مجلة جامعة سبها للعلوم البحتة والتطبيقية
Sebha University Journal of Pure & Applied Sciences

Journal homepage: www.sebhau.edu.ly/journal/index.php/jopas

The Ratio Predator-Prey Model with Random Initial Conditions

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Keywords:	**A B S T R A C T**
Uncertainty Ratio Predator-Prey Model Random initial Conditions Stability Normal Distribution	In this work, the predator-prey model with the ratio-dependent functional response is considered, where the randomness enters into the equations only through their initial conditions. It is done by assuming normal distribution as the initial states of the model to treat the randomness. The passage from the deterministic situation to the random one for these equations is also the most transparent. In addition, a numerical simulation will be offered using the modified approach founded on the fifth-order improved Runge-Kutta method. Furthermore, the stability of the equilibrium points, and certain statistical properties related to the random behaviour of predators and their prey, will be analyzed and discussed.

نموذج الفريسة والمفترس النسبي بشروط ابتدائية عشوائية

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الكلمات المفتاحية:	الملخص
عدم اليقين نموذج الفريسة والمفترس النسبي الشروط الابتدائية العشوائية الاستقرار التوزيع الاحصائي الطبيعي	في هذه الورقة, تم دراسة العشوائية في نموذج الفريسة والمفترس النسبي مع دالة الاستجابة وذلك باعتبار ان العشوائية موجودة فقط في الشروط الابتدائية للمعادلات التفاضلية المكونة للنموذج. تم استخدام التوزيع الطبيعي ليمثل الشروط الابتدائية للنموذج. ايضاً، عملية التحول من النموذج الطبيعي الى النموذج العشوائي تم بشكل واضح وجلي. بالإضافة الى ذلك، تم استخدام المحاكاة العددية لدراسة النموذج العشوائي وذلك لعدم وجود حل تحليلي لهذا النموذج. هذه المحاكاة تمت بنهج طريقة معدلة لطريقة رنج كوتا المطورة من الدرجة الخامسة. وكنتيجة لهذه المحاكاة، تم دراسة ومناقشة الاستقرارية وبعض الخواص الإحصائية للسلوك العشوائي لكل من الفريسة والمفترس.

Introduction

In statistics, uncertainty has been around for a long time. On the other hand, scientists and engineers have only recently begun carefully considering the consequences of stochastic in their various fields. They have realized that most real-world phenomena and physical tests cannot be adequately explained, partially because the complete information is not always accessible. Different types of uncertainty can be addressed in differential equations [1]. A random input phrase or source term distinguishes the first instance. The second scenario is when introduced via the parameters. Finally, when the beginning states are unpredictably variable. Fuzzy set theory is a helpful feature when ambiguous data cause uncertainty. The influence of fuzziness has been studied in [2-4], and the authors used different approaches to deal with uncertainty in the predator-prey model. Narayanamoorthy et al. analyzed the fractional-order predator-prey model by taking the initial conditions of the predator-prey model as fuzzy initial conditions [5]. Another powerful approach for dealing with uncertainty in models is probability theory, which is used when constructing a random mathematical model. Kegan and West investigated the effects of

unexpected initial conditions on the simple epidemic deterministic model [6]. The beta distribution is assumed to be the initial proportion of susceptible; they define a distribution that describes the ratio of susceptible in a population at any time during an epidemic. Additionally, they discussed the statistical properties of the random behaviour of the epidemic. Omar and Abu-Hasan wrer numerically simulated the random SIR model with random initial states distributed as a beta distribution [7]. Pollett et al. described a general strategy for including random initial conditions in population models where a deterministic model is sufficient to represent population dynamics [8]. They also showed that the total variation of a broad class of stochastic models is the sum of variation due to random initial conditions and variation due to random dynamics, which allowing them to quantify the variation not accounted for when random dynamics are neglected. Tu and Wilman investigated stability conditions for a relatively general predator-prey model, which exhibits self-limiting density effects and minimum viable population levels for both the predator and the prey [9]. The intrinsic rates of increase in the two populations

were assumed to be known only with error. Omar and Abu-Hasan studied the effect of randomness on the simple predator-prey model by considering the normal distribution as the initial stats of the populations [10], [11]. Many versions of the Lotka-Volterra model are investigated for parameter uncertainty [12]. The simulation tool was based on differential inclusions instead of ordinary differential equations. Mondal et al. studied the predator-prey model by modifying the Lotka–Volterra model, taking appropriate biological parameters as intervals [13]. Barhagh *et al.* employed a system dynamics method based on the predator-prey approach to model the restoration possibilities of Urmia Lake. A Monte Carlo simulation investigated the effect of unclear parameters on the lake level [14].

In this study, the initial conditions of the system of the ratio-dependent predator-prey model are normally distributed. The fifth order improved Runge-Kutta method is modified to compute the random interaction between prey and predators. Simulation is provided, and the effect of random initial conditions on the interaction between prey and their predators is investigated

Preliminary

In this section, the deterministic model will be introduced. The normal distribution used to enter the randomness in the deterministic model will be offered.

