well as in laboratory (see, for instance, [1–3], and the references quoted therein).

The life cycle of a sole can be divided into four stages: egg, larva, juvenile and adult.

The model proposed by Arino et al. in [2] takes as the state variables the densities of the four stages as functions of time, age and distance from the coast. However, it seems to be important to consider also the daily ascending migrations of larvae after sunset and the descending ones before sunrise.

Vertical displacements are the result of a number of factors: sea turbulence, reaction to light, quest for food and energy cost minimization (a possible explanation for night migration towards the surface, which is generally warmer than the deeper layers of the sea and thus, in particular, more suited for digestion). An evolutionary advantage of migration towards the lower layer of the sea during the day could be that it gives better protection to small fish from predation by large fish, [4].

Thus, we include the influence of depth in the demography of larvae, studying a model of an age-structured population divided into N spatial patches (with different mortality rates) that distinguishes the two time scales involved.

It is important to notice that, even if we shall talk about soles, the model we shall study in this paper covers a big variety of situations in the modelling of fish population dynamics, namely, the segment of fish life cycle where fish undergo movements in the water column, according to an essentially circadian rhythm, [4]. For example, in the case of the common anchovy, Engraulis encrasicholus, we have vertical migrations during its whole life, [5].

The evolution of the population is described in a standard way as follows, [3,6]:

$$\frac{\partial n_i}{\partial t} + \frac{\partial n_i}{\partial a} = -\mu_i(a)n_i + \frac{1}{\varepsilon}\left[\sum_{j=1}^{N} k_{ij}(a)n_j - \sum_{j=1}^{N} k_{ji}(a)n_i\right], \tag{1}$$