

Lotka-Volterra Modeling for Introducing Intraspecific Competition and Multi-Species Extension

Jinran Zeng

*School of Mathematical Sciences, Fudan University, Shanghai, China
23300180071@m.fudan.edu.cn*

Abstract. The classical Lotka-Volterra (LV) model, while foundational, exhibits limitations by neglecting the influence of intraspecific competition within prey and predator populations on their own dynamics, and by restricting interactions to only two species. This study addresses these shortcomings. Firstly, we incorporate intraspecific competition terms into the LV equations and rigorously analyze the structure and stability of the resulting singular (equilibrium) solutions. Sensitivity analysis quantifies the impact of the intraspecific competition strength on key system parameters. Secondly, acknowledging the LV model's similarity in derivation to the logistic model, we construct a generalized multi-species LV model capable of representing complex ecological communities. Crucially, we develop a novel method utilizing Taylor's formula and transfer matrices to compute short-term solutions for this multi-species system. Collectively, this work significantly extends the classical LV framework, provides a computationally feasible approach for multi-species dynamics, and establishes new analytical perspectives on predator-prey interactions incorporating density-dependent feedback.

Keywords: Lotka-Volterra models, Logistic models, singularity stability of planar autonomous systems, transfer matrices, biomathematics

1. Introduction

Predator-prey dynamics constitute a cornerstone of theoretical ecology, with the Lotka-Volterra (LV) model serving as a seminal framework for understanding the fundamental interactions between two species. The standard LV equations elegantly capture the mutual influence between predators and their prey, describing how predation reduces prey numbers while prey abundance fuels predator growth. However, this classical formulation makes simplifying assumptions that limit its applicability to more realistic ecological scenarios.

A key limitation lies in its omission of intraspecific competition. The original LV model derivation focuses solely on the interspecific effects: prey mortality due to predation and predator growth fueled by prey consumption. It implicitly assumes that populations grow or decline solely due to the interaction with the other species, neglecting the crucial reality that fluctuations in a population's own size can significantly regulate its future growth through density-dependent mechanisms like competition for resources (e.g., food, space). This omission overlooks the potential

impact of crowding effects within both prey and predator populations on their intrinsic growth rates and carrying capacities.

Furthermore, the inherent two-species structure of the classic LV model restricts its direct application to natural ecosystems, which are typically complex webs involving multiple interacting species. While the conceptual derivation of the LV model shares parallels with that of the single-species logistic model (which does incorporate intraspecific competition via a carrying capacity term), extending the LV framework to accommodate multiple species remains a significant challenge, particularly regarding analytical tractability and solution computation.

This thesis aims to bridge these gaps and extend the LV paradigm. First, we address the limitation concerning intraspecific competition by explicitly incorporating density-dependent feedback terms into the LV equations. We then conduct a detailed analysis of the modified system, focusing on the structure and stability properties of its singular (equilibrium) solutions. To understand the influence of the intraspecific competition strength, we derive functional relationships for relevant system parameters and perform sensitivity analyses. Second, motivated by the conceptual link between the LV and logistic model derivations, we propose a generalized multi-species LV model designed to represent communities with an arbitrary number of interacting species. A central contribution here is the development of a novel computational approach: leveraging Taylor's formula and transfer matrices, we provide a practical method for approximating short-term solutions to this complex multi-species system.

Through these extensions and the introduction of a new computational technique, this work significantly generalizes the classical Lotka-Volterra model. It provides a more ecologically realistic framework by incorporating intraspecific competition and offers a feasible pathway for analyzing dynamics in multi-species communities, thereby establishing a new perspective on modeling predator-prey and broader ecological interactions.

2. Analysis and improvement of the Lotka-Volterra model

Building upon the limitations of the classical Lotka-Volterra (LV) model identified in the Introduction, specifically its neglect of density-dependent feedback within populations, the following section 2.1 initiates our core analysis by incorporating explicit intraspecific competition terms for both prey and predator species. The primary objective here is to rigorously examine the mathematical and dynamical consequences of this crucial ecological realism. We focus on characterizing the singular points (equilibrium solutions) of the modified model, determining their existence conditions, and conducting a comprehensive stability analysis to understand the long-term behavioral repertoire of the system near these equilibria. Beyond mere stability classification, we quantify the rate of convergence for solutions initiating near the coexistence equilibrium, providing a finer-grained understanding of transient dynamics. Furthermore, recognizing the potential for complex oscillatory behavior, we systematically investigate the Hopf bifurcation phenomena induced by variations in the intraspecific competition strength parameters. This bifurcation analysis, complemented by numerical simulations and phase portraits, reveals the critical parameter thresholds where stable limit cycles emerge, signifying a qualitative shift from damped oscillations to persistent periodic population fluctuations. Collectively, these analyses provide profound insights into how intraspecific competition fundamentally reshapes the predictions of the foundational predator-prey model.

2.1. Lotka-Volterra model with the inclusion of an intraspecific competition term

We first give the original model of Lotka-Volterra [1,2]

$$\begin{cases} \frac{dx}{dt} = x(a - by) \\ \frac{dy}{dt} = y(-c + dx) \end{cases} \quad (1)$$

Here x, y represents the population size of the bait and predator, respectively, $a, -c$ represents the base growth (decline) rate of the population of the bait and predator, respectively, and b, d represents the factor influencing the growth rate of the predator on the bait and the factor influencing the growth rate of the bait on the predator, respectively.

