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A Mathematical Modeling Approach in Cybersecurity using Deep neural Learning

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ABSTRACT: Mathematical modeling has been proven to be a remarkably effective approach for bio-mathematician to study and understand the behavior of various malicious objects in a computer system. As a result of the similarities that exist between computer virus and disease infection, a SEIARS compartmental model has been proposed to model and analyses cyberspace attack where S stands for Susceptible, E for Exposed, I for Infected, A for Asymptomatic and R for Recovered. The dynamic of the model is governed by a set of differential equations that are usually solved by finite difference methods such as Euler method, Crank-Nicolson method, Runge-Kutta method. However, solutions obtained by these methods are stored in a discretized form that presents some limitations in terms of space memory occupied when high resolution result are required or an accumulation of approximation error on every step of a finite-difference methods. In that regard, a deep neural learning approach has been implemented to solve the system of ordinary differential equation of the epidemic model. It was found that neural network with one hidden layer shows good capacity in approximating the solution of the differential equation and it required less storage comparing to the traditional finite difference methods and the resulting solutions have been validated showing satisfactory relative error margins. For the convergence of the neural network model, BFGS has been a good optimization method comparing to the Conjugate Gradient as well as the Limited Memory BFGS methods.

I. INTRODUCTION

The growth of technology is beneficial to the modern industrial world with the use of computer software in various sector of our life such as: In medicine by improving the ability to analyze health information, in agriculture to enhance crop productivity and decrease the use of fertilizer and pesticides which in turn keeps food prices down as well as in telecommunication by seamlessly connecting and sharing information [1]. However, this growth in digitization of information has created a new sort of crime known as cyber-crime that occurs when cybercriminals install malicious software on someone's device without their knowledge in order to access personal information, usually for financial gain or damaging the device. The risks associated with these cyber-attacks in new paradigms such as the Industry 4.0 [2], the Artificial Intelligence [3], the Internet of Things [4]just to name the few, are important and, therefore, should be properly managed.

Malicious software are computer programs that operate on behalf of a potential intruder to attack a system or network. Computer programs such as worm or Trojan horses resemble to the way plagues can spread through a population [5]. In the same way viruses transmit diseases from one person to another, these programs can also spread through an interconnected computer system. Hence, based on these similarities, several mathematical models have been proposed to simulate the spreading of various malicious objects through a system. The design and computational implementation of these mathematical models are particularly important since it allows prediction of the behavior and the evolution of malware as well as in understanding the efficiency of different countermeasures.

Several researchers have proposed different mathematical models for malware propagation [6],[7]. These models are mostly compartmental and deterministic. They are compartmental model due to the fact that devices are classified into different compartments: Susceptible (S), Infected (I), Recovered (R), Quarantined (Q), Exposed (E), Asymptomatic (A)

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among others, according to their status. By considering the dynamics between these compartments, different type of models can be obtained [8]: SI, SIR, SIS, SEIR, SCIR just to name a few. They are deterministic models considering that the temporal evolution of these compartments is ruled by a system of different equations. The importance of these models lies in the fact that the theory behind the differential equations can be used to study the behavior and dynamics of their solutions. Ordinary Differential Equations (ODEs) are generally solved by discretization methods such as Euler method, Crank-Nicolson method, Runge-Kutta method among others [9]. Solutions obtained by these methods are stored in a discretized form such as an array. However, these solutions have some limitations in terms of huge amount of storage occupied when high resolution result are required or an accumulation of approximation error on every evolution step. Hence, Artificial Neural Network (ANN) approaches have been proposed [10] to address the limitations of solutions obtained when using discretization methods. It has been established that an ANN with a nonlinear activation function and a hidden layer can approximate any function provided that many hidden neurons are available [11].

Therefore, an efficient and accurate mathematical model will be developed in this work that helps in understanding thebehavior of various malicious objects through a device network. Moreover, a details analysis of the attack free and endemic equilibrium points of the model for local and global stabilities will be performed in order to obtain efficient control measures that involve several parameters and lastly, a deep learning-based approach will be used to obtain solutions of the model and discuss the results. The rest of the paper is organized as follows: In section 2 a detailed description of the mathematical model is formulated as well as the stability analysis of the equilibrium points is performed; in section 3 the numerical simulation and discussion of the result is presented, and finally the conclusion and suggestions.

II. MATERIAL AND METHODS

A. MODEL FORMULATION

Mathematical modeling is one of the most important tools used in understanding the dynamics of virus transmission. The model developed consider the case where devices' users that have been infected with malicious software can be controlled without them being aware. The objective of such an attack is to control the device system anonymously and increase the scope of the attacks. In epidemiological jargon these kinds of devices are called *asymptomatic devices*. Analogous to the spread of some disease in a population, asymptomatic devices can carry the infection without showing the symptoms. They are infectious and contribute to the distribution of the virus. However, they are much harder to detect since they do not show symptoms.
In this regard, a *SEIARS* compartmental model is proposed where *S* stand for Susceptible, *E* for Exposed, *I* for Infectious, *A* for Asymptomatic and *R* for Recovered as shown in Figure 1

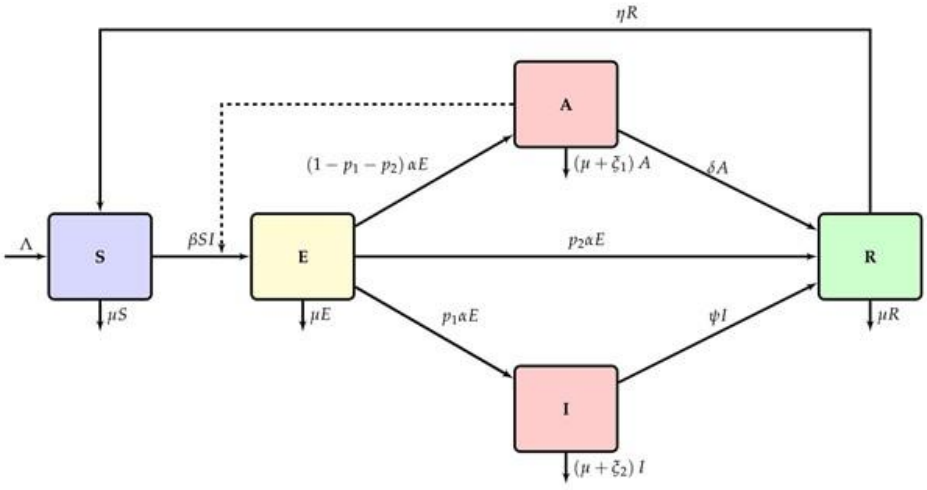

Figure 1: Flowchart of the SEIARS model

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The notation for the *SEIARS* model is summarized in Table 3.1. An asymptomatic compartment is included in addition to the infectious compartment I and it is denoted by A. They are assumed to be infectious at a reduced transmission rate $\beta\lambda$ as represented by a dashed line in Figure 1. The Exposed devices are infected but not infectious yet and they can acquire temporal immunity to malware attack at a rate of $p_2\alpha$. If security software can detect and removes the malware then the Asymptomatic and Infectious devices will acquire temporal immunity at rates δA and ψI, respectively. Otherwise, devices will be removed from the system at rates $(\mu + \xi_1)A$ and $(\mu + \xi_2)I$ where μ denotes the normal device damaged rate, ξ_1 and ξ_2 are device damaged rates due to an attack from A and I compartments, respectively. Finally, recovered devices lose their temporal immunity and return to the susceptible compartment at a rate of ηR. The dynamic of the model in Figure 1is governed by the set of ordinary differential equations given in equation 1.

$$\begin{cases} \frac{dS}{dt} = \Lambda - \beta S(I + \lambda A) - \mu S + \eta R, \quad S(0) = S_0. \\ \frac{dE}{dt} = \beta S(I + \lambda A) - (\alpha + \mu)E, \quad E(0) = E_0. \\ \frac{dI}{dt} = p_1\alpha E - (\psi + \mu + \xi_2)I, \quad I(0) = I_0. \\ \frac{dA}{dt} = (1 - p_1 - p_2)\alpha E - (\delta + \mu + \xi_1)A, \quad A(0) = A_0. \\ \frac{dR}{dt} = \psi I + \delta A + p_2\alpha E - (\eta + \mu)R, \quad R(0) = R_0. \end{cases} \tag{1}$$