1. The Deterministic Predator-Prey Model with Ratio Functional Response

The predator-prey model with the equivalent form of the Monod functional response (type II) has the form

$$\frac{dx}{dt} = ax\left(1 - \frac{x}{K}\right) - \frac{bxy}{1 + bHx}, \quad x(0) = x_0 \geq 0, \qquad (1a)$$

$$\frac{dy}{dt} = \frac{cbxy}{1 + bHx} - dy, \qquad y(0) = y_0 \geq 0. \qquad (1b)$$

The parameters $a, b, c,$ and d represent the intrinsic growth rate of prey, a total attack rate for the predator, interpreted as conversion efficiency ($0<c<1$), and a predator death rate in the absence of their prey, respectively. The parameters K, H denote the carrying capacity for the prey population and the time it takes a predator to digest one unit of prey. Equations **1** are sometimes called the traditional prey-dependent predator-prey model. Recent evidence from biological and physiological communities supports the classic prey-dependent predator-prey model, which is verifiable in many circumstances, especially when food resources are scarce compared to predator population density and predators must search for that resource. Predators must share and compete for food in such a circumstance. To address this disadvantage, functional and numerical responses should depend on prey and predator populations. Arditi et al. proposed a simple way of incorporating predator reliance into the functional response by replacing x with the ratio $\frac{x}{y}$ in the functional response [15]. The dynamics of the so-called ***ratio-dependent predator-prey model*** can be represented as follows with these assumptions [16]:

$$\frac{dx}{dt} = ax\left(1 - \frac{x}{K}\right) - \frac{bxy}{y + bHx}, \quad x(0) = x_0 \geq 0, \qquad (2a)$$

$$\frac{dy}{dt} = \frac{cbxy}{y + bHx} - dy, \qquad y(0) = y_0 \geq 0. \qquad (2b)$$

The possible population **equilibriums** of the model (2) can be calculated by setting

$$\frac{dx}{dt} = 0, \qquad \frac{dy}{dt} = 0. \qquad (3)$$

Substituting conditions **3** into the time-dependent population model **2** yields the three equlibrioum points

$$e_1 = (0,0), \qquad (4a)$$
$$e_2 = (K, 0), \quad and \qquad (4b)$$
$$e_3 = \left(\frac{K(ac - bc + bdH)}{ac}, \frac{b(c - dH)x^*}{d}\right). \qquad (4c)$$

According to [17], [18], [19] and [20], the origin e_1 is a singular equilibria, which makes the model **2** is not able directly to linearize at this state. The equilibrium point e_2 called axial equilibrium point and e_3 is called positive equilibrium point. The latter is equilibria without absences of any species (predator and prey), and it is more interesting from the viewpoint of ecologists. Generally, studying the stability of the predator prey model **2** allows us to understand what happens when we distribute the system near the equilibria e_is.
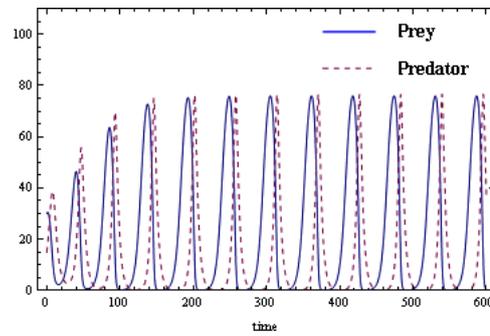
Fig. 1. The behaviours of prey and predators over time for the parametric values $a = 0.2, b = 0.02, H = 3, c = 0.95, d = 0.25, and\ K = 90,$
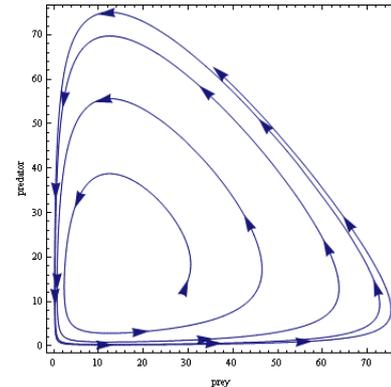
Fig. 2. The interaction of prey and predators over time for the parametric values $a = 0.2, b = 0.02, H = 3, c = 0.95, d = 0.25, and\ K = 90$, where $x(0) = 30$ and $y(0) = 15$.

2. The Normal Distribution

The normal distribution is the most widely known and used class of all statistical distributions. It is a continuous distribution for all values of X, and it is symmetric and has a bell-shaped curve with a single peak. The normal distribution is helpful for many reasons; for instance, it is directly related to some mathematical properties and is easy to work with mathematically. Also, many scientists have seen that many observations in various physical experiments and natural phenomena are normally distributed or close to normal. For example, the people population, the distributions of heights and weights are usually approximately close to normal. Another reason is the advantage of the central limit theorem, which makes a powerful connection between the sample size and the extent to which a sampling distribution approaches the standard form. In other words, the distribution of the sample means will approximate the normality even though this random sample is taken from some distributions that are not approximately normal. The normal distribution often describes at least roughly any variable that clusters around the mean [21]. It is given by the following probability density function (PDF):

$$f(x) = \frac{1}{\sigma\sqrt{2\pi}} e^{-\frac{1}{2}\left(\frac{x-\mu}{\sigma}\right)^2}. \qquad (5)$$

The cumulative distribution function (CDF) is given by

$$F_X(x) = \frac{1}{\sigma\sqrt{2\pi}} \int_{-\infty}^{x} e^{-\frac{1}{2}\left(\frac{t-\mu}{\sigma}\right)^2} dt. \qquad (6)$$

Methodology

This section gives an outline that was followed in the study. It provides information on entering the randomness in the deterministic model through the initial conditions of the system of differential equations. Also, discuss the methods used to simulate the random model by using Mathematica software.