However, when we consider the real natural community, because the number of each population is limited by the environmental capacity, when the number of populations is large, the intraspecific competition will cause the growth rate of the population to decline accordingly, so following the form of the original model of Lotka-Volterra, we can give the modified form of the equation by adding the factor of the influence of intraspecific competition [3].

$$\begin{cases} \frac{dx}{dt} = x(a - by - \varepsilon x) \\ \frac{dy}{dt} = y(-c + dx - \delta y) \end{cases} \quad (2)$$

Here $\varepsilon, \delta > 0$, and assuming $\varepsilon, \delta \ll b, d$, since the main body of the equation is still studying the interaction between the bait and the predator.

2.1.1. Singularity analysis of planar autonomous systems

The above system of differential equations is a planar autonomous system, and to reveal some stability and periodicity properties of this autonomous system, we need to calculate its singularities and analyze its stability and other properties.

2.1.2. Singularity calculation and analysis of the corresponding practical implications

seek to solve (an equation)

$$\begin{cases} x(a - by - \varepsilon x) = 0 \\ y(-c + dx - \delta y) = 0 \end{cases} \quad (3)$$

Four solutions can be obtained $(0,0)$, $(\frac{a}{\varepsilon}, 0)$, $(0, -\frac{c}{\delta})$, (x_0, y_0)
included among these $x_0 = \frac{bc+ad}{\varepsilon\delta+bd}$, $y_0 = \frac{ad-c\varepsilon}{\varepsilon\delta+bd}$

It is easy to see that $(0,0)$ corresponds to a time when both the bait and predator populations are at zero, at which point there will be no change in the system.

$(\frac{a}{\varepsilon}, 0)$. This corresponds to the stable solution of the system in the absence of predators, when the number of baits remains at a stable value. In fact, the equation can be rewritten as $\frac{dx}{dt} = ax(1 - \frac{a}{\varepsilon}x)$ when $y = 0$ is used, which is the same as the differential equation of the logistic model, where the environmental capacity, $K = \frac{a}{\varepsilon}$, corresponds to the number of predators when the population size of the predator remains stable, as described by the singularity. And $(0, -\frac{c}{\delta})$ has no practical significance because the predator cannot survive alone when the bait is not present, so there is no solution with a positive population size. Singularities related to population extinction have already been systematically studied [4], so we focus our attention on coexistence equilibrium points (x_0, y_0) . The counterpart is the coexistence equilibrium when both bait and predator are present, and is what we need to focus on in the following parts.

2.1.3. Singularity type analysis of coexisting equilibria

In order to analyze the singularity type of the coexistence equilibrium (x_0, y_0) of (2), we can first compute the singularity type of the primary approximation system of (2) in the vicinity of the coexistence equilibrium, and then use Perron's theorem to determine the singularity type of the coexistence equilibrium of (2).

To do this, we set the two functions on the right-hand side of the system of equations (2) to be

$$\begin{cases} P(x, y) = x(a - by - \varepsilon x) \\ Q(x, y) = y(-c + dx - \delta y) \end{cases} \quad (4)$$

and compute the Jacobi matrix of the right-hand side vector-valued function as

$$\frac{\partial(P, Q)}{\partial(x, y)} = \begin{pmatrix} a - by - 2\varepsilon x & -bx \\ dy & -c + dx - 2\delta y \end{pmatrix} \quad (5)$$

Substituting in the coexistence equilibrium point gives

$$\frac{\partial(P, Q)}{\partial(x, y)}(x_0, y_0) = \begin{pmatrix} -\varepsilon x_0 & -bx_0 \\ dy_0 & -\delta y_0 \end{pmatrix} \quad (6)$$

Thus, the one-time approximation system is

$$\begin{cases} \frac{dx}{dt} = -\varepsilon x_0(x - x_0) - bx_0(y - y_0) \\ \frac{dy}{dt} = dy_0(x - x_0) - \delta y_0(y - y_0) \end{cases} \quad (7)$$

Calculate its eigenvalues:
$$\begin{vmatrix} \lambda + \varepsilon x_0 & bx_0 \\ -dy_0 & \lambda + \delta y_0 \end{vmatrix} = 0$$
,

$\Delta = (\varepsilon x_0 + \delta y_0)^2 - 4(\varepsilon\delta + bd)x_0y_0 = (\varepsilon x_0 - \delta y_0)^2 - 4bdx_0y_0 < 0$ and $\varepsilon x_0 + \delta y_0 > 0$, indicating that its eigenvalues are a pair of conjugate complexes of the real part < 0 , i.e. $-\frac{\varepsilon x_0 + \delta y_0}{2} \pm \sqrt{4bdx_0y_0 - (\varepsilon x_0 - \delta y_0)^2} \triangleq u \pm iv$

Thus the coexisting equilibrium point is a stable focus for the type of singularity in (7). nevertheless, the design

$$\begin{pmatrix} -\varepsilon x_0 & -bx_0 \\ dy_0 & -\delta y_0 \end{pmatrix} \begin{pmatrix} x-x_0 \\ y-y_0 \end{pmatrix} + \begin{pmatrix} g_1(x,y) \\ g_2(x,y) \end{pmatrix} = \begin{pmatrix} x(a-by-\varepsilon x) \\ y(-c+dx-\delta y) \end{pmatrix} \quad (8)$$