Table 1: Notation of the SEIARS model

Symbol	*Explanation*
$S(t)$	Total number of Susceptible computers at time t.
$E(t)$	Total number of Exposed computers at time t.
$I(t)$	Total number of Infected computers at time t.
$A(t)$	Total number of Asymptomatic computers at time t.
$R(t)$	Total number of Recovered/Removed computer at time t.
Λ	Number of new devices that come into the system. It is called birth rate.
μ	Rate at which device crushes due to number of times it has been used. It is called naturally death.
λ	Infection rate of an Asymptomatic device.
ξ	Rate at which device get damaged due to an attack that occur at the Asymptomatic (ξ_1) or the Infected stage (ξ_2).
β	Contact rate.
p_1 and p_2	Proportions at which devices leave the Exposed compartment to the Infected or Recovered stage respectively.
α	Rate at which devices leave Exposed compartment either to the Infected, the Recovered or the Asymptomatic stage with the proportions p_1, p_2 and $1 - (p_1 + p_2)$ respectively.
δ and ψ	Rates at which device leave respectively Asymptomatic and Infected compartment to the Recovered compartment.
η	Recovery rate at which devices lose their temporal immunity and return back to the susceptible compartment.

The total number of devices N is the sum of all the devices in all compartments which vary with time. Hence:

$$N(t) = S(t) + E(t) + I(t) + A(t) + R(t).$$

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B. Analysis of the model

B.1 Positively invariant region

This section will provide the positivity and boundedness analysis of the solutions of the model governed by the set of differential equation given in equation 1 with initial conditions $(S_0, E_0, I_0, A_0, R_0)^T$ which belong to the positive orthant ${\mathbb{R}_+}^5$.

Lemma1[12]: Suppose $\Omega \subset \mathbb{R}^5$ is open, $f_i \in \mathcal{C}(\Omega),\ i = 1,2,3,4,5.$ If$f_i|_{x_i(t)\geq 0, X_t \in {\mathbb{R}_+}^5} \geq 0, X_t = (x_{1t}, x_{2t}, x_{3t}, x_{4t}, x_{5t})^T, i = 1,2,3,4,5,$ then ${\mathbb{R}_+}^5$is the invariant domain of the following equations

$$\frac{dx_i(t)}{dt} = f_i(t, X_t),\ t \leq 0,\ i = 1,2,3,4,5.$$

Theorem 1: For all $t \geq 0$, each solution $(S(t), E(t), I(t), A(t), R(t))$ of the model given in equation1 with non-negative initial conditions is non-negative.

Proof. Let consider $X = (S, E, I, A, R)^T$ and $f(X) = (f_1(X), f_2(X), f_3(X), f_4(X), f_5(X))^T$, then the system of equations 1 can be rewritten as follow

$$\frac{dX}{dt} = f(X),$$

where

$$f(X) = \begin{pmatrix} f_1(X) \\ f_2(X) \\ f_3(X) \\ f_4(X) \\ f_5(X) \end{pmatrix} = \begin{pmatrix} \Lambda - \beta S(I + \lambda A) - \mu S + \eta R \\ \beta S(I + \lambda A) - (\alpha + \mu)E \\ p_1 \alpha E - (\psi + \mu + \xi_2)I \\ (1 - p_1 - p_2)\alpha E - (\delta + \mu + \xi_1)A \\ \psi I + \delta A + p_2 \alpha E - (\eta + \mu)R \end{pmatrix}.$$

- Note that for:

$$\begin{aligned} \frac{dS(t)}{dt} &= \Lambda - \beta S(I + \lambda A) - \mu S + \eta R. \ \Rightarrow\ \frac{dS(t)}{dt} \geq -(\beta I + \beta\lambda A + \mu)S. \\ \int \frac{dS(t)}{S} &\geq -\int (\beta I + \beta\lambda A + \mu)dt. \ \Rightarrow\ \ln S(t) \geq -\Gamma(t) + C. \\ S(t) &\geq K e^{-\Gamma(t)}. \text{ where } \Gamma(t) = \int (\beta I + \beta\lambda A + \mu)dt. \text{ and } \ K = e^C \text{ a constant of integration.} \end{aligned}$$

for $t = 0,\ S(0) = S_0 \geq K.$ Thus $S(t) \geq S_0 e^{-\Gamma(t)} \geq 0,\ \forall t \geq 0$ since S_0 is positive.

- For

$$\begin{aligned} \frac{dE(t)}{dt} &= \beta S(I + \lambda A) - (\alpha + \mu)E. \ \Rightarrow\ \frac{dE(t)}{dt} \geq -(\alpha + \mu)E. \\ \int \frac{dE(t)}{E} &\geq -\int (\alpha + \mu)dt. \ \Rightarrow\ \ln E(t) \geq -\Gamma(t) + D. \\ E(t) &\geq K e^{-\Gamma(t)}. \text{ where } \Gamma(t) = \int (\alpha + \mu)dt \text{ and } \ K \text{ a constant of integration.} \end{aligned}$$

for $t = 0,\ E(0) = E_0 \geq K.$ Thus $E(t) \geq E_0 e^{-\Gamma(t)} \geq 0,\ \forall t \geq 0$ since E_0 is positive.

- For

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$$\begin{aligned} \frac{dI(t)}{dt} &= p_1\alpha E - (\psi+\mu+\xi_2)I. \;\Rightarrow\; \frac{dI(t)}{dt} \geq -(\psi+\mu+\xi_2)I. \\ \int \frac{dI(t)}{I} &\geq -\int (\psi+\mu+\xi_2)dt. \;\Rightarrow\; \ln I(t) \geq -\Gamma(t) + E. \\ I(t) &\geq Ke^{-\Gamma(t)} \text{ where } \Gamma(t) = \int (\psi+\mu+\xi_2)dt \text{ and } K \text{ a constant of integration.} \end{aligned}$$

for $t = 0,\ I(0) = I_0 \geq K.$ Thus $I(t) \geq I_0 e^{-\Gamma(t)} \geq 0,\ \forall t \geq 0$ since I_0 is positive.

- For

$$\begin{aligned} \frac{dA(t)}{dt} &= (1-p_1-p_2)\alpha E - (\delta+\mu+\xi_1)A. \;\Rightarrow\; \frac{dA(t)}{dt} \geq -(\delta+\mu+\xi_1)A. \\ \int \frac{dA(t)}{A} &\geq -\int (\delta+\mu+\xi_1)dt. \;\Rightarrow\; \ln A(t) \geq -\Gamma(t) + F. \\ A(t) &\geq Ke^{-\Gamma(t)} \text{ where } \Gamma(t) = \int (\delta+\mu+\xi_1)dt \text{ and } K \text{ a constant of integration.} \end{aligned}$$

for $t = 0,\ A(0) = A_0 \geq K.$ Thus $A(t) \geq A_0 e^{-\Gamma(t)} \geq 0,\ \forall t \geq 0$ since A_0 is positive.

- For

$$\begin{aligned} \frac{dR(t)}{dt} &= \psi I + \delta A + p_2\alpha E - (\eta+\mu)R. \;\Rightarrow\; \frac{dR(t)}{dt} \geq -(\eta+\mu)R. \\ \int \frac{dR(t)}{R} &\geq -\int (\eta+\mu)dt. \;\Rightarrow\; \ln R(t) \geq -\Gamma(t) + G. \\ R(t) &\geq Ke^{-\Gamma(t)} \text{ where } \Gamma(t) = \int (\eta+\mu)dt \text{ and } K \text{ a constant of integration.} \end{aligned}$$

for $t = 0,\ R(0) = R_0 \geq K.$ Thus $R(t) \geq R_0 e^{-\Gamma(t)} \geq 0,\ \forall t \geq 0$ since R_0 is positive.