1. The Predator-Prey Model with the Random Initial States

In the nondimensional system **2**, the initial sizes of x_0 and y_0 are nonnegative deterministic values. In this model, the initial states of

population processes may be available, but they cannot be known with certainty. We want to investigate the behaviour of the solutions when the initial populations' sizes are in the neighbourhood of the deterministic values x_0 and y_0. We pick our neighborhoods to have symmetrical distributions of probabilities. For this reason, we will treat the initial population sizes as random variables with a certain probability distribution, namely the normal distribution. As was previously stated, the nondimensional random predator-prey model with the ratio-dependent functional response can be written as:

$$\frac{dX}{dT} = aX\left(1 - \frac{X}{K}\right) - \frac{bXY}{Y + bHX}, \quad X(0) = X_0 \sim N(\mu_1, \sigma_1), \quad (7a)$$

$$\frac{dY}{dT} = \frac{cbXY}{Y + bHX} - dY, \quad\quad Y(0) = Y_0. \sim N(\mu_2, \sigma_2). \quad (7b)$$

The symbols μ_1, σ_1, μ_2 and σ_2 represent the means and the standard deviations of the normal distributions, where the mean determines the location, and the variance measures the width of the distribution.

2. The numerical method

The system **7** is a nonlinear differential equation system with no analytical solution. So, the method defined in [22] will be applied to solve the random system (7). The modified method is based on the fifth-order improved Runge-Kutta.

To achieve that, we first consider the set

$$\{X_0^q, q = 1, \cdots, m\},$$

to be a random sample selected from a random variable X_0, and the set

$$\{Y_0^q, q = 1, \cdots, m\},$$

to be a random sample drawn from a random variable Y_0. Therefore, we can rewrite the equations 7 as follows

$$\frac{dX}{dT} = aX\left(1 - \frac{X}{K}\right) - \frac{bXY}{Y + bHX}, \quad X(0) = X_0^q, q = 1, \cdots, m, \quad (8a)$$

$$\frac{dY}{dT} = \frac{cbXY}{Y + bHX} - dY, \quad\quad Y(0) = Y_0^q, q = 1, \cdots, m. \quad (8b)$$

By using the numerical method, the random solution of the equations **8** seems to be a family of order pairs of curves

$$\{(X^q(T), Y^q(T)): q = 1, \cdots, m\}.$$

Where every pair of curves

$$\left(X^{q^*}(T), Y^{q^*}(T)\right), q^* \in \{1, \dots, m\},$$

describe the behaviour of the prey and their predators over time for a specific initial populations size

$$\left(X_0^{q^*}, Y_0^{q^*}\right), q^* \in \{1, \dots, m\}.$$

For $q = 1, \dots, m$, the method defines an algebraic transformation of the random sample into

$$\left\{\left(X^q(T_r), Y^q(T_r)\right)\right\}, \ \forall \ T_r,$$

starting from the random sample of the initial population's size $\left\{(X_0^q, Y_0^q)\right\}$.

The Results

1. The effect of the randomness on the stability of the random system

The points e_1, e_2 and e_3 that are defined in equations **4a**, **4b**, and **4c**, respectively, represent the equilibrium points of the system of the equations **8** (For the random model we will denote to e_1, e_2 and e_3 by E_1, E_2 and E_3, respectively). The following formula can obtain the Jacobian matrix of the model **8**

$$\begin{pmatrix} X^q \dfrac{\partial F_1(X^q, Y^q)}{\partial X^q} + F_1(X^q, Y^q) & X^q \dfrac{\partial F_1(X^q, Y^q)}{\partial Y^q} \\ Y^q \dfrac{\partial F_2(X^q, Y^q)}{\partial X^q} & Y^q \dfrac{\partial F_2(X^q, Y^q)}{\partial Y^q} + F_2(X^q, Y^q) \end{pmatrix},$$

where $q = 1, \dots, m$. and

$$F_1(X^q, Y^q) = 1 - X^q - \frac{vY^q}{X^Q + Y^q}, \quad (9a)$$

$$F_2(X^q, Y^q) = \frac{\beta X^q}{X^Q + Y^q} - \delta. \quad (9a)$$

Thus, linearization of the equations **9** yields the given Jacobian matrices

$$\begin{pmatrix} -X^q + \dfrac{vY^q}{(X^Q + Y^q)^2} & -\dfrac{v(X^2)^q}{(X^Q + Y^q)^2} \\ \dfrac{\beta(Y^2)^q}{(X^Q + Y^q)^2} & \dfrac{\delta X^q Y^q}{(X^Q + Y^q)^2} \end{pmatrix}; \quad q = 1, \dots, m,$$

where for every $q = 1, \dots, m$, the Jacobian matrix at the equilibrium point $E_2^q(1,0)$ is

$$\begin{pmatrix} -1 & -v \\ 0 & \beta - \delta \end{pmatrix}.$$

Since this matrix only depends on the parameters v, β, and δ for every $q = 1, \dots, m$, and according to [16], the equilibrium $E_2 = (1,0)$ is a saddle point. Hence, we can conclude that the equilibrium $E_2 = (1,0)$ is a saddle point for the random interaction as well, and it is stable along the x-direction and is not for the y-direction.