With
$$\begin{cases} g_1(x,y) = -\varepsilon(x-x_0)^2 - b(x-x_0)(y-y_0) \\ g_2(x,y) = -\delta(y-y_0)^2 + d(x-x_0)(y-y_0) \end{cases}$$

Thus, at $(x,y) \rightarrow (x_0,y_0)$, $g_1(x,y), g_2(x,y) = o(\|(x-x_0, y-y_0)\|_2)$

By Perron's First Theorem, the type of singularity of the equilibrium stabilizer of (2) is also a stable focus.

This is actually roughly in line with what happens in reality, where the two populations grow in numbers and grow in numbers and grow in numbers, gradually approaching stabilization in the absence of human intervention.

2.2. Analysis of the behavior of the system near the equilibrium stability point

Since at $(x,y) \rightarrow (x_0,y_0)$, $g_1(x,y), g_2(x,y) = o(\|(x-x_0, y-y_0)\|_2)$

Thus in the neighborhood of the coexistence equilibrium, we can use the correlation properties of (7) to approximate the correlation properties of (2).

So below we consider some properties of planar autonomous systems [5]

$$\begin{pmatrix} \frac{dx}{dt} \\ \frac{dy}{dt} \end{pmatrix} = \begin{pmatrix} a_0 & b_0 \\ c_0 & d_0 \end{pmatrix} \begin{pmatrix} x \\ y \end{pmatrix} \quad (9)$$

Suppose that $\begin{pmatrix} a_0 & b_0 \\ c_0 & d_0 \end{pmatrix}$ has two conjugate complex roots $u \pm iv$, then there exists a non-isomorphic array P such that

After variable substitution $\begin{pmatrix} x' \\ y' \end{pmatrix} = P^{-1} \begin{pmatrix} x \\ y \end{pmatrix}$, the

$$P^{-1} \begin{pmatrix} a_0 & b_0 \\ c_0 & d_0 \end{pmatrix} P = \begin{pmatrix} u & v \\ -v & u \end{pmatrix}$$

$$\begin{pmatrix} \frac{dx'}{dt} \\ \frac{dy'}{dt} \end{pmatrix} = \begin{pmatrix} u & v \\ -v & u \end{pmatrix} \begin{pmatrix} x' \\ y' \end{pmatrix} \quad (10)$$

The commutator $\begin{cases} x' = r \cos \theta \\ y' = r \sin \theta \end{cases}$, then

$$\begin{cases} \frac{dr}{dt} = ur \\ \frac{d\theta}{dt} = -v \end{cases} \Rightarrow \begin{cases} r(t) = C_1 e^{ut} \\ \theta(t) = -vt + C_2 \end{cases} \quad (11)$$

And in (7), $\begin{pmatrix} a_0 & b_0 \\ c_0 & d_0 \end{pmatrix} = \begin{pmatrix} -\varepsilon x_0 & -bx_0 \\ dy_0 & -\delta y_0 \end{pmatrix}$, $u = -\frac{\varepsilon x_0 + \delta y_0}{2}$, $v = \sqrt{4bdx_0y_0 - (\varepsilon x_0 - \delta y_0)^2}$

Thus, near the coexistence equilibrium point, the system's cyclic cycle of carrying out one of this and one of the other, this and the other, ecological behaviors is [6]

$$T = \frac{2\pi}{v} = \frac{2\pi}{\sqrt{4bdx_0y_0 - (\varepsilon x_0 - \delta y_0)^2}} \quad (12)$$

Rate of contraction of the system towards the equilibrium stabilization point [7]

$$\frac{dr}{dt} = O(ue^{ut}) = O\left(-\frac{\varepsilon x_0 + \delta y_0}{2} e^{-\frac{\varepsilon x_0 + \delta y_0}{2} t}\right) \quad (13)$$

Let's revisit this Jacobi matrix and its eigenvalues

$$\frac{\partial(P, Q)}{\partial(x, y)}(x_0, y_0) = \begin{pmatrix} -\varepsilon x_0 & -bx_0 \\ dy_0 & -\delta y_0 \end{pmatrix}$$

$$\lambda_{1,2} = -\frac{\varepsilon x_0 + \delta y_0}{2} \pm \sqrt{4bdx_0y_0 - (\varepsilon x_0 - \delta y_0)^2}i$$

We control for ε, δ with the same number, and the original hypothesis $\varepsilon, \delta \ll b, d$.

When $\varepsilon, \delta > 0$, the eigenvalues are a pair of conjugate complexes with negative real parts, when $\varepsilon, \delta = 0$, the eigenvalues are a pair of conjugate pure imaginary numbers, and when $\varepsilon, \delta < 0$, the eigenvalues are a pair of conjugate complexes with positive real parts. Thus we find that when (ε, δ) is continuously transformed from the first quadrant through the origin to the third quadrant, the eigenvalues cross the imaginary axis from left to right, resulting in the destabilization of the system's immobile point. The coexisting stabilized points will form a small amplitude limit ring.