Therefore, it follows from lemma**111** that $\mathbb{R}_+^5$is an invariant set of the system of equations1. □

Theorem 2: Let$\mathbb{D} = \{(S,E,I,A,R)^T \in \mathbb{R}_+^5, \exists\, \mathrm{k} \in \mathbb{R}:\ 0 \leq \mathrm{S}+\mathrm{E}+\mathrm{I}+\mathrm{A}+\mathrm{R} \leq \mathrm{k}\}$ is a positively invariant set of the model given in equation1.

Proof. Let consider the total population $N(t) = S(t) + E(t) + I(t) + A(t) + R(t)$ of the model given in equation1. A direct computation of the previous expression will lead to the following:

$$\begin{aligned} \frac{dN(t)}{dt} &= \frac{dS(t)}{dt} + \frac{dE(t)}{dt} + \frac{dI(t)}{dt} + \frac{dA(t)}{dt} + \frac{dR(t)}{dt}. \\ \frac{dN(t)}{dt} &= \Lambda - \mu N(t) - (\xi_2 I(t) + \xi_1 A(t)). \\ \frac{dN(t)}{dt} &\leq \Lambda - \mu N(t) \text{ since } (\xi_2 I(t) + \xi_1 A(t)) \text{ is positive.} \end{aligned}$$

Let denote $N(t) = N$ for simplicity. When integrating both sides, we get:

$$\begin{aligned} \int \frac{dN}{\Lambda - \mu N} &\leq \int dt. \;\Rightarrow\; -\frac{1}{\mu}\ln(\Lambda - \mu N) \leq t + C. \\ \ln(\Lambda - \mu N) &\geq -(\mu t + k). \text{ with } k = \mu C. \;\Rightarrow\; \Lambda - \mu N \geq Ke^{-\mu t}. \quad \text{with } K = e^{-k} \text{ a constant.} \end{aligned}$$

At $t = 0,\ N(0) = N_0 \Longrightarrow \Lambda - \mu N_0 \geq K.$ Then

$$N(t) \leq \frac{\Lambda}{\mu} - \frac{\Lambda - \mu N_0}{\mu} e^{-\mu t}.$$

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Hence, $\lim_{t\to\infty} N(t) \to \frac{\Lambda}{\mu}$. Thus $N(t) \in \left[0, \frac{\Lambda}{\mu}\right]$. Therefore, the set $\mathbb{D}$ is a positively invariant set for the model describe in equation 1. □

B.2 Existence of equilibrium points

In this section, existence of equilibrium points will be considered. They are two equilibria points for the model in equation 1 : one is the virus free equilibrium, and the other is the endemic equilibrium.

B.2.1 Virus Free Equilibrium

A Virus Free Equilibrium (VFE) is a state of a system in which no virus is present in the population of devices. The VFE of the model is defined as $\Xi_* = (S_*(t),0,0,0,0)$ satisfying the following equation:

$$\frac{dS}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dA}{dt} = \frac{dR}{dt} = 0,$$

$$\begin{aligned} \frac{dS}{dt} &= \Lambda - \mu S \ \ since\ I = E = A = R = 0. \ \ then \\ 0 &= \Lambda - \mu S_*. \ \ since\ \frac{dS}{dt} = 0. \\ S_* &= \frac{\Lambda}{\mu}. \end{aligned}$$

Therefore, the VFE is obtained as:

$$\Xi_* = \left(\frac{\Lambda}{\mu}, 0,0,0,0\right).$$

B.2.2 Endemic Equilibrium

The endemic equilibrium point (EEP) is the state where the infection cannot be totally eradicated but remains in the population. The EEP of the model is defined as $\Xi^* = (S^*(t), E^*(t), I^*(t), A^*(t), R^*(t))$ satisfying the following equation:

$$\frac{dS(t)}{dt} = \frac{dE(t)}{dt} = \frac{dI(t)}{dt} = \frac{dA(t)}{dt} = \frac{dR(t)}{dt} = 0.$$

Hence

$$\begin{cases} \boldsymbol{\Lambda - \beta S(I + \lambda A) - \mu S + \eta R} &= \mathbf{0}, \\ \boldsymbol{\beta S(I + \lambda A) - (\alpha + \mu)E} &= \mathbf{0}, \\ \boldsymbol{p_1 \alpha E - (\psi + \mu + \xi_2)I} &= \mathbf{0}, \\ \boldsymbol{(1 - p_1 - p_2)\alpha E - (\delta + \mu + \xi_1)A} &= \mathbf{0}, \\ \boldsymbol{\psi I + \delta A + p_2 \alpha E - (\eta + \mu)R} &= \mathbf{0}. \end{cases} \quad \textbf{(2)}$$

It follows from the third and the fourth equations of the system2 that:

$$E^*(t) = \frac{\psi + \mu + \xi_2}{p_1 \alpha} I^*(t), \qquad (3) \qquad A^*(t) = \frac{(1 - p_1 - p_2)(\psi + \mu + \xi_2)}{p_1(\delta + \mu + \xi_1)} I^*(t). \qquad (4)$$

Replacing equations3 and 4 in the second and fifth equations of the system 2 yield respectively

$$S^*(t) = \frac{(\alpha + \mu)(\psi + \mu + \xi_2)(\delta + \mu + \xi_1)}{\alpha\beta[p_1(\delta + \mu + \xi_1) + \lambda(1 - p_1 - p_2)(\psi + \mu + \xi_2)]},$$

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and

$$R^*(t) = \frac{1}{p_1(\eta+\mu)}\left[p_1\psi + p_2(\psi+\mu+\xi_2) + (1-p_1-p_2)\delta\frac{(\psi+\mu+\xi_2)}{(\delta+\mu+\xi_1)}\right] I^*(t).$$

Hence all the variables are strictly positive since $I^*(t) > 0 \ \ \forall t$ and $I^*(t) = 0$ at the Virus Free Equilibrium. Therefore, the Endemic Equilibrium Point exist.The uniqueness of the Virus Free Equilibrium and the Endemic Equilibrium point can be obtained through the basic reproductive number.

Definition 1(Basic reproductive number)

In Epidemiology, the basic reproductive number R_0 is a threshold parameter that provide the number of secondary cases that one infected device will produce in a susceptible population during its infective period as defined in [13]. The next generation matrix approach is used to compute the basic reproductive number.The basic reproduction number is the largest eigenvalue (called spectral radius) of the next generation matrix FV^{-1} of the system, where

$$F = \left[\frac{\partial F_i(x_0)}{\partial x_j}\right] \quad \text{and} \quad V = \left[\frac{\partial V_i(x_0)}{\partial x_j}\right]$$

F_i denotes the transmission part which describe the production of new infections in compartment i, V_i transfers the infections from one compartment to another and x_0 denotes the virus free equilibrium state[14].

$$F_i - V_i = \begin{bmatrix}\frac{dE}{dt}\\ \frac{dA}{dt}\\ \frac{dI}{dt}\end{bmatrix} \text{ where } E, A, I \text{ are considered to be infected compartments and } i = 1,2,3.$$

$$= \begin{bmatrix}\beta S(I+\lambda A) - (\alpha+\mu)E\\ p_1\alpha E - (\psi+\mu+\xi_2)I\\ (1-p_1-p_2)\alpha E - (\delta+\mu+\xi_1)A\end{bmatrix}.$$

Hence,

$$F_i = \begin{bmatrix}\beta S(I+\lambda A)\\ p_1\alpha E\\ (1-p_1-p_2)\alpha E\end{bmatrix} \qquad \text{and} \qquad V_i = \begin{bmatrix}(\alpha+\mu)E\\ (\psi+\mu+\xi_2)I\\ (\delta+\mu+\xi_1)A\end{bmatrix}.$$

