Approximate Analytic Solution to the Three Species Lotka – Volterra Differential Equation Model

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Abstract

This paper provides an approximate analytic solution to the three species Lotka – Volterra differential equations by symbolic regression. The approximate analytic solution through symbolic regression is made as close as desired to the actual analytic solution by using the Jacobian system. This is proposed as the equilibrium will be stabilized if and only if the real parts of each of the eigenvalues are negative. As a result, the symbolic regression approach is found to provide an approximation to the faster convergence that can be expected with a more refined Euler numerical approach.

Keywords: approximation, analytic solution, Lotka-Volterra, differential equation model

1.0 Introduction

The famous Lotka – Volterra model is a pair of differential equations representing the populations of predator-prey species that interact with each other. The model was individually proposed in 1925 by Lotka (1925) and Voltera (1926). Suppose that the model extends the two-species model and considers the three-species model with one species at the bottom of the food chain, one in the middle, and one at the top Chauvet et al. (2002). Let these species be x, y, and z and denote the differential equations modeling their behavior by:

$$\frac{dx}{dt} = \alpha x - \beta xy$$

$$\frac{dy}{dt} = -\gamma y + \delta xy - \sigma yz \qquad (1)$$

$$\frac{dz}{dt} = -\varphi z + \mu yz$$

where $x(t)$ represents the population of the species at the bottom of the food chain the producer and $y(t)$ represents the population of the species in the middle of the primary consumer and $z(t)$ represents the population of the top of the food chain or the predator. Equation (1) is independent in the sense that the right-hand side is not explicitly expressed in terms of time. The Lotka–Volterra predator-prey model (Volterra, 1926), is used to study a differential equation system with diffusion and time delays which model the dynamics of predator-prey interactions within three biological species (Wei, 2007). Pekalski and Stauffer (1998) studied of the dynamics of three-species predator-prey models with time delays. Early studies such as those by Guerrero et al. (2009) focused on obtaining analytical solutions for the transport equations, whereas recently numerical solutions have become increasingly popular using widely available computer software.

Regardless of the rising number of Lotka – Volterra applications, this model is a minor generalization of the two-species model: it adds a third species, but it only allows for a chain of predation. Still, considerable interest remains in analytical solutions because they may be used as relatively simple screening models in regulatory decision making by Devireddy (2016); Regalado and Castillano (2019), and because analytical solutions may serve as benchmarks for testing numerical solutions.

Since 1970s, there have been some interesting and impressive results to the analytic solution on the dynamics of three species predator-prey systems. In the past years, Hsu et al. (2015) analyzed the three species Lotka–Volterra food web model with omnivore which was defined as feeding on more than one trophic level. Pontedeiro et al. (2007) obtained solutions on a finite domain using a semi-analytical approach to perform sensitivity analyses and risk assessments of technologically enhanced, naturally occurring radioactive material (TENORM) disposed in an industrial landfill. The paper solved the decay chain problem using a semi-analytic approach known as the Generalized Integral Transform Technique (GITT), which is a generalization of the Classic Integral Transform Technique, or CITT (Cotta & Mikhailov, 1993). Recently, Cassol et al. (2009) combined GITT and CITT techniques with Laplace transforms and matrix diagonalization methods to develop an analytical solution for transient two-dimensional atmospheric pollutant dispersion on a semi-infinite spatial domain.

There are many papers focused on obtaining analytical solutions for the transport equations, whereas more recent numerical solutions have become increasingly popular using widely available computer software. However, there is no closed-form shown that analytic solution to this three-species predator-prey model exists in the literature. The analytic solutions are still a problem for the three species Lotka–Volterra Equation. Hence, this paper intends to find approximate analytic solutions to the Extended Lotka – Volterra equations.

2. 0 Three-Species Model

Suppose that Lotka – Volterra model would be extended from the two-species model into a three-species model with one species at the bottom of the food chain, one in the middle, and one at the top. Let these species be x, y, and z and denote the differential equations modeling their behavior by equation (1).

The three – species model is a very minor generalization of the two-species model: it adds a third species, but it only agrees for a chain of predation (i.e. this model does not agree us to consider the case where both y and z prey on x or where x and y are at the bottom of the food chain and z preys on both).