And this process of making changes in the qualitative structure of the system yielding limit rings as the parameters change is known as Hopf bifurcation in the study of differential equations [8].

In order to visualize this bifurcation using code, here, let us assume $\varepsilon = \delta$ and let the two-parameter transform continuously from the first quadrant to the third quadrant along the line $y = x$. And for better visualization, let's say $\gamma = -\varepsilon$, then the equation takes the following form:

$$\begin{cases} \frac{dx}{dt} = x(a - by + \gamma x) \\ \frac{dy}{dt} = y(-c + dx + \gamma y) \end{cases} \quad (14)$$

We set the initial parameter as $a, b, c, d = 0.8, 0.7, 1.5, 0.3$, we assume $\gamma \in (-0.005, 0.005)$, satisfy the condition $\gamma \ll b, d$, and the initial value condition selects a point $\left(\frac{bc-a\gamma}{\gamma^2+bd} + 0.1, \frac{ad+c\gamma}{\gamma^2+bd} + 0.1\right)$ near the equilibrium point. Then we use the RK45 method in python to numerically simulate the trajectory plots of the population size of the bait and the predator over time with different parameters γ , where we use the parameter γ as the z axis, and record the trajectory plots against in the $\mathbb{R}^2 \times \{\gamma\}$ plane, and make a three-dimensional visualization of the three-dimensional plot to reflect the effect of parameter changes on the stability of the system as well as the phenomenon of the Hopf bifurcation [9].

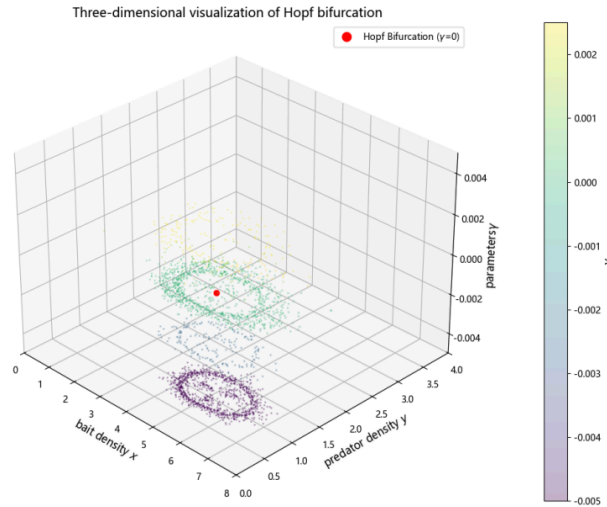


Figure 1. Three-dimensional visualization of Hopf bifurcation

Taking out the cross sections at each γ value can make it easier for us to look at the system near the singularity at specific parameter values.

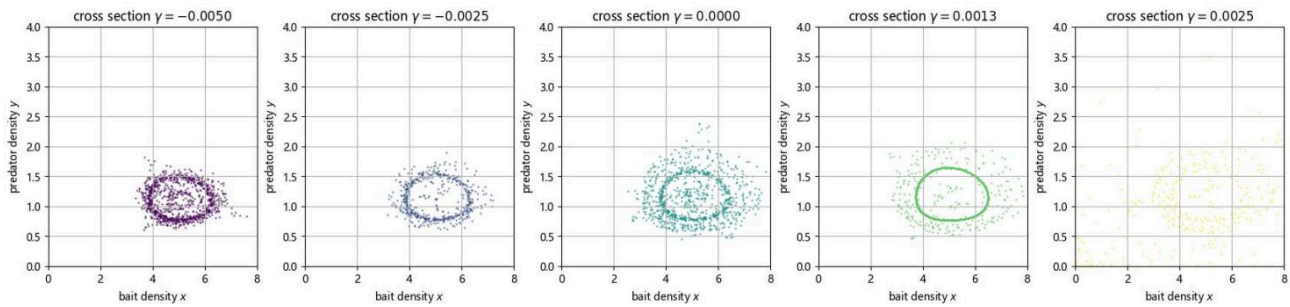


Figure 2. Cross sections of three-dimensional visualization of Hopf bifurcation

We find that when γ is negative, the coexistence equilibrium point is a stable focus, and the rate of contraction toward the coexistence equilibrium point is fast when the absolute value is large, as shown by the purple dots. And when $\gamma \rightarrow 0^-$, the trend of inward contraction of the trajectory line is weakened and the coexistence equilibrium point evolves toward the center. At $\gamma = 0$, the neighborhood of the coexistence equilibrium point is a circle of closed rails. When $\gamma \rightarrow 0^+$, the coexistence equilibrium point becomes a small amplitude limit circle as shown by the light green dot. This 3D diagram shows from bottom to top, the coexisting equilibrium point changes from a stable focus to the center to having an unstable focus with a limit circle wrapped around it, which is the process of Hopf bifurcation. Also, the yellow dots tell us that the coexisting equilibrium point is poorly stabilized when γ is large.