The matrix F and V are obtained as follow

$$F = \begin{bmatrix}\frac{\partial F_1(x_0)}{\partial E} & \frac{\partial F_1(x_0)}{\partial A} & \frac{\partial F_1(x_0)}{\partial I}\\ \frac{\partial F_2(x_0)}{\partial E} & \frac{\partial F_2(x_0)}{\partial A} & \frac{\partial F_2(x_0)}{\partial I}\\ \frac{\partial F_3(x_0)}{\partial E} & \frac{\partial F_3(x_0)}{\partial A} & \frac{\partial F_3(x_0)}{\partial I}\end{bmatrix} = \begin{bmatrix}0 & \frac{\lambda\beta\Lambda}{\mu} & \frac{\beta\Lambda}{\mu}\\ p_1\alpha & 0 & 0\\ (1-p_1-p_2)\alpha & 0 & 0\end{bmatrix},$$

$$V = \begin{bmatrix}\frac{\partial V_1(x_0)}{\partial E} & \frac{\partial V_1(x_0)}{\partial A} & \frac{\partial V_1(x_0)}{\partial I}\\ \frac{\partial V_2(x_0)}{\partial E} & \frac{\partial V_2(x_0)}{\partial A} & \frac{\partial V_2(x_0)}{\partial I}\\ \frac{\partial V_3(x_0)}{\partial E} & \frac{\partial V_3(x_0)}{\partial A} & \frac{\partial V_3(x_0)}{\partial I}\end{bmatrix} = \begin{bmatrix}\alpha+\mu & 0 & 0\\ 0 & 0 & \psi+\mu+\xi_2\\ 0 & \delta+\mu+\xi_1 & 0\end{bmatrix}.$$

Accordingly,

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$$V^{-1} = \begin{bmatrix} \frac{1}{\alpha+\mu} & 0 & 0 \\ 0 & 0 & \frac{1}{\delta+\mu+\xi_1} \\ 0 & \frac{1}{\psi+\mu+\xi_2} & 0 \end{bmatrix}.$$

Thus, the next generation matrix is given by

$$FV^{-1} = \begin{bmatrix} 0 & \frac{\beta\Lambda}{\mu(\psi+\mu+\xi_2)} & \frac{\lambda\beta\Lambda}{\mu(\delta+\mu+\xi_1)} \\ \frac{p_1\alpha}{\alpha+\mu} & 0 & 0 \\ \frac{(1-p_1-p_2)\alpha}{\alpha+\mu} & 0 & 0 \end{bmatrix}.$$

The spectral radius of the next generation matrix is

$$\rho(FV^{-1}) = \sqrt{\frac{\alpha\beta\Lambda}{\mu(\alpha+\mu)}\left[\frac{\lambda(1-p_1-p_2)}{\delta+\mu+\xi_1} + \frac{p_1}{\psi+\mu+\xi_2}\right]}.$$

Therefore, the basic reproduction number of the system 1 is given by

$$R_0 = \sqrt{\frac{\alpha\beta\Lambda}{\mu(\alpha+\mu)}\left[\frac{\lambda(1-p_1-p_2)}{\delta+\mu+\xi_1} + \frac{p_1}{\psi+\mu+\xi_2}\right]}.$$

The reproduction number is positive; it is zero if there is no transmission of virus from one device to another, that is when $\beta = 0$ and it can be interpreted as the number of secondary cases. Therefore, one can see that $\beta\lambda\Lambda/\mu$ is the number of newly exposed devices generated by one asymptomatic device per unit of time in an entirely susceptible device. A fraction of devices $\alpha(1-p_1-p_2)/(\alpha+\mu)$ survives the Exposed compartment and progress to the Asymptomatic compartment. An asymptomatic device remains asymptomatic to susceptible devices and infect other devices as asymptomatic for $1/(\delta+\mu+\xi_1)$ units. Therefore,

$$R_a = \frac{\alpha\beta\Lambda}{\mu(\alpha+\mu)}\left[\frac{\lambda(1-p_1-p_2)}{\delta+\mu+\xi_1}\right].$$

is the number of secondary infections that one asymptomatic device will produce in an entirely susceptible population during its lifetime as asymptomatic. Likewise, $\beta\Lambda/\mu$ is the number of newly exposed devices generated by one infectious device per unit of time in an entirely susceptible device. A fraction of devices $\alpha p_1/(\alpha+\mu)$ survives the Exposed compartment and progress to the Symptomatic compartment. A symptomatic device remains infectious and infect other devices for $1/(\psi+\mu+\xi_2)$ units. Hence,

$$R_i = \frac{\alpha\beta\Lambda}{\mu(\alpha+\mu)}\left[\frac{p_1}{\psi+\mu+\xi_2}\right].$$

is the number of secondary infections that infectious device will produce in an entirely susceptible population during its lifetime. Therefore,

$$R_0 = \sqrt{R_a + R_i}.$$

From the reproductive number, we have the following result:

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Proposition 1[8]: If $R_0 \leq 1$, the system of equations 1 has a unique virus free equilibrium Ξ_*. If $R_0 > 1$, the system has a unique endemic equilibrium $\Xi^* = (S^*(t), E^*(t), I^*(t), A^*(t), R^*(t))$, where

$$E^*(t) = \frac{\psi + \mu + \xi_2}{p_1 \alpha} I^*(t), \qquad A^*(t) = \frac{(1 - p_1 - p_2)(\psi + \mu + \xi_2)}{p_1(\delta + \mu + \xi_1)} I^*(t),$$

$$S^*(t) = \frac{(\alpha+\mu)(\psi+\mu+\xi_2)(\delta+\mu+\xi_1)}{\alpha\beta[p_1(\delta+\mu+\xi_1)+\lambda(1-p_1-p_2)(\psi+\mu+\xi_2)]}, \text{and}$$

$$R^*(t) = \frac{1}{p_1(\eta + \mu)}\left[p_1\psi + p_2(\psi + \mu + \xi_2) + (1 - p_1 - p_2)\delta\frac{(\psi + \mu + \xi_2)}{(\delta + \mu + \xi_1)}\right] I^*(t).$$

B.3 Stability analysis of the model

Equilibrium points of a system can be classified in to three categories: *stable, unstable or asymptotically stable* depending on the nature of the eigenvalues of the coefficient matrix (linear system) or the Jacobian matrix (nonlinear system) about the equilibrium point[14].

B.3.1 Local Asymptotic Stability Analysis

Definition 2 (Locally asymptotically stable)

An equilibrium point of a dynamical system is said to be locally asymptotically stable if the system stays in the neighborhood of that point after perturbing the initial conditions slightly such that all trajectories of its solutions tend to the equilibrium point when t becomes large [8].

Theorem 3: The virus free equilibrium point $\Xi_* = \left(\frac{\Lambda}{\mu}, 0,0,0,0\right)$ is locally asymptotically stable if $R_0 < 1$. If $R_0 > 1$, the virus free equilibrium is unstable.

Proof. Let consider the Jacobian of the system of equations 1

$$J = \begin{bmatrix} -\beta(I + \delta A) - \mu & 0 & -\beta S & -\beta S\lambda & \eta \\ \beta(I + \delta A) & -(\alpha + \mu) & 0 & \beta S\lambda & 0 \\ 0 & p_1\alpha & -(\psi + \mu + \xi_2) & 0 & 0 \\ 0 & (1 - p_1 - p_2)\alpha & 0 & -(\delta + \mu + \xi_1) & 0 \\ 0 & p_2\alpha & \psi & \delta & -(\eta + \mu) \end{bmatrix}.$$

To determine the local stability of the virus free equilibrium, the Jacobian matrix has to be evaluated at Ξ_*. In particular, the equation $P(\theta)$ must be shown that it has only negative roots or roots with negative real part.

$$J|_{\Xi_*} = \begin{bmatrix} -\mu & 0 & -\beta\frac{\Lambda}{\mu} & -\beta\frac{\Lambda}{\mu}\lambda & \eta \\ 0 & -(\alpha + \mu) & 0 & \beta\frac{\Lambda}{\mu}\lambda & 0 \\ 0 & p_1\alpha & -(\psi + \mu + \xi_2) & 0 & 0 \\ 0 & (1 - p_1 - p_2)\alpha & 0 & -(\delta + \mu + \xi_1) & 0 \\ 0 & p_2\alpha & \psi & \delta & -(\eta + \mu) \end{bmatrix}.$$

Subtracting θ along the main diagonal, one can see that the characteristic equation $P(\theta) = |J|_{\Xi_*} - \theta I|$ yield the following roots:

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$$\begin{cases} \theta_1 &= -\mu, \\ \theta_2 &= -(\eta+\mu), \\ \theta_3 &= -(\psi+\mu+\xi_2), \\ \theta_4 &= -\frac{1}{2}\left[M+\sqrt{M^2-4N}\right], \\ \theta_4 &= -\frac{1}{2}\left[M-\sqrt{M^2-4N}\right]. \end{cases}$$

with $M=(\alpha+\mu)+(\delta+\mu+\xi_1)$ and $N=(\alpha+\mu)(\delta+\mu+\xi_1)-\beta\lambda(1-p_1-p_2)\alpha\frac{\Lambda}{\mu}$.

