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# On Dynamical Analysis of a Prey-Diseased Predator Model with Refuge in Prey

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**Abstract:** In this paper, we propose a mathematical model of a prey-diseased predator model with refuge in prey system. In other words, a prey-predator model with an infectious disease in the prey population is formulated. This model is constituted by a system of three nonlinear ordinary differential equations of first order, which describe the interaction between the infected prey, non-infected prey and predator. The equilibria of the system are derived and the stability analyses of the disease-free and the endemic equilibria are conducted.

**Keywords:** Non-linear differential equations, Prey-predator model, Equilibria, Stability.

## 1 Introduction

The interactions of prey and predator species have been studied by many scientists, engineers and researchers since Lotka-Volterra model [1]. Similarly, the interactions among infected, susceptible and recovered population are becoming an interesting and important research work since Kermack-Kendrick work [2]. Nowadays, the dynamic systems involving diseased species in the eco-epidemiology research is playing an important role. Anderson and May were first introduced in [3] the combination of these two systems, and the term "eco-epidemiology" is used for the first time by Chattopadhyay and Arino in [4] for such type of models. In [5], the authors proposed and analyzed a mathematical model dealing with two species of prey-predator system, in which the prey population was divided as immature and mature prey population. It has a refuge capability as a defensive property against the predation. Many researchers and engineers have been studying various dynamics systems involving the prey and predator with different effects of biological factors, see, for example [6–10], and various mathematical models have been created in epidemiology using different types of incidence rates and diseases.

The aim of this paper is to propose a mathematical model of a prey-diseased predator model with refuge in prey system. In detail, in the proposed prey-predator model, an infectious disease is considered in the population of the prey and it is assumed that there is harvesting from the predator. In this model, there are three first-order nonlinear ordinary differential equations, these equations describe the interaction between the species infected prey, non-infected prey and predator. The disease-free and the endemic equilibria of the system are derived and the stability analyses of the two equilibria are conducted. Numerical simulations are presented to justify analytical results. The rest of the paper is arranged as follows. In Section 2, we present the formulation of mathematical model, Section 3 computes the disease-free equilibrium and endemic equilibrium points of the proposed model, Section 4 discusses the stability analyses of disease-free equilibrium and endemic equilibrium of the model, and finally Section 5 gives the conclusion.

## 2 Mathematical Model Formulation

The proposed model studies a prey-predator system involving infected disease in prey. We assumed that there is harvesting from the predator and a defensive property against predation. In this model, we make some hypotheses.

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### 2.1 Assumptions

- The population density of prey is divided into two parts namely, the susceptible population density at time $t$ given by $X(t)$ and the infected population density at time $t$ denoted by $I(t)$, and the population density of predator at time $t$ is given by $Y(t)$.
- The predator population consumes both prey populations according to modified Holling type-II functional response for the predation [11] with half saturation constant $b > 0$ and maximum attack rates $a_1 > 0$ and $a_2 > 0$ for susceptible prey and infected prey respectively. Since there is a vulnerability of infected prey relative to susceptible prey the vulnerability constant rate $\theta > 0$ is used in the functional response. Moreover the constants $e_1 \in (0,1)$ and $e_2 \in (0,1)$ are the conversion rates from susceptible and infected preys to predator respectively.
- The disease causes a death in the infected population that is represented by diseased death rate $d > 0$.
- The prey and predator populations growth rates are $\alpha_1 > 0$ and $\alpha_2 > 0$ respectively.
- There is a type of protection of prey population from the predation by predator, which is represented by a constant prey's refuge rate $p \in (0,1)$ that leaves $(1-p)X$ of prey available to be hunted by the predator.
- Let $\beta > 0$ be the rate of infection.

Under the above assumptions, the dynamics of the prey-predator model can be described as follows.

$$\frac{dX}{dt} = \alpha_1 X - \left(\frac{e_1 a_1(1-p)Y + e_2 a_2(1-p)I}{b+(1-p)Y+\theta(1-p)I}\right)X, \qquad (1)$$

$$\frac{dY}{dt} = \alpha_2 Y + \frac{a_1(1-p)XY}{b+(1-p)Y+\theta(1-p)I} - \beta YI, \qquad (2)$$

$$\frac{dI}{dt} = \beta YI + \frac{a_2(1-p)XI}{b+(1-p)Y+\theta(1-p)I} - dI, \qquad (3)$$

with the non-negative initial conditions $X(0) \geq 0, Y(0) \geq 0, I(0) \geq 0$.