3. Multi-species Lotka-Volterra model based on logistic modeling

While Section 2.1 addressed a critical limitation of the Lotka-Volterra model by incorporating intraspecific competition, it remained confined to the essential, yet simplified, two-species predator-prey paradigm. However, natural ecosystems are rarely this simplistic; they typically comprise intricate networks of interactions among multiple species. Directly applying the classical pairwise LV framework to such complex communities is conceptually challenging and computationally prohibitive due to the combinatorial explosion of interaction terms and the inherent nonlinearity of the equations. Recognizing this fundamental gap, this section aims to significantly broaden the scope of the LV model. Motivated by the observation that the derivation logic underlying the original LV equations bears resemblance to that of the logistic growth model (which inherently handles a single species with self-limitation), we propose a principled extension: the Generalized Multi-Species Lotka-Volterra (GMS-LV) Model. This model framework explicitly incorporates both interspecific interactions (predation, competition, mutualism, etc.) and intraspecific competition for an arbitrary number of species. The central challenge then shifts towards solving this high-dimensional, nonlinear system. To address the critical need for computational feasibility, especially for understanding short-term dynamics, we introduce a novel analytical-numerical method in section 3. Leveraging Taylor's formula, we approximate the system's solution over a finite time horizon. Crucially, we demonstrate how this approximation can be efficiently computed using the concept of a transfer matrix, effectively encapsulating the complex web of interactions and initial conditions. This approach provides a practical and scalable pathway to obtain approximate short-term trajectories for complex ecological communities under the GMS-LV framework, overcoming a significant barrier in applying generalized LV models to realistic multi-species scenarios.

3.1. Preliminary Lotka-Volterra modeling for generalization

As we analyzed in 2.1, the original Lotka-Volterra model (1) employs a similar biological modeling approach as the Logistic model, since the consideration of the

$$\begin{cases} \frac{dx}{dt} = ax \left(1 - \frac{y}{b}\right) \\ \frac{dy}{dt} = -cy \left(1 - \frac{x}{d}\right) \end{cases}$$

Here we assume that the base growth rate of the bait-feeding population is a and the base extinction rate of the predator is c , which is the same form as the differential equation of the logistic model $\frac{dx}{dt} = rx \left(1 - \frac{x}{K}\right)$. In the Logistic model, the population itself is too large to inhibit population growth. In contrast, in the original Lotka-Volterra model, an oversize population of predators inhibits the extinction of the number of predators, and an oversize population of predators inhibits the growth of the number of predators.

Accordingly, the model can be generalized to any number of competing species. In fact, the competitive Lotka-Volterra model utilizes this type of modeling: for n competing species, the equation for the i th species is [10]:

$$\frac{dx_i}{dt} = r_i x_i \left(1 - \frac{\sum_{j=1}^n \alpha_{ij} x_j}{K_i}\right) \quad (15)$$

where the base rate of population growth for the i population $r_i > 0$, the influence factor of the j population species on the i population species $\alpha_{ij} > 0$, and the environmental capacity of the i population $K_i > 0$, $\forall 1 \leq i, j \leq n$.

However, when we consider systems in which both bait and predators are present, such as the original Lotka-Volterra model, it takes a different form than the competitive Lotka-Volterra model. Because in the original Lotka-Volterra model, when only predators are present, we assume that it is the i th population, and the rate of change of the population base r_i is negative, so the corresponding α_{ij} may also have some negative numbers (due to ecological competition, other predator populations may inhibit its population growth, and the j th population is a predator population competing with it as an example, then $\alpha_{ij} < 0$).

We may therefore wish to rewrite the competitive Lotka-Volterra model as follows

$$\frac{dx_i}{dt} = r_i x_i \left(1 - \sum_{j=1}^n \alpha_{ij} x_j\right) (i \in [1, n] \cap \mathbb{Z}) \quad (16)$$

where the rate of change in the population base of the i population is r_i and the influence factor of the j population on the i population is α_{ij} .

3.2. Extended Lotka-Volterra model for short-time solution methods

It is shown that the original Lotka-Volterra model also does not have an analytic solution, under this premise, for the equation (16), the time complexity is very high if it is solved directly using the Runge-Kutta method without any treatment, so we need to use some approximation to provide a way to compute a short time solution for the equation.

If $u_i = \ln(x_i)$, then (16) can be rewritten as [11]

$$\frac{du_i}{dt} = r_i \left(1 - \sum_{j=1}^n \alpha_{ij} e^{u_j} \right) \quad (i \in [1, n] \cap \mathbb{Z}) \quad (17)$$

$$\mathbf{u} = \begin{pmatrix} u_1 \\ u_2 \\ \vdots \\ u_n \end{pmatrix}, \quad \mathbf{f}(\mathbf{u}) = \begin{pmatrix} f_1(\mathbf{u}) \\ f_2(\mathbf{u}) \\ \vdots \\ f_n(\mathbf{u}) \end{pmatrix}$$

$$f_i(\mathbf{u}) = r_i \left(1 - \sum_{j=1}^n \alpha_{ij} e^{u_j} \right)$$

Then the equation (17) is abbreviated as:

$$\frac{d\mathbf{u}}{dt} = \mathbf{f}(\mathbf{u}) \quad (18)$$

Here, we use the polynomial approximation method to approximate $\mathbf{u}(t)$ [12] [13]:

By the Weierstrass Approximation Theorem: we can approximate by a polynomial in the series $\mathbf{u}(t)$

$$\mathbf{u}(t) = \begin{pmatrix} u_1(t) \\ u_2(t) \\ \vdots \\ u_n(t) \end{pmatrix} = \begin{pmatrix} \sum_{k \geq 0} \frac{u_{1k} t^k}{k!} \\ \sum_{k \geq 0} \frac{u_{2k} t^k}{k!} \\ \vdots \\ \sum_{k \geq 0} \frac{u_{nk} t^k}{k!} \end{pmatrix} \quad (19)$$

To find these polynomial coefficients, we now set:

$$u_{i(m)}(t) = \sum_{k=0}^m \frac{u_{ik} t^k}{k!}. \quad \text{For the first } m \text{ part of } u_i(t) = \sum_{k \geq 0} \frac{u_{ik} t^k}{k!} \text{ and the function}$$

$$\mathbf{u}_m(t) = \begin{pmatrix} u_{1(m)}(t) \\ u_{2(m)}(t) \\ \vdots \\ u_{n(m)}(t) \end{pmatrix}$$

Here, $\{u_{i0}\}_{i=1}^n$ is a known quantity for the initial population state.

Thus, to approximate the fitted polynomial to $\mathbf{u}(t)$, we have the recurrence relation:

$$\frac{d\mathbf{u}_m}{dt} = \mathbf{f}(\mathbf{u}_{m-1}), \quad \forall m \in \mathbb{N}^*$$

to continually determine higher order coefficients.

So $t \ll 1$ time:

$$\begin{aligned}
 \frac{d\mathbf{u}_{i(m)}}{dt} &= r_i \left(1 - \sum_{j=1}^n \alpha_{ij} e^{u_{j(m-1)}} \right) \\
 &= r_i \left(1 - \sum_{j=1}^n \alpha_{ij} e^{u_{j0}} e^{u_{j1}t + \frac{u_{j2}}{2}t^2 + \dots + \frac{u_{j,m-1}}{(m-1)!}t^{m-1}} \right) \\
 &= r_i \left(1 - \sum_{j=1}^n \alpha_{ij} e^{u_{j0}} \left(1 + u_{j1}t + \frac{u_{j2}}{2}t^2 + \dots + \frac{u_{j,m-1}}{(m-1)!}t^{m-1} \right) \right) + o(1) \\
 &= r_i \left(1 - \sum_{j=1}^n \alpha_{ij} e^{u_{j0}} \right) - r_i \sum_{j=1}^n \alpha_{ij} e^{u_{j0}} u_{j1}t - \dots - r_i \sum_{j=1}^n \alpha_{ij} e^{u_{j0}} u_{j,m-1} \frac{t^{m-1}}{(m-1)!} \\
 &= u_{i1} + u_{i2}t + \dots + \frac{u_{im}}{(m-1)!} t^{m-1}
 \end{aligned}$$

Comparison coefficients are available:

$$u_{il} = \begin{cases} r_i \left(1 - \sum_{j=1}^n \alpha_{ij} e^{u_{j0}} \right) & (l = 1) \\ -r_i \sum_{j=1}^n \alpha_{ij} e^{u_{j0}} u_{j,l-1} & (2 \leq l \leq m) \end{cases}$$

Since the above equation holds for $\forall m \in \mathbb{N}^*$, the coefficients we determine by polynomial approximation are:

$$u_{im} = \begin{cases} r_i \left(1 - \sum_{j=1}^n \alpha_{ij} e^{u_{j0}} \right) & (m = 1) \\ -r_i \sum_{j=1}^n \alpha_{ij} e^{u_{j0}} u_{j,m-1} & (m \geq 2) \end{cases} \quad (20)$$

Thus, we can store the recurrence relations of the coefficients in matrices and vectors [14]:

$$\begin{pmatrix} u_{1m} \\ u_{2m} \\ \vdots \\ u_{nm} \end{pmatrix} = \begin{pmatrix} -r_1 e^{u_{10}} \alpha_{11} & -r_1 e^{u_{20}} \alpha_{12} & \cdots & -r_1 e^{u_{n0}} \alpha_{1n} \\ -r_2 e^{u_{10}} \alpha_{21} & -r_2 e^{u_{20}} \alpha_{22} & \cdots & -r_2 e^{u_{n0}} \alpha_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ -r_n e^{u_{10}} \alpha_{n1} & -r_n e^{u_{20}} \alpha_{n2} & \cdots & -r_n e^{u_{n0}} \alpha_{nn} \end{pmatrix} (m \geq 2)$$

$$= - \begin{pmatrix} r_1 & 0 & \cdots & 0 \\ 0 & r_2 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & r_n \end{pmatrix} \begin{pmatrix} \alpha_{11} & \alpha_{12} & \cdots & \alpha_{1n} \\ \alpha_{21} & \alpha_{22} & \cdots & \alpha_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ \alpha_{n1} & \alpha_{n2} & \cdots & \alpha_{nn} \end{pmatrix} \begin{pmatrix} e^{u_{10}} & 0 & \cdots & 0 \\ 0 & e^{u_{20}} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & e^{u_{n0}} \end{pmatrix} \begin{pmatrix} u_{1,m-1} \\ u_{2,m-1} \\ \vdots \\ u_{n,m-1} \end{pmatrix}$$

4. Discussion

In this section, we will discuss the rationality and feasibility of the method described in 3.2 in actual short-term forecasting operations and in which scenarios is it appropriate to use the polynomial approximation method in section 3.2, and how should it be used.