Clearly, one can see that all the eigenvalues of the Jacobian matrix are strictly negative provided $M>\sqrt{M^2-4N}$. This follow that Ξ_* is locally asymptotically stable. □

Theorem 4: The endemic equilibrium point Ξ^* is locally asymptotically stable if $R_0>1$.

Proof. To show that the endemic equilibrium Ξ^* is locally asymptotically stable for $R_0>1$, the Routh-Hurwitz criterion [8] will be applied which give necessary and sufficient conditions for the eigenvalues to have negative real parts.

Let consider the Jacobian matrix at Ξ^*

$$J=\begin{bmatrix} -\beta(I^*+\delta A^*)-\mu & 0 & -\beta S^* & -\beta S^*\lambda & \eta \\ \beta(I^*+\delta A^*) & -(\alpha+\mu) & 0 & \beta S^*\lambda & 0 \\ 0 & p_1\alpha & -(\psi+\mu+\xi_2) & 0 & 0 \\ 0 & (1-p_1-p_2)\alpha & 0 & -(\delta+\mu+\xi_1) & 0 \\ 0 & p_2\alpha & \psi & \delta & -(\eta+\mu) \end{bmatrix}.$$

The characteristic equation is

$$a_5\theta^5+a_4\theta^4+a_3\theta^3+a_2\theta^2++a_1\theta+a_0=0.$$

with

$$\begin{aligned} a_5 &= 1, \\ a_4 &= (\alpha+5\mu+p_2\alpha+\psi+\delta+\eta+\xi_1+\xi_2+\beta(I^*+\delta A^*)), \\ a_3 &= (\alpha+\mu)(\psi+\mu+\xi_2)+(\alpha+2\mu+\psi+\xi_2)(\delta+\mu+\xi_1)+(\eta+\mu)(\beta(I^*+\delta A^*)+\mu) \\ &\quad +(\alpha+3\mu+p_2\alpha+\psi+\delta+\xi_1+\xi_2)(\eta+2\mu+\beta(I^*+\delta A^*))-\beta S^*\lambda(1-p_1-p_2)\alpha, \\ a_2 &= (\eta+2\mu+\beta(I^*+\delta A^*))((\alpha+\mu)(\psi+\mu+\xi_2)+(\alpha+2\mu+p_2\alpha+\psi+\xi_2)(\delta+\mu+\xi_1)) \\ &\quad +(\alpha+\mu+\gamma)(\psi+\mu+\xi_2)(\delta+\mu+\xi_1)+(\eta+\mu)(\beta(I^*+\delta A^*)+\mu)(\alpha+3\mu+p_2\alpha+\psi+\delta+\xi_1+\xi_2) \\ &\quad -(\eta+2\mu+\beta(I^*+\delta A^*))\beta S^*\lambda(1-p_1-p_2)\alpha-\beta S^*\lambda(1-p)\alpha(\psi+\mu+\xi_2), \\ a_1 &= (\eta+2\mu+\beta(I^*+\delta A^*))(\alpha+\mu)(\psi+\mu+\xi_2)(\delta+\mu+\xi_1)+((\alpha+\mu)(\psi+\mu+\xi_2) \\ &\quad +(\alpha+3\mu+\xi_2)(\delta+\mu+\xi_1))(\eta+\mu)(\beta(I^*+\delta A^*)+\mu)-(\eta+\mu)(\beta(I^*+\delta A^*)+\mu)\beta S^*\lambda(1-p_1 \\ &\quad -p_2)\alpha-(\eta+2\mu+\beta(I^*+\delta A^*))\beta S^*\lambda(1-p_1-p_2)\alpha(\psi+\mu+\xi_2), \\ a_0 &= (\eta+\mu)(\beta(I^*+\delta A^*)+\mu)(\psi+\mu+\xi_2)[(\alpha+\mu)(\delta+\mu+\xi_1)-\beta S^*\lambda(1-p_1-p_2)\alpha]. \end{aligned}$$

Therefore, by applying Routh-Hurwitz approach, provided that $a_5>0$, $a_4>0$, $a_3>0$, $a_2>0$, $a_1>0$, $a_0>0$, we get additional conditions shown inTable 2.

Table 2: Routh-Hurwitz criteria

Power of each term	*Coefficients of the polynomial*		
θ^5	a_5	a_3	a_1
θ^4	a_4	a_2	a_0

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θ^3	b_1	b_2	b_3
θ^2	c_1	c_2	-
θ	-	-	-

Where $b_1 > 0$, $c_1 > 0$ and $d_1 > 0$ are additional conditions to be verified for the endemic equilibrium point Ξ^* to be locally asymptotically stable and b_2, b_3, c_2 are coefficients that will be used in the computation of b_1, c_1 and d_1. Hence, fromTable 2:

$$b_1 = \frac{a_4a_3 - a_1a_5}{a_4} b_2 = \frac{a_4a_1 - a_0a_5}{a_4} b_1 = 0 c_1 = \frac{b_1a_2 - b_2a_4}{b_1} c_2 = \frac{b_1a_0 - b_3a_4}{b_1} d_1 = \frac{c_1b_2 - b_1c_2}{c_1}$$

Then, the following conditions can be deduced:

$$\begin{cases} a_4a_3 > a_1a_5 \text{ for } b_1 > 0, \\ a_4a_3a_2 + a_0a_5a_4 > a_2^2a_5 + a_4^2a_1 \text{ for } c_1 > 0, \\ (a_4a_1 - a_0a_5)[(a_4a_3a_2 + a_0a_5a_4) - (a_2^2a_5 + a_4^2a_1)] > (a_0a_4a_3 - a_0a_1a_5)(a_4a_3 - a_2a_5) \text{ for } d_1 > 0. \end{cases}$$

Consequently, the claimed result follows from Routh-Hurwitz criterion. □

B.3.2 Global Asymptotic Stability Analysis

The virus free equilibrium for global asymptotic stability (g.a.s) will be investigated by following the procedure implemented in [15].

Let the system of equations 1 be written in the form:

$$\begin{cases} \frac{dX}{dt} = F(X,Y), \\ \frac{dY}{dt} = G(X,Y). \end{cases}$$

where $X = (S,R)$ denotes the uninfected devices, $Y = (E,I,A)$ denotes the infected devices and $\Xi_* = (X^*,0)$ denotes the virus free equilibrium of the system.

Theorem 4: The virus free equilibrium $\Xi_* = (X^*,0)$ is said to be a globally asymptotic stable (g.a.s) equilibrium of the system provided that $R_0 < 1$ $(l.a.s)$ and those assumptions

$$(H1): \quad \text{For } \frac{dX}{dt} = F(X,0),\ \Xi_* \text{ is a globally asymptotically stable,}$$
$$(H2): \quad G(X,Y) = AY - G^*(X,Y),\ G^*(X,Y) \geq 0 \text{ for } (X,Y) \in \Omega.$$

are satisfied. Where Ω is the feasible region of the model and A an M-matrix.

Proof. Let

$$F(X,0) = \begin{cases} \Lambda - \mu S + \eta R, \\ -(\eta + \mu)R. \end{cases}$$

Let us prove that $\Xi_* = \left(\frac{\Lambda}{\mu}, 0,0,0,0\right)$ is globally asymptotically stable for $\frac{dX}{dt} = F(X,0)$ by solving the equation using the Integrating Factor (I.F) method.