Simplified Solution of the Three-Species Model

To find the balances of this model, the researcher considers the values x, y, z for which $\frac{dx}{dt} = \frac{dy}{dt} = \frac{dz}{dt} = 0$. Thus:

$$\begin{cases} \frac{dx}{dt} = x(a - \beta y) \\ \frac{dy}{dt} = y(\delta x - \gamma - \sigma z) \\ \frac{dz}{dt} = z(\mu y - \varphi) \end{cases} \tag{2}$$

This model has related parameters as the classic model: x has a growth rate denoted by ax

while y and z have a natural death rate denoted by $-\gamma y$ and $-\varphi z$, respectively. δxy and μyz denote the growth rate of y and z from hunting their prey and $-\beta xy$ and $-\sigma yz$ denote the death rate of the prey as a result of being hunted. It is interesting to note that the authors chose to give species y a death rate (the negative sign in front of – γy) instead of a growth rate in the absence of a predator z.

Qualitative Solutions Using Equilibrium Points

Without expressly solving the differential equations, the equilibrium points can be analyzed. Equilibrium points are points for which the derivatives with respect to time are zero. Thus, for the classical Lotka-Voltera model illustrates:

$$x(\alpha - \beta y = 0) \; and - y(\gamma - \delta x\,) = \;0 \tag{3}$$

which yields:

$$x = 0, y = 0 \; and \; x = \frac{\gamma}{\delta}\,, y = \;\frac{\alpha}{\beta} \tag{4}$$

The first solution comes when the two species become nonexistent. The second solution represents a set point at which the populations sustain their present number indefinitely. The Jacobian matrix of the LV model is given by

$$\mathrm{J} = \begin{bmatrix} \alpha - \beta y & -\beta \mathrm{x} & 0 \\ \delta x & -\gamma + \delta x - & \sigma z \\ 0 & \mu z & \mu y - \varphi \end{bmatrix}$$

Likewise, for the trivial equilibrium position $(0, 0, 0)$, of the three species Lotka - Volterra model, we consider the case where *(a – βy) = (μy – φ) = (δx – γ – σz) = 0*. The $y = \dfrac{\alpha}{\beta} = \dfrac{\varphi}{\mu}$. Therefore, a second equilibrium position exists only when the constant parameters $\mu\alpha = \varphi\beta$.

The Jacobian of the system was proposed. Taking the appropriate partial derivatives, it has been found that:

$$\begin{aligned}(\,J(x,y,z) - \lambda I) = [\alpha - \beta y - \lambda \; - \beta x \; 0 \; \delta y \\ - \gamma + \delta x - \sigma z - \lambda \\ - \sigma y \; 0 \; \mu z \; \mu y - \varphi - \lambda\,]\end{aligned} \tag{5}$$

The system will have an asymptotical order solution if and only if all the real parts of the eigenvalues of the Jacobian are negative. Consider the roots of the characteristic equation of the above Jacobian, given by

$$\begin{aligned}det(J(x,y,z) - \lambda I) = [\alpha - \beta y - \lambda \; - \beta x \; 0 \; \delta y \\ - \gamma + \delta x - \sigma z - \lambda \\ - \sigma y \; 0 \; \mu z \; \mu y - \varphi - \lambda\,]\end{aligned} \tag{6}$$

To attempt the order of an equilibrium position (*x, y, z*) of a system with constants a b, etc. by working these values into the Jacobian and finding the eigenvalues. The equilibrium will be stabilized if and only if the real parts of each of the eigenvalues are negative.