4.1. Discussion on the rationality of polynomial approximation methods in section 3.2

We use both the Runge-Kutta method and polynomial approximation for (16) .

We set $n = 2$, $\begin{pmatrix} r_1 \\ r_2 \end{pmatrix} = \begin{pmatrix} 1.2 \\ 0.8 \end{pmatrix}$, $\begin{pmatrix} \alpha_{11} & \alpha_{12} \\ \alpha_{21} & \alpha_{22} \end{pmatrix} = \begin{pmatrix} -0.5 & 0.3 \\ 0.4 & -0.6 \end{pmatrix}$, $\begin{pmatrix} u_{10} \\ u_{20} \end{pmatrix} = \begin{pmatrix} \ln(x_{10}) \\ \ln(x_{20}) \end{pmatrix} = \begin{pmatrix} 0 \\ 0 \end{pmatrix}$

to represent populations of two species in a mutually beneficial symbiotic relationship.

We take the first 15 terms of the infinite polynomial to approximate the fitted short-time solution and output the simulated values of the numbers of the two populations over a period of $t = 1$ years and calculate the relative errors by comparing them with the results obtained using the Runge-Kutta method. Here, we use the fourth-order Long-Gouta method, which can basically be considered to yield accurate results [15].

Table 1. Comparison of Runge-Kutta method and polynomial method

Time	Runge-Kutta Method Solution u_1	Runge-Kutta Method Solution u_2	Polynomial method of solving u_1	Polynomial method of solving u_2	Relative error
0.0	0.000000	0.000000	0.000000	0.000000	0.00%
0.1	0.024978	0.016640	0.024978	0.016640	0.00%
0.2	0.049993	0.033280	0.049992	0.033280	0.00%
0.3	0.075047	0.049919	0.075042	0.049920	0.01%
0.4	0.100141	0.066556	0.100128	0.066560	0.01%
0.5	0.125275	0.083193	0.125251	0.083199	0.02%
0.6	0.150452	0.099828	0.150410	0.099838	0.03%
0.7	0.175672	0.116460	0.175606	0.116477	0.04%
0.8	0.200938	0.133090	0.200838	0.133116	0.05%
0.9	0.226251	0.149717	0.226106	0.149754	0.06%

From Table 1, we can see that the population size predicted using the polynomial method and the results obtained by directly solving the differential equation using the Runge-Kutta method are highly consistent, as we can see that the relative error values do not exceed 0.1%. Accordingly, the results obtained by the polynomial approximation are very close to those obtained by the Runge-Kutta method, which confirms the reasonable predictability of the theory developed in this article.

4.2. Real-world applications of polynomial approximation methods

Beyond the theoretical extensions to the Lotka-Volterra framework presented in section 3.2 (incorporating intraspecific competition and generalizing to multi-species systems), the development of the Taylor series approximation coupled with the transfer matrix method for solving the GMS-LV equations offers significant practical potential. The primary advantage of this approach lies in its computational efficiency for generating short-term forecasts. Traditional numerical integrators, while highly accurate, become computationally burdensome for high-dimensional systems like our GMS-LV model, especially when numerous simulations are required for parameter exploration or sensitivity analysis. The transfer matrix method transforms the ODE solution into an algebraic computation of the matrix exponential, which can be implemented very efficiently. This computational advantage opens doors for applications demanding rapid feedback or handling high complexity. For instance:

In invasion ecology, managers could use this method to rapidly simulate the initial population trajectories of both invasive and native species following an introduction event under various hypothetical control scenarios (e.g., different removal rates), aiding in the timely design of mitigation strategies before the invasion becomes entrenched.

Fisheries science often relies on short-term projections to set annual quotas. This solver could enable quick exploration of how different harvesting pressures might affect target fish stocks and their interacting species (predators, competitors) over the next fishing season, providing more agile decision support.

The core idea could be adapted to model early-stage outbreaks in complex multi-host epidemic systems, where quickly assessing initial transmission risks or the short-term impact of interventions is critical.

It is crucial to acknowledge the inherent limitation of polynomial approximation: its accuracy degrades over longer time horizons due to truncation errors. Therefore, this method is specifically targeted at short-term prediction and rapid computation tasks, not as a replacement for high-fidelity integrators in studying long-term asymptotic behavior or chaotic dynamics. The trade-off here is accepting a controlled level of approximation over a limited time window in exchange for substantial gains in computational speed. This trade-off is often necessary and acceptable in applications like rapid risk assessment, real-time management support, or large-scale parameter screening.

Looking forward, integrating this solver with data assimilation techniques (e.g., Kalman filtering) could create powerful tools for near-real-time ecosystem monitoring and short-term forecasting by continuously updating model states with incoming observations. Further research could also explore its application to spatially explicit models, investigate adaptive strategies for choosing the Taylor expansion order, or develop robust error estimators to better quantify the approximation validity period for specific systems. Ultimately, by providing a computationally feasible pathway to tackle high-dimensional interaction networks, this method enhances our capacity to apply generalized Lotka-Volterra models to increasingly realistic and complex ecological scenarios.