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$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - \mu S + \eta R, \\
\frac{dS}{dt} + \mu S &= \Lambda + \eta R. \quad \text{where the } I.F = e^{\int \mu dt}. \text{ Therefore :} \\
\left(\frac{dS}{dt} + \mu S\right) e^{\mu t} &= (\Lambda + \eta R) e^{\mu t}, \\
\frac{d}{dt}(S e^{\mu t}) &= (\Lambda + \eta R) e^{\mu t}. \text{ When integrating both side, we get :} \\
S &= \frac{\Lambda}{\mu} + \frac{\eta}{e^{\mu t}} \int R e^{\mu t} dt.
\end{aligned}$$

Thus, $S \to \frac{\Lambda}{\mu}$ as $t \to \infty$ which implies the global convergence of $F(X,0)$ in Ω. Therefore, $\Xi_* = \left(\frac{\Lambda}{\mu}, 0,0,0,0\right)$ is globally asymptotically stable for $F(X,0)$. Hence $(H1)$ is verified.

For $(H2)$, let

$$G(X,Y) = \begin{cases} \beta S(I + \lambda A) - (\alpha + \mu)E, \\ p_1 \alpha E - (\psi + \mu + \xi_2)I, \\ (1 - p_1 - p_2)\alpha E - (\delta + \mu + \xi_1)A. \end{cases} = AY - G^*(X,Y).$$

where

$$A = \begin{bmatrix} -(\alpha + \mu) & \beta & \beta\lambda \\ p_1 \alpha & -(\psi + \mu + \xi_2) & 0 \\ (1 - p_1 - p_2)\alpha & 0 & -(\delta + \mu + \xi_1) \end{bmatrix}.$$

an M-matrix with its off-diagonal elements non-negative. And

$$G^*(X,Y) = \begin{bmatrix} \beta(I + \lambda A)(S - 1) \\ 0 \\ 0 \end{bmatrix}.$$

Since $G^*(X,Y) \geq 0$, that is $(H2)$ is satisfied. Therefore, $\Xi_* = (X^*, 0)$ is a globally asymptotic stable (g.a.s) equilibrium point of the system for $R_0 < 1$. □

B.3.3 Model parameters-based control strategies

The basic reproductive number R_0 also called propagation threshold of the model described by the system of differential equation is particularly important in establishing efficient control measures. The main goal of all control measures is to reduce the value of R_0 and to analyze the propagation threshold such that explicit expressions for the control of the malware epidemic can be provided. From the expression of the basic reproductive number, the following can be obtained:

$$\begin{aligned}
\frac{\partial R_0}{\partial \alpha} &= -\frac{1}{2}\frac{R_0 \mu}{\alpha(\alpha + \mu)} < 0 \\
\frac{\partial R_0}{\partial \beta} &= \frac{1}{2}\frac{R_0}{\beta} > 0 \\
\frac{\partial R_0}{\partial \Lambda} &= \frac{1}{2}\frac{R_0}{\Lambda} > 0 \\
\frac{\partial R_0}{\partial \lambda} &= \frac{R_0}{2K}\frac{(1 - p_1 - p_2)}{\delta + \mu + \xi_1} > 0 \\
\frac{\partial R_0}{\partial p_1} &= \frac{R_0}{2K}\frac{(\delta + \xi_1) - (\psi + \xi_2)}{(\delta + \mu + \xi_1)(psi + \mu + \xi_2)} \begin{cases} < 0, \ if \ (\delta + \xi_1) < (\psi + \xi_2) \\ > 0, \ if \ (\delta + \xi_1) > (\psi + \xi_2) \end{cases}
\end{aligned}$$

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$$\frac{\partial R_0}{\partial p_2} = -\frac{R_0}{2K}\frac{\lambda}{\delta+\mu+\xi_1} < 0$$
$$\frac{\partial R_0}{\partial \delta} = \frac{\partial R_0}{\partial \xi_1} = -\frac{R_0}{2K}\frac{\lambda(1-p_1-p_2)}{(\delta+\mu+\xi_1)^2} < 0$$
$$\frac{\partial R_0}{\partial \mu} = -\frac{R_0}{2K}\left[\frac{\alpha+2\mu}{\mu(\alpha+\mu)}\left(\frac{\lambda(1-p_1-p_2)}{\delta+\mu+\xi_1}+\frac{p_1}{\psi+\mu+\xi_2}\right)+\left(\frac{\lambda(1-p_1-p_2)}{(\delta+\mu+\xi_1)^2}+\frac{p_1}{(\psi+\mu+\xi_2)^2}\right)\right] < 0$$
$$\frac{\partial R_0}{\partial \psi} = \frac{\partial R_0}{\partial \xi_2} = -\frac{R_0}{2K}\frac{p_1}{(\psi+\mu+\xi_2)^2} < 0$$

with $K = \left[\frac{\lambda(1-p_1-p_2)}{\delta+\mu+\xi_1}+\frac{p_1}{\psi+\mu+\xi_2}\right]$.

Considering that $\alpha, \beta, \Lambda, \lambda, p_1, p_2, \delta, \mu, \psi, \xi_1, \xi_2$ are within a certain interval, from these results one can notice that R_0 decreases as $\alpha, p_2, \delta, \psi, \mu, \xi_1$ and ξ_2 increases provided that the rest of parameters remain constant. However, if β, Λ or λ decreases then R_0 decreases as well. Additionally, if p_1 decreases when $(\delta+\xi_1) > (\psi+\xi_2)$ or p_1 increases when $(\delta+\xi_1) < (\psi+\xi_2)$ then R_0 decreases. Hence, considering the above conditions can help in controlling the virus propagation.

C. Solving Ordinary Differential Equations using Deep Neural Learning.

Let consider a neural network connected to the system of differential equations by two operators Id and $\frac{d}{dt}$ that can approximate the solutions of the system of ODEs as illustrated inFigure 2: Neural network for system of differential equations. For simplicity, let rewrite the system of equations 1 as follow

$$\begin{cases} S'(t) = F_1(S(t),E(t),I(t),A(t),R(t),t), & S(t_0)=S_0 \\ E'(t) = F_2(S(t),E(t),I(t),A(t),R(t),t), & E(t_0)=E_0 \\ I'(t) = F_3(S(t),E(t),I(t),A(t),R(t),t), & I(t_0)=I_0 \\ A'(t) = F_4(S(t),E(t),I(t),A(t),R(t),t), & A(t_0)=A_0 \\ R'(t) = F_5(S(t),E(t),I(t),A(t),R(t),t), & R(t_0)=R_0 \end{cases}$$

which can be reduced to

$$\frac{dy_r}{dt} = y_r{}'(t) = F(y_1(t),y_2(t),y_3(t),y_4(t),y_5(t),t)\ r = 1,2,3,4,5\ t \in [t_0,t_n] \text{ and } n \in \mathbb{N},$$

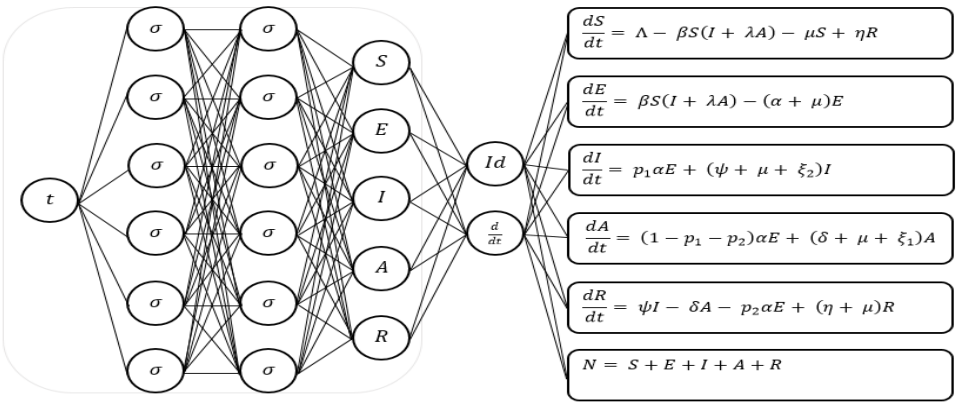

Figure 2: Neural network for system of differential equations

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where $y_1(t) = S(t),\ y_2(t) = E(t),\ y_3(t) = I(t),\ y_4(t) = A(t)$ and $y_5(t) = R(t)$, with initial conditions $y_r(t_0) = y_r r = 1,2,3,4,5$. The corresponding solution of the neural network can be written as:

$$\widetilde{y_r}(t, p_r) = y_r + (t - t_0)N_r(t, p_r) \text{ for } r = 1,2,3,4,5.$$

For each r, $N_r(t, p_r)$ is the output of the multilayer neural network with input x and parameter p_r. Then, the error function can be written as

$$E(t,p) = \sum_{i=1}^{n}\sum_{r=1}^{5}\frac{1}{2}\left[\frac{d\widetilde{y_r}(t_i,p_r)}{dt} - F_r(\widetilde{y_1}(t_i,p_1),\widetilde{y_2}(t_i,p_2),\widetilde{y_3}(t_i,p_3),\widetilde{y_4}(t_i,p_4),\widetilde{y_5}(t_i,p_5),t_i)\right]^2.$$

The objective is to optimize the error function by making it as close as possible to 0 through a learning process. In general, this process can be seen as an optimization problem where parameters (weights and biases) are adjusted for the loss function to be minimized. There are several approaches that are used in optimization problem. In this project, we used 3 of them to find theminimum loss function which are: the Conjugate Gradient method (CG), the Broyden-Fretcher-Goldfard-Shanno method (BFGS) and the Limited Memory BFGS for Bound constrained method (L-BFGS-B).