Numerical Finite Difference Method

Let x be the bottom species or producer density, y be the middle species or primary consumer density and z be the top species or predator density, thus:

$$\begin{aligned} \frac{dx}{dt} &= ax\left(1 - \frac{x}{K}\right) - \frac{\beta xyz}{1+\beta x} \\ \frac{dy}{dt} &= \gamma y\left(1 - \frac{y}{kx}\right) + \left(\frac{\delta xy}{1+\delta y}\right) - \left(\frac{\sigma yz}{1+\sigma y}\right) \\ \frac{dz}{dt} &= \varphi z\left(1 - \frac{z}{kxy}\right) \end{aligned} \tag{7}$$

where βxyz is the interaction rate between the species, $\dfrac{\beta xyz}{1+\beta x}$ is the effective rate of eating bottom species, γ is the mortality rate of the predators, K and k are the carrying capacitance of each population. x has a growth rate denoted by ax while y and z have a natural death rate denoted by $-\gamma y$ and $-\varphi z$, respectively, δxy and σyz denote the growth rate of y and z from hunting their prey and $-\beta xy$ and $-\sigma yz$ denote the death rate of the prey as a result of being hunted.

Example: Let x=100, y=100, z=100. Then, a=15, γ=0.05, δ=0.09, K=500, k=0.82, β=0.01, φ=1.9, σ=0.5, $x(0)$=100, $y(0)$=100, $z(0)$=100

The Euler's recursive relation is,

$$\begin{aligned} x_i &= x_{i-1} + xs_{i-1}\Delta t \\ y_i &= y_{i-1} + ys_{i-1}\Delta t \\ z_i &= z_{i-1} + zs_{i-1}\Delta t \end{aligned} \tag{8}$$

where $S_{(i-1)}$ in the equation (8) represent of the slope of every species and Δt represent of the change of time.

This leads to the recurrence:

$$\begin{aligned} x_i &= x_{i-1} + \left(15x_{i-1}\left(1 - \frac{x_{i-1}}{500}\right) - \left(\frac{0.01x_{i-1}y_{i-1}z_{i-1}}{0.01+1x_{i-1}}\right)\right)(0.1) \\ y_i &= y_{i-1} + \left(0.05y_{i-1}\left(1 - \frac{y_{i-1}}{0.82x_{i-1}}\right)\right. \\ &\quad \left. - \left(\frac{0.09x_{i-1}y_{i-1}}{1+0.09y_{i-1}}\right) + \left(\frac{0.5y_{i-1}z_{i-1}}{1+0.5y_{i-1}}\right)\right)(0.1) \\ z_i &= z_{i-1} + \left(1.9z_{i-1}\left(1 - \frac{z_{i-1}}{0.82x_{i-1}y_{i-1}}\right)\right)(0.1) \end{aligned} \tag{9}$$

3.0 Three-Species Model using Symbolic Regression Approach

The symbolic regression approach is a type of regression analysis that searches the space of mathematical expressions to find the model that best fits a given data set. No model is provided as a starting point to the algorithm. Instead, initial expressions are formed by randomly combining mathematical building blocks such as mathematical operators, analytic functions, constant, and state variables. New equations are then formed by recombining previous equations, using genetic programming.

The values are then entered into symbolic regression software with generated ordered pairs $\{(t_i, x_i)\}_{i=0}^{n}$ for the population of the species at the bottom, $\{(t_i, y_i)\}_{i=0}^{n}$ for the population of the species at the middle and $\{(t_i, z_i)\}_{i=0}^{n}$ for the population of the species at the top. Let $t_i = ih$, $i=0, 1,2,\ldots,n$, and step size h, where $h = 0.001$.

Table 1. *The result of the first iteration*

T	Producer	Primary Consumer	Top Predator
0	100	100	100
0.001	96.2	99.95870636	100.1876829
0.002	92.45503286	99.89916516	100.3756209
0.003	88.76825685	99.82163294	100.563807
0.004	85.14280942	99.72638952	100.7522337
0.005	81.58179248	99.61373724	100.9408929
0.006	78.08825643	99.4840001	101.1297755
0.007	74.66518313	99.33752279	101.3188717
0.008	71.31546787	99.17466962	101.5081706
⋮	⋮	⋮	⋮
1.489	8.648208124	12.25357802	14.99960432
1.49	8.761057434	12.24801042	15.02318419
1.491	8.875348481	12.24248318	15.04685473
1.492	8.991098972	12.23699646	15.07061565
1.493	9.108326815	12.23155042	15.09446667
1.494	9.227050124	12.22614522	15.1184075
1.495	9.347287215	12.22078106	15.14243787
1.496	9.469056614	12.21545811	15.16655749
1.497	9.592377053	12.21017658	15.19076611
1.498	9.717267476	12.20493667	15.21506346
1.499	9.843747041	12.1997386	15.23944928
1.5	9.971835119	12.19458258	15.26392331