At the most exciting equilibrium points

$$E_3^q = \left(1 - \left[\frac{v(\beta - \delta)}{\beta}\right], \frac{(\beta - \delta)X^q}{\delta}\right); \quad q = 1, \dots, m.$$

The Jacobian matrices can be defined as

$$\begin{pmatrix} -X_{\blacksquare}^q + \dfrac{vY_{\blacksquare}^q}{\left(X_{\blacksquare}^q + Y_{\blacksquare}^q\right)^2} & -\dfrac{v(X_{\blacksquare}^2)^q}{\left(X_{\blacksquare}^q + Y_{\blacksquare}^q\right)^2} \\ \dfrac{\beta(Y_{\blacksquare}^2)^q}{\left(X_{\blacksquare}^q + Y_{\blacksquare}^q\right)^2} & \dfrac{\delta X_{\blacksquare}^q Y_{\blacksquare}^q}{\left(X_{\blacksquare}^q + Y_{\blacksquare}^q\right)^2} \end{pmatrix}; \quad q = 1, \dots, m.$$

The Symbols $X_{\blacksquare}^q$ and $Y_{\blacksquare}^q$ denote the coordinates of the interior equilibrium $E_3^q = \left(X_{\blacksquare}^q, Y_{\blacksquare}^q\right)$, where $X_{\blacksquare}^q = 1 - \left[\frac{v(\beta - \delta)}{\beta}\right]$ and $Y_{\blacksquare}^q = \frac{(\beta - \delta)X_{\blacksquare}^q}{\delta}$. At a specific q^* the behaviour around the equilibrium point $E_3^{q^*}$ of the model **8** is extensively discussed in [16]. The authors show under which conditions the equilibrium point $E_3^{q^*}$ is locally unstable, and there exists at least one limit cycle around this equilibrium point as well as the conditions for the existence of a Hopf-bifurcating small-amplitude periodic solution. Logically, these conditions will also be satisfied at every equilibrium point E_3^q where $q \in \{1, 2, \dots, m\}$. Hence, the equilibrium points E_3^q generally satisfy the same situations for the random interaction between the prey and the predators.

2. Statistical Properties of the Random Solution of the Predator-Prey Model

Here, we are interested in the statistical properties of the random solution of the ratio-dependent predator-prey model **7**.

2.1. Test the Normality of the Random System

Since we assume that the initial states of population sizes are normally distributed, the first thing that comes to mind is to check whether the random solution remains normally distributed or significantly different from a normal distribution. Many statistical tools can be used for departures from normality. The *Shapiro Wilk* (S-W) and *Kolmogorov-Smirnov* (K-S) are widely used tests for the normality of unknown population distribution functions [23], [24]. They perform the goodness-of-fit test with a null hypothesis H_0 that the random sample was drawn from a normal distribution with unknown mean and variance, and the alternative hypothesis H_1 is that it was not drawn from a normal distribution. By default, a probability value or p-value where a small p-value suggests that it is unlikely that the random sample is normally distributed. In this study, we use both to test the random solution of the model **7** for normality over time. **Fig. 3** represents the p-values at a different time of the behavior of the prey and its predators with different initial sample sizes by using the S-W test. In contrast, **Fig. 4** represents the p-values by using the K-S test.
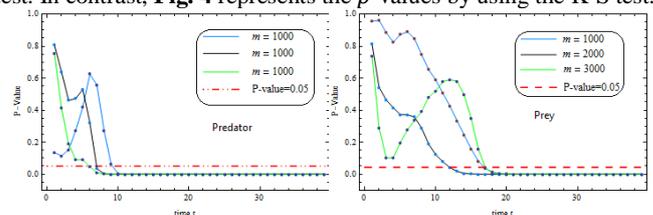
Fig. 3. P-values by using the S-W test at different times and with different initial sample sizes where $X_0 \sim N(0.3, 0.05)$ and $Y_0 \sim N(0.15, 0.02)$.
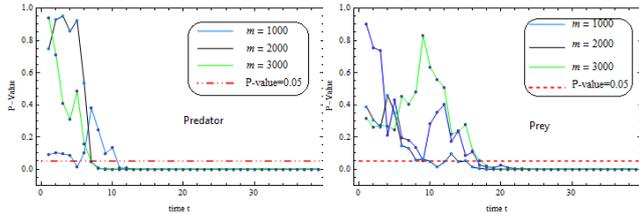
Fig. 4. P-values by using the K-S test at different times and with different initial sample sizes where $X_0 \sim N(0.3, 0.05)$ and $Y_0 \sim N(0.15, 0.02)$.

The figures show that the p-values decrease and increase over time; that is, the random samples representing the random solution are normally distributed or close to the normal, sometimes not. Hence, keeping the random solution normally distributed does not depend on the random sample size m.