C.1 Parameter estimation.

Ordinary Differential Equations based models usually contain many unknown parameters. Hence, parameter estimation is an important step to the understanding of the process. For the proposed model, the Metropolis-Hastings algorithm based on the Markov Chain Monte Carlo (MCMC) described in [16] has been used for the estimation of some parameters of the model. Other's parameters were taken from the literature. The parameter values are determined based on the references provided against the values inTable 3 and Figure 3 displays the parameter estimation of the SEIARS model using MCMC.

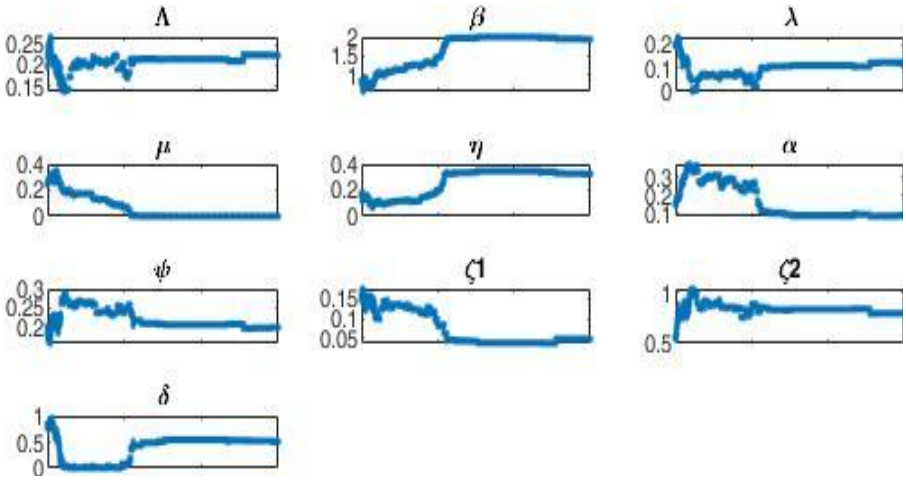

Figure 3: Parameter estimation using Markov Chain Monte Carlo Simulation of the SEIARS

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Table 3: Estimation of parameters used in the model

Symbol	*Model parameter name*	*Values*	*References*
Λ	Birth rate.	0.0613	Estimate (MCMC)
β	Contact rate.	0.0002	[6]
λ	Infection rate of an Asymptomatic device.	0.3583	Estimate (MCMC)
μ	Natural crush of a device	0.0688	[6]
η	Recovery rate.	0.0018	[17]
p_1	Proportion of Exposed to Infected devices.	0.2	Estimate
p_2	Proportion of Exposed to Recovered devices.	0.6	Estimate
α	Rate of node from Exposed class either to Infected, Recovered or Asymptomatic class with proportions p_1, p_2 and $1-(p_1+p_2)$ respectively.	0.0218	Estimate (MCMC)
ψ	Rate of node from Infected class to Recovered class.	0.0001	Estimate (MCMC)
ξ_1	Damaged rate of devices due to an attack at the Asymptomatic stage.	0.0448	Estimate (MCMC)
ξ_2	Damaged rate of devices due to an attack at the Infected stage.	0.0595	[6]
δ	Rate of node from Asymptomatic class to Recovered class	0.0034	[17]
R_0	Basic reproductive number.	0.0796	Estimate

III. SIMULATION AND DISCUSSIONS OF RESULTS

To simulate the behavior of the model, 1000 interconnected devices were considered such that all devices are susceptible at $t = t_0$ with the exception of two devices: one is Infectious and another is Asymptomatic: $S(t_0) = 998$, $E(t_0) = 0$, $I(t_0) = 1$, $A(t_0) = 1$, $R(t_0) = 0$. Moreover, the time is measured in years and the simulation period comprises the first five years after the first infected device has been discovered. The devices were categorized in two classes: The infected and the infected devices.

A. Uninfected device

Devices are not infected when they are in the susceptible and in the recovered compartment. They are susceptible since they are at risk of infection while being connected. The model developed confer a temporal recovered state after being infected by a malware and Figure 4 indicates that the number of susceptible devices decreases due to the awareness of the devices users towards the attack and because of the progression from the susceptible class to the exposed class. However, the number of recovered devices increases in size due to the efficacy of the anti-virus software used as well as the effectiveness of the firewall.

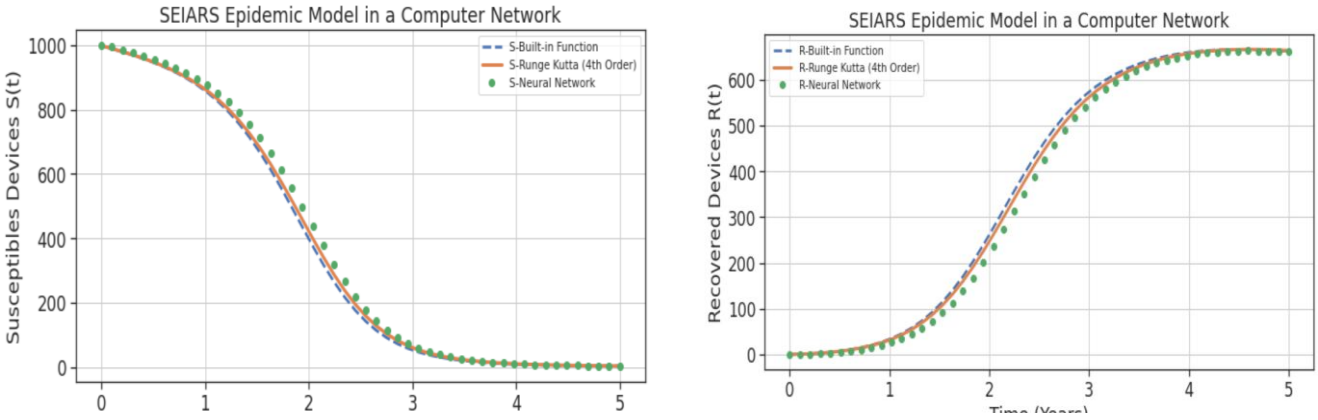

Figure 4: Neural network versus numerical solution for Susceptible and Recovered devices.

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B. Infected devices

Figure 5 presents the infected compartments: Exposed, Infected and Asymptomatic. As one can see, the exposed devices experience a rapid growth within the first two years since they have been hacked but still not aware of the attack which occur when devices move from the susceptible state to the exposed. After the two years, they start decreasing while the infected and asymptomatic devices have reached their pick. From the third year, they start recovered due to use of anti-virus software or through any other maintenance process. However, the virus will not disappear completely due to the reinfection process of the system.

One can noticed that the number of infected devices is not more than the asymptomatic devices almost throughout the infective period, despite the assumption of having the same proportion of devices going to both infected and asymptomatic stage from the exposed compartments. The main reason, which is in line with the real case scenario, is asymptomatic devices can carry the virus without showing symptoms and, therefore, are much harder to detect.