Table 2. *Result Statistics for the Symbolic Regression Analysis*

Species	**MSE**	$\boldsymbol{R^2}$	**Equation**
$x(t)$	138.28192	0.9889	$x = 0.922t^{14} \, sin(0.014t^2) + 1.0t^2 \, exp(8.09t \, cos(0.92t^4))$
$y(t)$	12.671713	0.9954	$y = 6.33 + 11.1t + 11.1t \, sin\left(sin(2.86 + 2.26t + 2.26t^2)\right)$ $+ 39.6 \, exp\left(3.78 \, sin(2.86 + 2.26t + 2.26t^2)\right)$ $- 3.78 \, sin(2.86 + 2.26t + 2.26t^2)$ $- 33.77t \, exp\left(3.78 \, sin(2.86 + 2.26t + 2.26t^2)\right)$
$z(t)$	65.35765	0.8906	$z = 153 + 1416.86t^2 + 377.65t \, sin(3.18t) - 1076t - 446.4t^3$ $- 251.7t^2 \, sin(3.18t) - 85.5t^2 \, sin(3.18t)^2$

Table 1 shows the first iteration of the simulated data using equation (9). These data are used to approximate the analytic solution to the extended Lotka –Volterra differential equation model.

Table 2 shows summary statistics for the symbolic regression analysis. The Bottom species (producer) was more fluctuate than the Middle species (primary consumer) and the Top Species (predator).

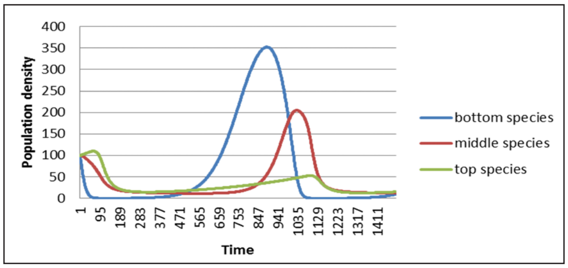

Figure 1. *Plot of $x(t)$, $y(t)$ and $z(t)$*

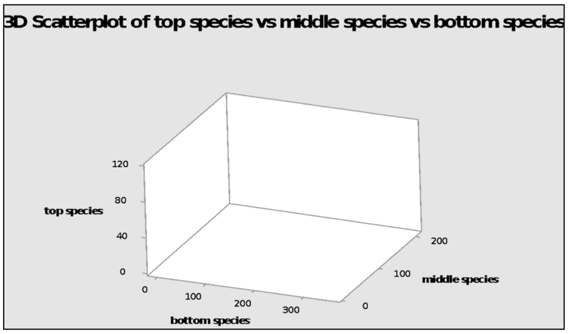

Figure 2. *Plot of $x(t)$ vs. $y(t)$ vs. $z(t)$*

Figure 1 shows the graph of the solutions $x(t)$, $y(t)$ and $z(t)$. The best fitting of the symbolic regression curve of the $x(t)$ gives an r – squared value of 98.89% with mean squared error (MSE) of 138.28, $y(t)$ gives an r – squared value of 99.54% with mean squared error (MSE) of 12.67 and for the $z(t)$ gives an r – squared value of 89.06% with mean squared error (MSE) of 65.36 This implies that the approximate solution of the $x(t)$, $y(t)$ and $z(t)$ is the best analytic solution to the extended Lotka – Volterra differential equations model.

Figure 2 shows the plot of $x(t)$ vs $y(t)$ vs $z(t)$ Note the closed trajectory as expected.

4.0 Conclusion and Recommendation

The symbolic regression analysis provides a proper means to determine an approximate analytic solution to the Three Species Lotka-Volterra non-linear differential equations. Therefore, the researcher recommends that the approximate analytic solution be made as close as the desired analytic solution of the three species Lotka-Volterra differential equation model problem. Likewise, since the finite difference approach is one method for arriving at a numerical solution of the differential equation, faster convergence can be expected with more sophisticated Euler numerical methods.

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