Fig. 5 illustrates a comparison between statistic values and p-values of the random solution of the prey by using the S-W test. **Fig. 6** compares the values of the unexpected solution of the predator by using the same test. It supports the previous result that the random solution does not need to have normal distribution over time and the normality does not depend on whether the initial sample sizes are small or large.
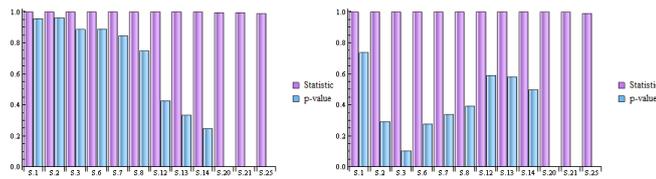
Fig. 5. Comparison between statistics values and P-values of the random solution of the prey by using the S-W test at different times and with different initial sample sizes where $X_0 \sim N(0.3, 0.05)$ and $Y_0 \sim N(0.15, 0.02)$.
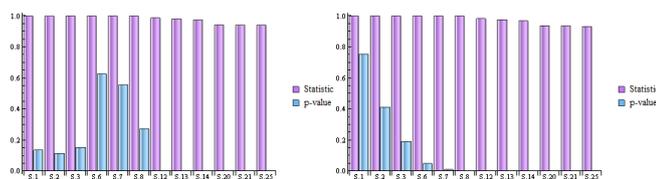
Fig. 6. Comparison between statistics values and P-values of the random solution of the predator by using the S-W test at different times and with different initial sample sizes where $X_0 \sim N(0.3, 0.05)$ and $Y_0 \sim N(0.15, 0.02)$.
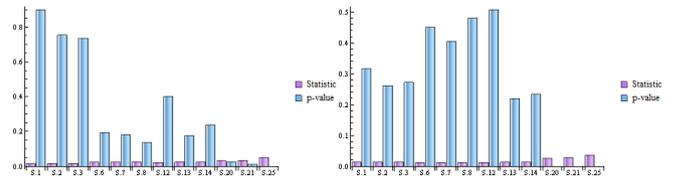
Fig. 7. Comparison between statistics values and P-values of the random solution of the prey by using the K-S test at different times and with different initial sample sizes where $X_0 \sim N(0.3, 0.05)$ and $Y_0 \sim N(0.15, 0.02)$.
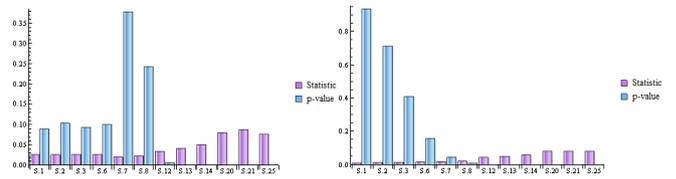
Fig. 8. Comparison between statistics values and P-values of the random solution of the prey by using the K-S test at different times and with different initial sample sizes where $X_0 \sim N(0.3, 0.05)$ and $Y_0 \sim N(0.15, 0.02)$.

The same results are observed when we use the K-S test, as illustrated in **Fig. 7** for the prey, and **Fig. 8** for predators.

Similarly, **Table 1** and **Table 2** give numerical simulation results of the p-values of the random solution of the prey and their predators, respectively, by using the S-W test and the K-S test for normality. These numerical results confirm what we have said previously.

Table 1. Simulation results of the p-values of the prey based on the S-W test and K-S test with different random initial samples where $X_0 \sim N(0.3, 0.05)$ and $Y_0 \sim N(0.15, 0.02)$.

Sample	S-W $m = 1000$	S-W $m = 2000$	S-W $m = 3000$	K-W $m = 1000$	K-W $m = 2000$	K-W $m = 3000$
$\{X_1\}$	0.9561	0.8115	0.7362	0.8993	0.3887	0.3161
$\{X_2\}$	0.9599	0.5419	0.2899	0.7554	0.3060	0.2609
$\{X_3\}$	0.8846	0.4640	0.1024	0.7356	0.2611	0.2718
$\{X_6\}$	0.8891	0.3712	0.2767	0.1933	0.1464	0.4504
$\{X_7\}$	0.8450	0.3566	0.3377	0.1807	0.1291	0.4055
$\{X_8\}$	0.7460	0.2873	0.3927	0.1350	0.0565	0.4797
$\{X_{12}\}$	0.4253	0.0174	0.5906	0.4018	0.0443	0.5071
$\{X_{13}\}$	0.3333	0.0053	0.5808	0.0173	0.0950	0.2187
$\{X_{14}\}$	0.2451	0.0000	0.4941	0.2380	0.0441	0.2332
$\{X_{20}\}$	0.0000	0.0000	0.0000	0.0242	0.0000	0.0000
$\{X_{21}\}$	0.0000	0.0000	0.0000	0.0102	0.0000	0.0000
$\{X_{25}\}$	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

Table 2. Simulation results of the p-values of the predator based on the S-W test and K-S test with different random initial samples where $X_0 \sim N(0.3, 0.05)$ and $Y_0 \sim N(0.15, 0.02)$.

Sample	S-W $m = 1000$	S-W $m = 2000$	S-W $m = 3000$	K-W $m = 1000$	K-W $m = 2000$	K-W $m = 3000$
$\{Y_1\}$	0.1344	0.8057	0.7539	0.0889	0.7502	0.9377
$\{Y_2\}$	0.1447	0.6384	0.4113	0.1035	0.9299	0.7119
$\{Y_3\}$	0.1528	0.4607	0.1904	0.9348	0.9498	0.4099
$\{Y_6\}$	0.6251	0.3216	0.0474	0.1002	0.5340	0.1569
$\{Y_7\}$	0.5549	0.0345	0.0088	0.3784	0.0444	0.0452
$\{Y_8\}$	0.2726	0.0019	0.0002	0.2433	0.0042	0.0075
$\{Y_{12}\}$	0.0000	0.0000	0.0000	0.0060	0.0000	0.0000
$\{Y_{13}\}$	0.0000	0.0000	0.0000	0.0002	0.0000	0.0000
$\{Y_{14}\}$	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
$\{Y_{20}\}$	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
$\{X_{21}\}$	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
$\{X_{25}\}$	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

The ratio-dependent predator-prey model (7) is nonlinear, and the normal distribution is closed under linear transformation. Therefore, the random solution will theoretically lose its normality after one unit. There are other ideas of using the principles of normal distribution even though the given solution is a non-normal random solution.