## 3 Equilibrium Points of the Model

In this section, we find the disease-free equilibrium and endemic equilibrium points of the proposed model.

### 3.1 Disease-free Equilibrium

The Disease-free equilibrium point can be calculated by substituting $I = 0$ in the system of (1)-(3). Now, from (1), we have

$$\alpha_1 X - \left(\frac{e_1 a_1(1-p)Y}{b+(1-p)Y}\right)X = 0.$$

Solving above equation, we get $X = 0$ or $Y = \frac{\alpha_1 b}{(1-p)(e_1 a_1 - \alpha_1)}$. Now from (2), we have

$$\alpha_2 Y + \frac{a_1(1-p)XY}{b+(1-p)Y} = 0.$$

Solving this equation, we get $Y = 0$ or $X = \frac{\alpha_2 e_1 b}{(1-p)(\alpha_1 - e_1 a_1)}$. Hence, the disease vanishes in the population at the point

$$\begin{aligned} D_0 &= (X_0, Y_0, I_0) \\ &= \left(\frac{\alpha_2 e_1 b}{(1-p)(\alpha_1 - e_1 a_1)}, \frac{\alpha_1 b}{(1-p)(e_1 a_1 - \alpha_1)}, 0\right). \end{aligned} \qquad (4)$$

### 3.2 Endemic Equilibrium

Expand (3) and notice that each variable is non-negative, we have

$$\begin{aligned} &I^*(\beta Y^*(b+(1-p)Y^*+\theta(1-p)I^*)+a_2(1-p)X^* \\ &\quad -d(b+(1-p)Y^*+\theta(1-p)I^*)) = 0, \end{aligned} \qquad (5)$$

from this equation, we get $I^* = 0$ which corresponds to disease-free equilibrium or

$$I^* = \frac{db+d(1-p)Y^*-a_2(1-p)X^*-\beta Y^* b-\beta(1-p)Y^{*2}}{\beta Y^*\theta(1-p)-d\theta(1-p)}. \qquad (6)$$

Notice that (5) is true for two values of $I^*$, i.e., $I^* = 0$ which corresponds to the disease-free equilibrium and (6) that gives the population of the infective when the infection invaded the ecosystem.

Substituting $I^* = 0$ into (1) and (2), we have

$$\alpha_1 X^* b + \alpha_1(1-p)X^*Y^* - e_1 a_1(1-p)X^*Y^* = 0 \qquad (7)$$

$$\alpha_2 Y^* b + \alpha_2 Y^{*2}(1-p) + a_1(1-p)X^*Y^* = 0. \qquad (8)$$

Given that $X^*$ and $Y^*$ are non-negative then from (7), we have

$$Y^* = \frac{\alpha_1 b}{N}, \qquad (9)$$

where $N = (1-p)(\alpha_1 - e_1 a_1)$. Putting (9) into (8), we get

$$X^* = \frac{\alpha_2 b(a_1 e_1 - 2\alpha_2)}{a_1 N}. \qquad (10)$$

Now putting (9) and (10) into (6), we get

$$I^* = \frac{I_n^*}{I_d^*}, \qquad (11)$$

where

$$\begin{aligned} I_n^* =& b(N^2 a_1^2 d - N a_1 \alpha_1 b\beta + N a_1 \alpha_1 d(1-p) \\ & - \alpha_1^2 b\beta(1-p) - N a_1 a_2 \alpha_2(1-p)(a_1 e_1 - 2\alpha_1)) \\ I_d^* =& N a_1 \theta(1-p)(\alpha_1 b\beta - N a_1 d). \end{aligned}$$