5. Conclusion

This study systematically expands the limitations of the classical Lotka-Volterra model, and promotes the improvement and application of the model from the dimensions of theoretical analysis and computational methods. The core contributions of the paper can be summarized in the following three aspects:

The first one is the introduction of intraspecific competition mechanism and stability reconstruction:

While the traditional model only focuses on the predator-prey binary relationship between species, this paper incorporates the effect of density constraints within the population into the dynamical framework by introducing the intraspecific competition term. Based on the improved system of equations, the paper analyzes the structural characteristics of the system's singularity solution, and reveals the regulation law of intraspecific competition intensity on the stability of the equilibrium state. By constructing the functional relationship between the key parameters and the competition factors, the sensitive influence of intraspecific competition on the population dynamics is further quantified, which provides a theoretical basis for the stability regulation of the ecosystem.

The second one is the construction of generalized multi-species model and innovation of computational paradigm: Aiming at the shortcomings of the original model which is difficult to describe complex communities, the paper draws on the idea of Logistic model and proposes the generalized multi-species Lotka-Volterra equation. In order to break through the bottleneck of solving high-dimensional nonlinear systems, the thesis creatively applies the polynomial fitting method to develop a fast computational framework for short-time analytic solution. The method significantly reduces the computational complexity of the multi-species coupled system through recursive coefficient generation, and provides a feasible tool for real-time simulation and prediction of real ecosystems.

The third one is the construction of generalized multi-species model and innovation of computational paradigm: the study not only accomplished the mathematical generalization of the model, but also focused on the deepening of the ecological connotation:

(1) The critical role of intraspecific competition in suppressing explosive population growth was elucidated by stability analysis;

(2) Parameter sensitivity analysis provides quantitative criteria for the identification of critical factors in ecosystem management.

The innovation of this study lies in breaking through the theoretical boundaries of the classical model, and realizing an all-round expansion from simple two-population to complex communities, from ideal assumptions to practical constraints through structural improvement and algorithm design. The proposed method provides a new paradigm with both theoretical depth and computational efficiency for practical problems such as ecosystem modeling, biodiversity conservation and invasive species prevention and control, and also opens up cross-disciplinary perspectives for the study of nonlinear dynamical systems.

References

- [1] Lotka, A.J. (1910) Contribution to the Theory of Periodic Reaction. The Journal of Physical Chemistry, 14, 271-274.
- [2] Volterra, V. (1931) Variations and Fluctuations of the Number of Individuals in Animal Species Living Together. In: Chapman, R.N., Ed., Animal Ecology, McGraw-Hill, New York, 409-448.
- [3] Davis JD, Olivença DV, Brown SP and Voit EO. (2022) Methods of quantifying interactions among populations using Lotka-Volterra models. Front. Syst. Biol. 2: 1021897.
- [4] M. L. Zeeman. (1995) Extinction in competitive Lotka-Volterra systems. Proc. Amer. Math. Soc. 123, 87-96.
- [5] Kraaijevanger, J.F.B.M. (1991) Contractivity of Runge-Kutta methods. BIT 31, 482–528.
- [6] Genda, A., Fidin, A., Lenci, S. et al. (2025) Effects of seasonal hunting and food quantity variations on the Lotka-Volterra model. Nonlinear Dyn 113, 12351–12369.
- [7] Saeedian Meghdad, Pigani Emanuele, Maritan Amos, Suweis Samir and Azalee Sandro. (2022) Effect of delay on the emergent stability patterns in generalized Lotka–Volterra ecological dynamics. Phil. Trans. R. Soc. A.38020210245.
- [8] P Yu and A Y T Leung. (2003) Nonlinearity 16 277
- [9] Cui Q, Xu C, Ou W, Pang Y, Liu Z, Li P, Yao L. (2023) Bifurcation Behavior and Hybrid Controller Design of a 2D Lotka–Volterra Commensal Symbiosis System Accompanying Delay. Mathematics, 11(23): 4808.
- [10] Khaliq, A.; Ibrahim, T.F.; Alotaibi, A.M.; Shoaib, M.; El-Moneam, M.A. (2022) Dynamical Analysis of Discrete-Time Two-Predators One-Prey Lotka–Volterra Model. Mathematics, 10, 4015.
- [11] Imane Akjouj, Matthieu Barbier, Maxime Clenet, Walid Hachem, Mylène Maïda, et al. (2024) Complex systems in Ecology: A guided tour with large Lotka-Volterra models and random matrices. Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences, 2024, 480 (2285)
- [12] F.Verhulst. (1990) Nonlinear Differential Equations and Dynamical Systems (Springer Verlag, Berlin, 1990.)
- [13] H.T.Davies. (1962) Introduction to Nonlinear Differential and Integral Equations (Dover, New York, 1962.)
- [14] Maxime Clenet, Hamed El Ferchichi, Jamal Najim. (2022) EQUILIBRIUM IN A LARGE LOTKA-VOLTERRA SYSTEM WITH PAIRWISE CORRELATED INTERACTIONS. Stochastic Processes and their Applications, 2022, 153, pp.423-444.
- [15] Raymond J. Spiteri, Siqui Wei. (2023) Fractional-step Runge–Kutta methods: Representation and linear stability analysis. Journal of Computational Physics, Volume 476.