Transforming a non-normal distribution solution into the normal one is applicable. It is performed in several ways, such as taking a logarithm, square root, or arcsine square root. The concept of the sampling distribution is also helpful based on *the Central Limit Theorem*. The theorem states that if we add together many independent identically distributed random variables drawn from any distribution, the resulting sum will be normally distributed [25].

2.2. The Probability Density Function of the Solution

The initial population sizes of the ratio-dependent predator-prey model **7** are assumed to have a normal distribution which is entirely characterized by the parameters μ (mean) and σ^2 (variance). The crisp behavior of model **2** is periodic, which is also followed by all solutions that have initial states in the samples $\{X_0^q, q = 1, \cdots, m\}$ and $\{Y_0^q, q = 1, \cdots, m\}$, which will finally construct the random solution. The probability density function of the prey and their predators generally describes the distribution, relative likelihood, and probabilistic behavior of the prey and predators over time. The probability density functions of prey and predators are numerically calculated where they are initially symmetric around their means and take many shapes over time. Their skewness values start as zero and change positively and negatively over time. At first, the bulks of the values symmetrically lie around the means and change to be concentrated on the right and left when the distributions are negative skew and positive skew, respectively.
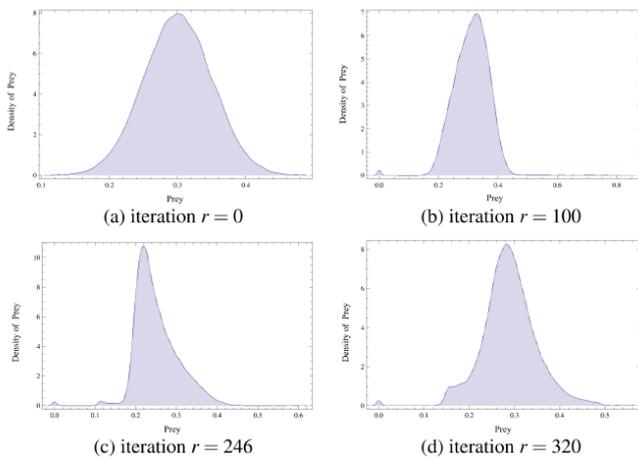
Fig. 9. Changing of the shapes of PDF of the prey over time, where $a = 0.2, b = 0.02, H = 3, c = 0.95, d = 0.25, and\ K = 90$ and $X_0 \sim N(0.3, 0.05)$ and $Y_0 \sim N(0.15, 0.02)$. with the sample distribution size $m = 60000$.

Fig. 9 shows the different shapes of the probability density function of the preys over time, and **Fig. 10** indicates the movement and changing of the shapes of the probability density function of the predators at different stages. The parameters in this simulation are chosen to show the model behavior. The random sample size is determined to be large enough to allow us to give a better description of the populations over time. Here, we are not interested in the quantitative aspect of the model but the qualitative one. So, any other parameter values should give the same qualitative behavior.

The cumulative distribution function is another helpful way to describe the distribution of the prey and predator. It can be calculated via the probability distribution function, which is beneficial to characterize the probability measure underlying the random variable by integrating the probability density function. It gives the probability that the variable will have a value less than or equal to any selected value. In the current study, the cumulative distribution functions of the prey and the predator are numerically obtained. Their curves allow us to infer whether the distribution has a low or high degree of kurtosis, which will give us information about how the prey and their predators are spread out.
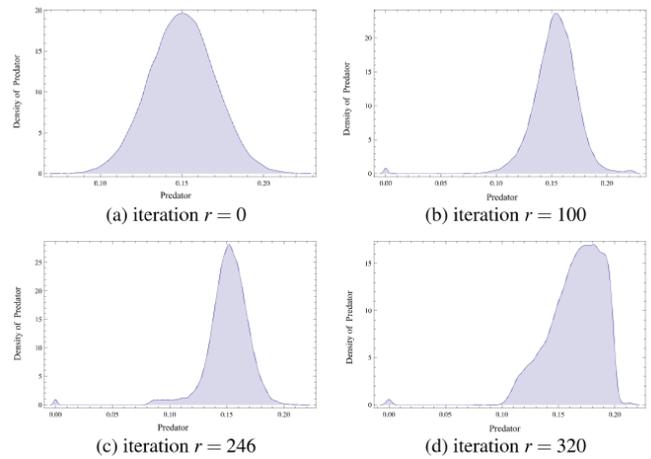
Fig. 10. Changing of the shapes of PDF of the prey over time, where $a = 0.2, b = 0.02, H = 3, c = 0.95, d = 0.25, and\ K = 90$ and $X_0 \sim N(0.3, 0.05)$ and $Y_0 \sim N(0.15, 0.02)$. with the sample distribution size $m = 60000$.
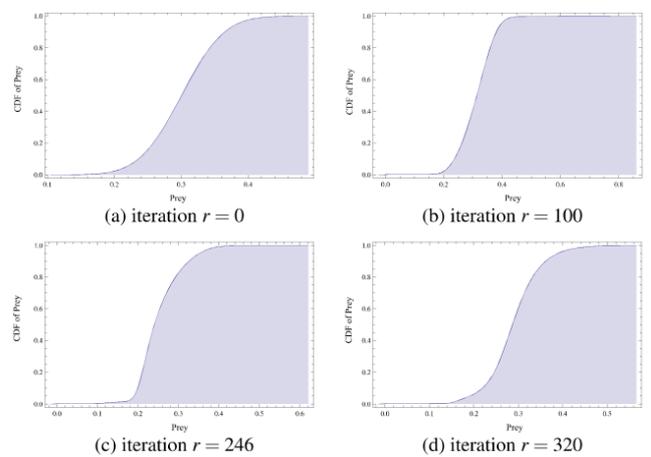
Fig. 11. Changing of the shapes of PDF of the prey over time, where $a = 0.2, b = 0.02, H = 3, c = 0.95, d = 0.25, and\ K = 90$ and $X_0 \sim N(0.3, 0.05)$ and $Y_0 \sim N(0.15, 0.02)$. with the sample distribution size $m = 60000$.