Hence, the endemic equilibrium point $D^* = (X^*, Y^*, I^*)$ is given by (9),(10) and (11), i.e.,

$$D^* = (D_1^*, D_2^*, D_3^*),$$

where

$$\begin{aligned} D_1^* &= \frac{\alpha_2 b(a_1 e_1 - 2\alpha_2)}{a_1 N} \\ D_2^* &= \frac{\alpha_1 b}{N}, \\ D_3^* &= \frac{D_{3n}^*}{D_{3d}^*}, \\ N &= (1-p)(\alpha_1 - e_1 a_1), \end{aligned}$$

where

$$\begin{aligned} D_{3n}^* =& b(N^2 a_1^2 d - N a_1 \alpha_1 b\beta + N a_1 \alpha_1 d(1-p) \\ & - \alpha_1^2 b\beta(1-p) - N a_1 a_2 \alpha_2 (1-p)(a_1 e_1 - 2\alpha_1)) \\ D_{3d}^* =& N a_1 \theta(1-p)(\alpha_1 b\beta - N a_1 d). \end{aligned}$$

## 4 Stability Analysis

In this section, we discuss the local stability analysis of disease-free equilibrium and endemic equilibrium of the model.

### *4.1 Stability Analysis of Disease-free Equilibrium*

To perform the local stability of the system around disease-free equilibrium, the Jacobian matrix of the model is derived and evaluated at disease-free equilibrium. The result is obtained as

$$J_{DFE} = \begin{pmatrix} 0 & J_{12} & J_{13} \\ J_{21} & J_{22} & J_{23} \\ 0 & 0 & J_{33} \end{pmatrix}, \tag{12}$$

where

$$\begin{aligned} J_{12} &= -\frac{e_1 a_1 (1-p) X_0}{b + (1-p) Y_0} + \frac{e_1 a_1 (1-p)^2 X_0 Y_0}{(b + (1-p) Y_0)^2}, \\ J_{13} &= -\frac{e_2 a_2 (1-p) X_0}{b + (1-p) Y_0} + \frac{e_1 a_1 \theta (1-p)^2 X_0 Y_0}{(b + (1-p) Y_0)^2}, \\ J_{21} &= \frac{a_1 (1-p) Y_0}{b + (1-p) Y_0}, \\ J_{22} &= \alpha_2 + \frac{a_1 (1-p) X_0}{b + (1-p) Y_0} - \frac{a_1 (1-p)^2 X_0 Y_0}{(b + (1-p) Y_0)^2}, \\ J_{23} &= -\frac{a_1 \theta (1-p)^2 X_0 Y_0}{(b + (1-p) Y_0)^2} - \beta Y_0, \\ J_{33} &= \beta Y_0 + \frac{a_2 (1-p) X_0}{b + (1-p) Y_0} - d. \end{aligned}$$

The disease-free equilibrium is locally asymptotically stable if all the eigenvalues of Eq. (12) are less than zero. If row reduced matrix operation is applied to Eq. (12) then

$$J_{DFE} = \begin{pmatrix} J_{21} & J_{22} & J_{23} \\ 0 & J_{12} & J_{13} \\ 0 & 0 & J_{33} \end{pmatrix}. \tag{13}$$

The eigenvalues of Eq. (13) are $\lambda_1 = J_{12}, \quad \lambda_2 = J_{21}, \quad \lambda_3 = J_{33}$. Hence, the disease-free equilibrium of the model is locally asymptotically stable if $\lambda_1 < 0, \lambda_2 < 0$ and $\lambda_3 < 0$.

### *4.2 Stability Analysis of Endemic Equilibrium*

The Jacobian matrix of the system (1)-(3) evaluated at the endemic equilibrium is obtained as

$$J_{EE} = \begin{pmatrix} X_1^* & Y_1^* & I_1^* \\ X_2^* & Y_2^* & I_2^* \\ X_3^* & Y_3^* & I_3^* \end{pmatrix}, \tag{14}$$