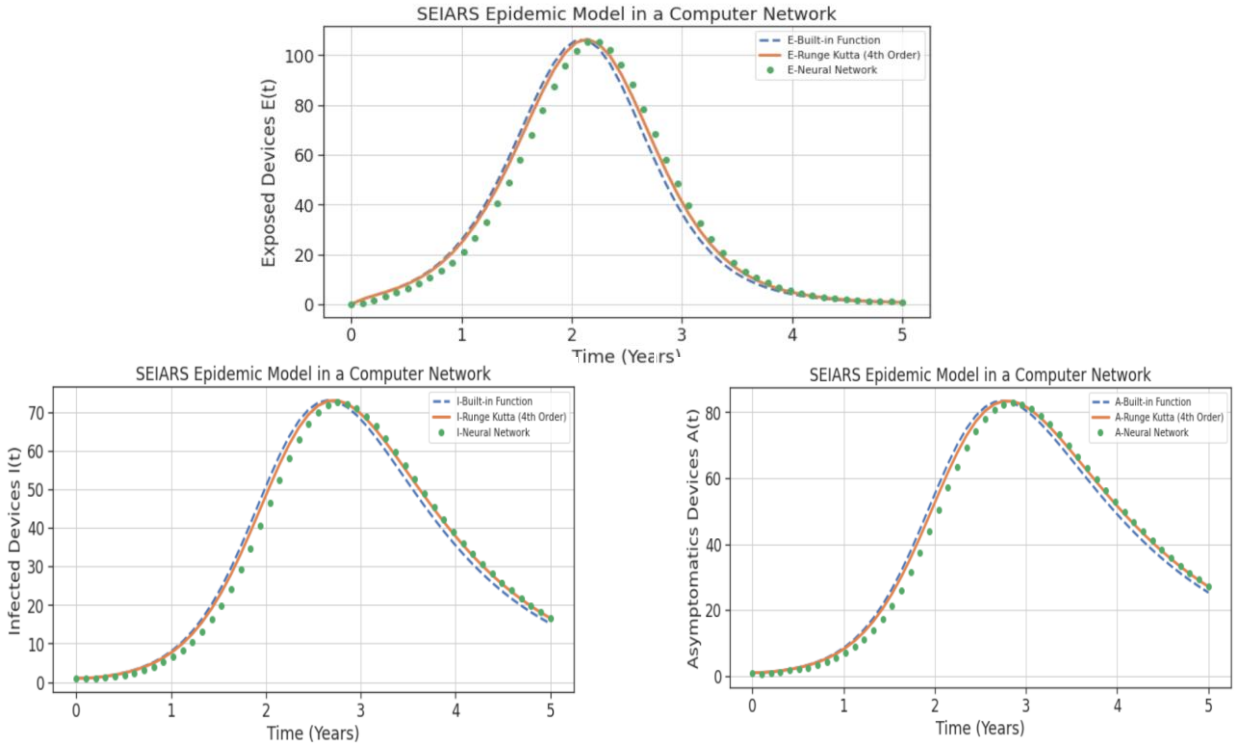

Figure 5: Neural network versus Numerical solutions for Exposed, Infected and Asymptomatic devices.

In this study, we used three optimizations' methods namely: The Conjugate Gradient method, the Broyden-Fretcher-Goldfard-Shanno method (BFGS) and the Limited BFGS for Bound constrained method (L-BFGS) to minimize the loss function such that the neural network can approximate the true solution of the system of ODEs. As shown inFigure 6 the BFGS is considered as a good optimization method since it attained the lowest log loss comparing to the other methods. However, it is more demanding in terms of time complexity.

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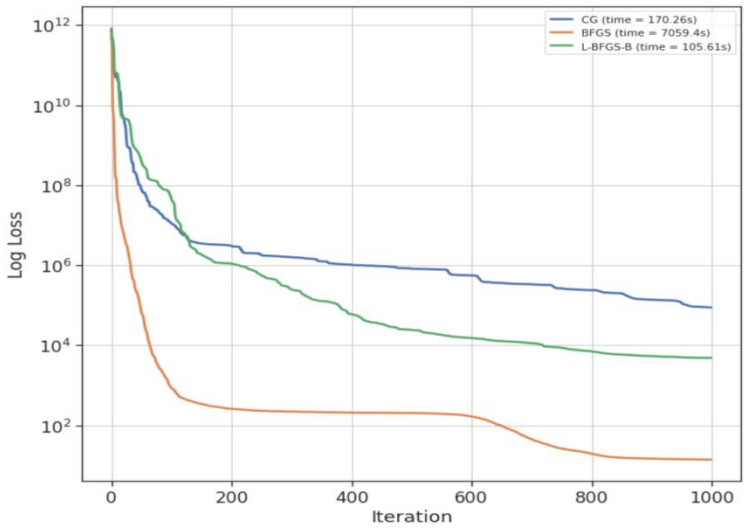

Figure 6: Comparing different optimization methods

To test the stability of the neural network approach, the model has been trained 100 times and a histogram of its performance over 100 fittings has been plotted. FromFigure 7, one can see that 38% of the fittings result is relatively good, getting remarkably close to the numerical solutions. The result can be improved by using more training data points.

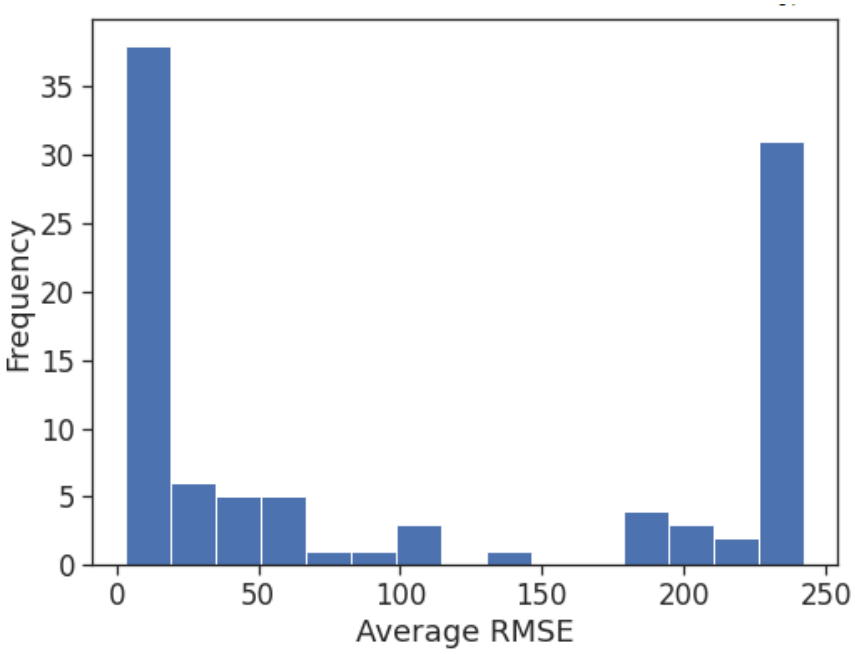

Figure 7: Performance of the neural network over 100 fittings

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In this work an efficient and accurate mathematical model that simulates malware attack in a network has been developed. It is a compartmental model where Asymptomatic devices have been considered as well as Susceptible, Exposed, Infectious and Recovered. Like the spread of some disease within a human population, asymptomatic devices can carry the virus without showing the symptoms. They are infectious and contribute to the spread of the malware. This additional type of devices is particularly important to consider for the cyber security models since the objective of several cyber-attack is to control the device system anonymously to access personal information.

The model developed was global and deterministic and its dynamics was governed by a set of ordinary differential equations. Therefore, the qualitative theory of differential equations has been used to study the stability of the virus free and endemic equilibrium points. Hence, it has been shown that the virus free equilibrium was stable globally and locally. Furthermore, a deep neural learning approach has been implemented to solve the system of ordinary differential equation of the epidemic model. It has been found that neural network with one hidden layer shows good capacity in approximating the solution of the differential equation and it required less storage comparing to the traditional finite difference methods. For the convergence of the neural network model, BFGS has been a good optimization method compering to the Conjugate Gradient as well as the Limited Memory BFGS methods in terms of its accuracy.

V. THANKS

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