The movement of the cumulative distribution function of preys over time is illustrated in **Fig. 11**, which shows different shapes. The behavior of the cumulative distribution function of predators over time is indicated in **Fig. 12** at other times. The CDF curve in **Fig. 11b** shows a higher variance than the one in **Fig. 11d**; that is, the uncertainty at iteration $r = 320$ is lower than at $r = 100$ and so on. The same can be said in **Fig. 12a** and **Fig. 12c**.
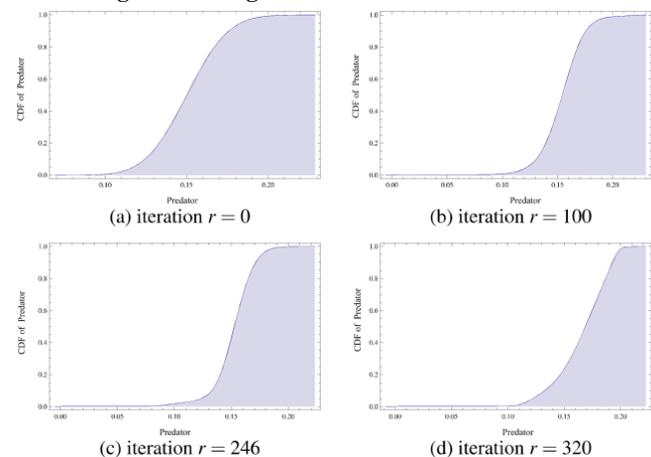
Fig. 12. Changing of the shapes of PDF of the prey over time, where $a = 0.2, b = 0.02, H = 3, c = 0.95, d = 0.25, and\ K = 90$ and $X_0 \sim N(0.3, 0.05)$ and $Y_0 \sim N(0.15, 0.02)$. with the sample distribution size $m = 60000$.

2.3. The Means of the Random Solution

The mean or the first moment is one of the essential properties of the random solution. It determines the location of the distribution of the prey. The predators were choosing various means, which will be the mean of the normal distribution, affecting the initial states of the populations and consequently influencing this population behavior. In the ratio-dependent predator-prey model (6), the mean of the random solution of predators and their prey follows the crisp, periodic solution in this simulation. For more accuracy, we calculate the 95% confidence intervals on all means of the predators and the prey, which means that in a 95% confidence interval, the mean μ will be between the endpoints. Still, in a 5% confidence interval, it will not be.

Fig. 13 describes how determining a 95% confidence interval on the mean of prey is affected by the sample size m. The parameters and the random initial conditions of the population are chosen as $v = 2$, $\beta = 0.7808$, $\delta = 0.5$, $X_0 \sim N(0.3,0.05)$ and $Y_0 \sim N(0.15,0.02)$. In these figures, the bold lines illustrate the boundaries of the 95% confidence interval, while the dashed line illustrates the computed mean.
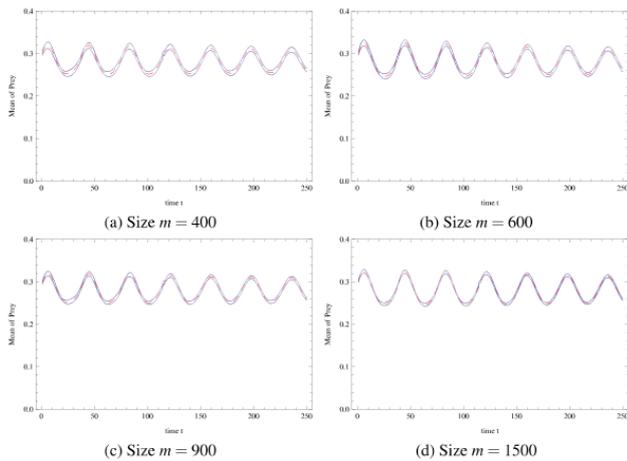
Fig. 13. Comparison of a 95% confidence interval of the means of the preys with different sample sizes m.
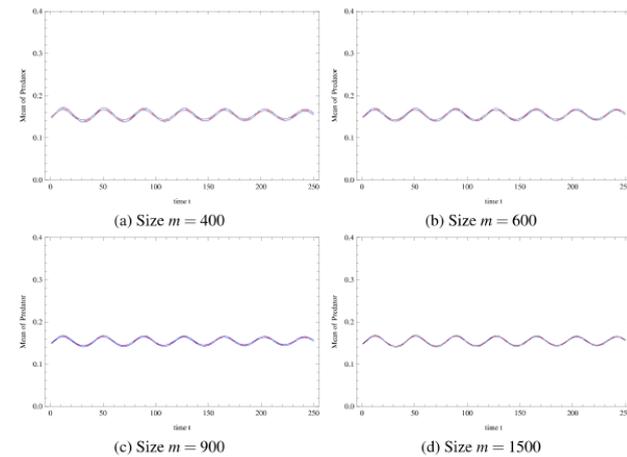
Fig. 14. Comparison of a 95% confidence interval of the means of the preys with different sample sizes m.

