

A METHOD FOR NUMERICAL ANALYSIS OF A LOTKA-VOLTERRA FOOD WEB MODEL

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Abstract. We study the existence, uniqueness and continuous dependence on initial data of the solution for a Lotka-Volterra cascade model with one basal species and hierarchal predation. A uniquely solvable, stable, semi-implicit finite-difference scheme is proposed for this system that converges to the true solution uniformly in a finite interval.

Key words. Finite difference scheme, convergence.

1. Introduction

In a food web, a species is called *basal* if it is prey but is not predatory, *intermediate* if it is both prey and predator and *top* if it is only a predator; the composition of predator and prey relationships in a food web is referred to as its *trophic structure* and individuals levels as *trophic levels*. We use the word *population* to mean abundance or biomass of a species. If we let $x(t)$, $y(t)$ and $z(t)$ represent the populations of basal, intermediate and top species respectively in a food web at time t , a sensible model for the trophic structure of a closed food-web population at time t is a generalized Lotka-Volterra system of the form

$$(1.1) \quad x' = ax - bx^2 - cxy - dxz,$$

$$(1.2) \quad y' = -ey + fxy - gyz,$$

$$(1.3) \quad z' = -hz + ixz + jyz,$$

$$(1.4) \quad x(0) = x_0, \quad y(0) = y_0 \text{ and } z(0) = z_0,$$

where $a, b, \dots, j > 0$. In this model, the basal species with population x has intrinsic growth rate a with environmental carrying capacity a/b and the strength of the effect of predation from the other two species is measured by interaction-term coefficients c and d . As the top species with population z preys on both the basal and intermediate species, its interaction terms xz and yz have positive coefficients since z increases under interaction with each of the other species. The intermediate species with population y grows through interaction with the basal species but declines through interaction with the top species.

This system is a special case of the well-known *Lotka-Volterra cascade model* (cf. [3]) given by

$$(1.5) \quad x'_i(t) = x_i(t) \left[e_i + \sum_{j=1}^n p_{ij} x_j(t) \right], \quad i = 1, 2, \dots, n$$

where $x_i(t)$ is the population of species i , e_i is the intrinsic growth or decline rate of species i and p_{ij} is the interaction coefficient between species i and j . The finite-difference scheme we introduce here for $n = 3$ applies to predict the population in the case of only one basal species, so that $p_{11} > 0$ and $p_{22} = p_{33} = 0$ in (1.5), and with *hierarchical predation*, meaning that each successive species preys on those below it. This means that in (1.5) species j preys on species i if and only if $i < j$, so that $p_{ij} < 0$ if $i < j$ and $p_{ij} > 0$ if $i > j$.

Although we present a numerical scheme only for the case of a trophic structure involving one basal and two non-basal species such as rabbits, foxes and wolves, our scheme can be applied to any geographically limited food web involving one basal species and any number of non-basal but hierarchical predators. We explain how this is done Section 3. Additionally, even though we analyze (1.1)-(1.4) specifically for three individual species, it may be thought of as representing an entire web of distinct basal species along with multiple species of intermediate and top predators, as long as no information about interaction between species at the same relative trophic level is sought.

The method used to discretize (1.1)-(1.4) in Section 3 is reminiscent of nonstandard finite difference schemes as proposed in [4] and [5], as well as in [6], [7] and [8] in the sense that it is not explicit in time. However, in these references, the methods proposed seek to find exact schemes that correctly exhibit the geometry of limit cycles when applied to various differential equations and systems. There it is demonstrated that a numerical scheme that is chosen semi-implicit in time and whose time step faithfully mimics the geometry of limit cycles by following certain rules has impressive numerical results. For an excellent summary of these methods, see [10].

The numerical method proposed in this paper uses a semi-implicit scheme as well, but in spirit more closely follows methods presented in [1], [2] and [11]. This is because we have little *a priori* global knowledge of the geometry of solutions, so although we use mixed time steps for the interaction terms of (1.1)-(1.4), this is done in a way that ensures nonnegativity and stability but still converges uniformly to the true solution. Therefore, instead of knowing properties of the solution and laying out a numerical method to match them as presented for a Lotka-Volterra system in [7], our numerical approach is to use a type of discretization that works for the system, prove that it converges to the solution of the system, then use these results to study the true solution.

It seems that there are very few results on the numerical solutions to the system (1.1)-(1.4) where a discretization is chosen that is shown to have all the desirable properties of a numerical method.

We organize this paper as follows. In Section 2, we prove the existence, uniqueness and global boundedness of the solution (x, y, z) of (1.1)-(1.4). In Section 3, we develop a semi-implicit finite difference scheme for this system and prove that the difference scheme is stable and the numerical approximation converges to the solution of (1.1)-(1.4). In Section 4, some numerical experiments are carried out to study the solution of this system, then finish with some notes on a Hopf bifurcation that arises at a certain critical value.

2. Existence, Uniqueness and Global Boundedness

In order to get a better analysis for the system, we reduce the number of parameters using the nondimensionalization method as in [9] as follows.