where

$$\begin{aligned} X_1^* &= \alpha_1 - \frac{e_1 a_1 (1-p) Y^* + e_2 a_2 (1-p) I^*}{b + (1-p) Y^* + \theta(1-p) I^*}, \\ Y_1^* &= -\frac{e_1 a_1 (1-p) X^*}{b + (1-p) Y^* + \theta(1-p) I^*} \\ &\quad + \frac{(e_1 a_1 (1-p) Y^* + e_2 a_2 (1-p) I^*) X^* (1-p)}{(b + (1-p) Y^* + \theta(1-p) I^*)^2}, \\ I_1^* &= -\frac{e_2 a_2 (1-p) X^*}{b + (1-p) Y^* + \theta(1-p) I^*} \\ &\quad + \frac{(e_1 a_1 (1-p) Y^* + e_2 a_2 (1-p) I^*) X^* \theta (1-p)}{(b + (1-p) Y^* + \theta(1-p) I^*)^2}, \\ X_2^* &= \frac{a_1 (1-p) Y^*}{b + (1-p) Y^* + \theta(1-p) I^*}, \\ Y_2^* &= \alpha_2 + \frac{a_1 (1-p) X^*}{b + (1-p) Y^* + \theta(1-p) I^*}, \\ &\quad - \frac{a_1 (1-p)^2 X^* Y^*}{(b + (1-p) Y^* + \theta(1-p) I^*)^2} - \beta I^*, \\ I_2^* &= -\frac{a_1 (1-p)^2 X^* Y^* \theta}{(b + (1-p) Y^* + \theta(1-p) I^*)^2} - \beta Y^*, \\ X_3^* &= \frac{a_2 (1-p) I^*}{b + (1-p) Y^* + \theta(1-p) I^*}, \\ Y_3^* &= \beta I^* - \frac{a_2 (1-p)^2 X^* I^*}{(b + (1-p) Y^* + \theta(1-p) I^*)^2}, \\ I_3^* &= \frac{a_2 (1-p) X^*}{b + (1-p) Y^* + \theta(1-p) I^*} \\ &\quad - \frac{a_2 (1-p)^2 X^* I^* \theta}{(b + (1-p) Y^* + \theta(1-p) I^*)^2} - d. \end{aligned}$$

The local asymptotic stability of the endemic equilibrium can be verified in two ways. The endemic equilibrium of the model is locally asymptotically stable if it is shown that $\det(J_{EE}) > 0$ whenever $\operatorname{trace}(J_{EE}) < 0$. Also, the endemic equilibrium of the model is locally asymptotically stable if all the eigenvalues of Eq. (14) have negative real parts. Assuming the second method is used to investigate the local asymptotic stability of the endemic equilibrium of the model and suppose that the matrix in Eq. (14) is reduced via row reduce matrix operation then we have

$$J_{EE} = \begin{pmatrix} X_1^* & Y_1^* & I_1^* \\ 0 & \frac{X_1^*Y_2^*}{X_2^*} - Y_1^* & \frac{X_1^*I_2^*}{X_2^*} - I_1^* \\ 0 & 0 & \frac{Y_1^*[X_1^*I_3^* - X_3^*I_1^*]}{X_1^*Y_3^* - X_3^*Y_1^*} - I_1^* \end{pmatrix}. \tag{15}$$

Note that $X^*, Y^*$ and $I^*$ are the values of $X, Y$ and $I$ at the endemic equilibrium. If the characteristic equation $|J_{EE} - \lambda I| = 0$ of Eq. (15) is solved then the eigenvalues are obtained as

$$\lambda_1 = X_1^*, \quad \lambda_2 = \frac{X_1^*Y_2^*}{X_2^*} - Y_1^*, \quad \lambda_3 = \frac{Y_1^*[X_1^*I_3^* - X_3^*I_1^*]}{X_1^*Y_3^* - X_3^*Y_1^*} - I_1^*.$$

The endemic equilibrium of the model is locally asymptotically stable if each of the eigenvalues are less than zero, i.e., $\lambda_1 < 0, \lambda_2 < 0$ and $\lambda_3 < 0$.