Similarly, **Fig. 14** depicts the 95% confidence interval of the mean of the predator. That means whichever value you pick in that interval will be close to the actual value. In these figures, we can observe that the ranges of the confidence intervals around the mean of the predator are pretty small compared with the fields of the prey in **Fig. 13**.

2.4. The Variances of the Random Solution

The variance defines the average squared deviations from the mean, representing the distribution of random variables around that mean. The starting variances of the prey and predators in the ratio-dependent predator-prey model (6) are identical to the conflicts of the standard distributions chosen as the beginning stages of the two populations, respectively. These differences increase and lessen as time passes. The width of the probability density function that characterizes the random solution is swaying, but the variances are finite over time, so the width is still limited. We compute the 95% confidence intervals on the variances over time to precisely extract the variances of the prey and their predators. The results reveal that the random sample size affects the width of the confidence intervals, which lowers as the sizes m rise.

Fig. 15 shows a 95% confidence interval for the preys variances, while **Fig. 16** displays a 95% confidence interval for the predators variances, with a different sample size m where the quantities in the simulation are set as $v = 2$, $\beta = 0.7808$ and $\delta = 0.5$, and $X_0 \sim N(0.3,0.05)$ and $Y_0 \sim N(0.15,0.02)$.The bold lines in these figures represent the 95% confidence interval limits, while the dashed line represents the computed variance.
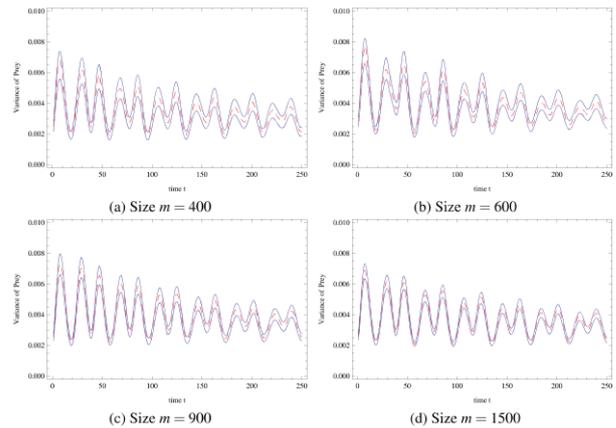
Fig. 15. Comparison of a 95% confidence interval of the variances of the preys with different sample sizes m.
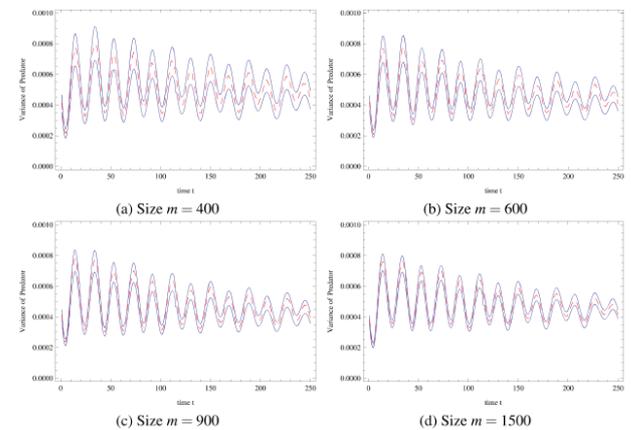
Fig. 16. Comparison of a 95% confidence interval of the variances of the preys with different sample sizes m.

In most cases, the result we arrive at after running these simulations is when uncertainty is considered. The ideas included inside the crisp models will be influenced and spread into random notions.

In addition, the lack of confidence over the initial values limits the solutions as they develop. The bound is distinct from the family of solutions in deterministic initial conditions, as the simulations have shown; yet, the distinctions between the bound and the family of solutions remain the same as the solution becomes.

Conclusion

The interaction between population models and uncertainty characteristics is the primary focus of this research. We frequently use the term "uncertainty" when we are confronted with situations in which we do not have adequate information or when the quantities necessary to define mathematical models of natural processes are unknown. To study the uncertainty present in population models, we used a more complicated predator-prey model that included a ratio-

dependent functional response. We have examined the uncertainty associated with the initial value. Our fundamental goal is to find a solution to the dilemma posed by the necessity of coping with and quantifying uncertainty. To overcome this obstacle, we relied heavily on the analytical strength of probability theory. The findings indicate that random behaviour can be constrained as a generalization of crisp behaviour, which makes the phenomenon description more realistic than the classical one. In addition, the interactions that take place between the various components of the model will not be classical. It will make itself known in the form of uncertainty, bounded by the range of probability density functions, which will shift with time.

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