## 5 Conclusion

This paper presents a mathematical model of a prey-diseased predator model with refuge in prey system. This model is constituted by a system of three nonlinear ordinary differential equations of first order, which describe the interaction between the infected prey, non-infected prey and predator. The equilibria of the system are derived and the stability analyses of the disease-free and the endemic equilibria are performed. At the disease-free equilibrium point, the model is locally asymptotically stable if $\frac{e_1a_1(1-p)^2X_0Y_0}{(b+(1-p)Y_0)^2} - \frac{e_1a_1(1-p)X_0}{b+(1-p)Y_0} < 0$, $\frac{a_1(1-p)Y_0}{b+(1-p)Y_0} < 0$ and $\beta Y_0 + \frac{a_2(1-p)X_0}{b+(1-p)Y_0} - d < 0$; and at the endemic equilibrium, the model is locally asymptotically stable if $X_1^* < 0$, $\frac{X_1^*Y_2^*}{X_2^*} - Y_1^* < 0$ and $\frac{Y_1^*[X_1^*I_3^* - X_3^*I_1^*]}{X_1^*Y_3^* - X_3^*Y_1^*} - I_1^* < 0$, where $X_i^*, Y_j^*$ are as in (14).

## Conflict of interest

The authors declare that they have no conflict of interest.

## References

[1] M. R. May: *Stability and Complexity in Model Ecosystems*. Princeton, NJ: Princeton University, 1973.

[2] W. O. Kermack, A. G. Mc Kendrick: *Contributions to the mathematical theory of epidemics, part1*. Proceedings of the Royal Society of London Series A, 115, 700–721, 1927.

[3] R. M. Anderson, R. M. May: *The invasion, persistence and spread of infectious diseases within animal and plant communities*. Philosophical Transactions of the Royal Society of London, Series B, 314:533–570, 1986.

[4] J. Chattopadhyay, O. Arino: *A predator-prey model with disease in the prey*. Nonlinear Analysis, 36:747–766, 1999.

[5] R. K. Naji, S. J. Majeed: *The Dynamical Analysis of a Prey-Predator Model with a Refuge-Stage Structure Prey Population*, Volume 2016, Article ID 2010464, 10 pages, 2016.

[6] S. Thota: *Prey-Predator Model for Awash National Park, Oromia, Ethiopia and Its Stability Analysis with Simulations*. Journal of Science and Sustainable Development, 7 (2), 15–21, 2019.

[7] S. Thota: *A mathematical study on a diseased prey-predator model with predator harvesting*. Asian Journal of Fuzzy and Applied Mathematics, 8 (2), 16–21, 2020.

[8] S. Thota: *On an Ecological Model of Mutualisim Between Two Species With a Mortal Predator*. Applications and Applied Mathematics, 15 (2), 1309–1322, 2020.

[9] A. S. Abdulghafour, R. K. Naji: *A Study of a Diseased Prey-Predator Model with Refuge in Prey and Harvesting from Predator*. Journal of Applied Mathematics, 2018, Article ID 2952791, 17 pages, 2018.

[10] Z. Ma, F. Chen, C. Wu, W. Chen: *Dynamic behaviors of a Lotka-Volterra predator-prey model incorporating a prey refuge and predator mutual interference*. Applied Mathematics and Computation, 219 (15), 7945–7953, 2013.

[11] S. Gakkhar, R. K. Naji: *Existence of chaos in two-prey, one-predator system*. Chaos, Solitons and Fractals, 17, 639–649, 2003.

[12] M. Awadalla, Y. Noupoue, K. Abuasbeh: *Population Growth Modeling via Rayleigh-Caputo Fractional Derivative*. J. Stat. Appl. Pro., 10, 11–16 2021: doi:10.18576/jsap/100102.

[13] A. Z. Al Rawashdeh, A. R. Al Arab, N. Alqahtani, Z.Hadmer: *The Sociological Understanding for Corona Crises and its Reflections on Society: An Inductive Analytical Vision*. J. Stat. Appl. Pro., 10, 267–286, 2021: doi:10.18576/jsap/100123

[14] Aafaq A. Rather, C. Subramanian: *A New Exponentiated Distribution with Engineering Science Applications*. J. Stat. Appl. Pro., 9, 127–137, 2020: doi:10.18576/jsap/090112

[15] T. Singh, R. Dubey, V. Narayan Mishra, M. Abdel-Aty. *Modeling of Diffusive Patterns in Predator–Prey System using Turing Instability and Amplitude Equations*. Inf. Sci. Lett., 10, 5–16, 2021: doi:10.18576/isl/100102

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