Stability analysis of a virulent code in a network of computers

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Introduction

A detailed analysis of the model is presented in this article. Particularly, we present the meaningfulness of the model, the reproduction number, and the equilibria stability. Theorems on the stability analysis are stated and proved using mathematical principles. The stability analysis is also validated by means of numerical methods. In this article, we solve the MSEIQR model using both pseudospectral methods and MATLAB's ode45 method. We show that the new pseudospectral method can be used as an alternative to MATLAB's ode45. The pseudospectral method entitled piecewise pseudospectral relaxation method (PPRM) is developed and presented in detail for a general system of initial values problems in this article. Results obtained are in excellent agreement with MATLAB's ode45. This method is robust, uses few nodes and obtains results in a fraction of a second.

Model formulation

The computer malware model consists of six compartments, namely, Immune node, susceptible node, exposed node, infectious node, quarantine node, and recovered node. Dynamical transfer assumptions are well governed by non-linear first order ordinary differential equations given by the model

$$
\begin{aligned}
\frac{dM}{dt} &= \beta + \phi R - (\eta + \mu)M,\\
\frac{dS}{dt} &= \pi - (\mu + \lambda I)S + \eta M + \xi R,\\
\frac{dE}{dt} &= \alpha\lambda SI + \mathrm{b}E - (\epsilon + \mu)E,\\
\frac{dI}{dt} &= (1-\alpha)\lambda SI + \epsilon E - (\sigma + \gamma + \delta + \mu)I,\\
\frac{dQ}{dt} &= \gamma I - (\rho + \delta + \mu)Q,\\
\frac{dR}{dt} &= \sigma I + \rho Q - (\phi + \xi + \mu)R.
\end{aligned} \tag{1}
$$

where β, π, μ and λ are positive constants and ϕ, η, ξ, α, b, ϵ, σ, γ, δ, and ρ are non-negative constants. The meanings can be obtained on the article given on the "For Further Information" section.

Pictorial elaboration of the model

Below, the model analysis is presented to justify the meaningfulness of the model using mathematical principles.

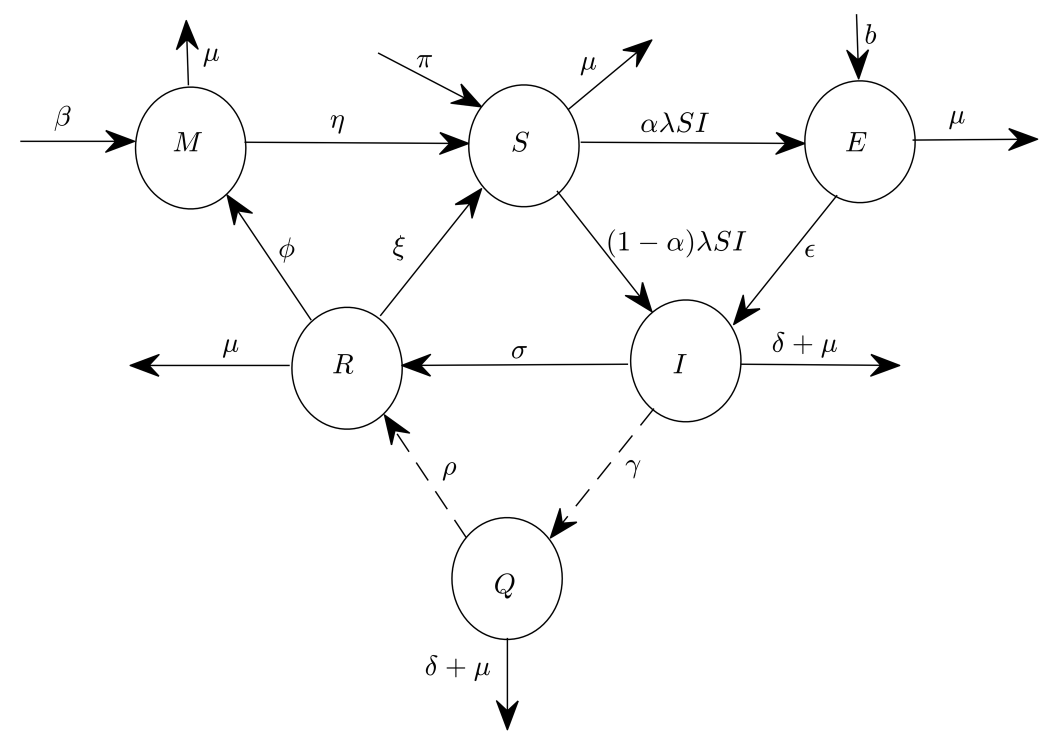

Figure: Flow diagram or pictorial representation of the MSEIQR model. The model is derived under assumption stated above and the diagram is presented for the purposes of visualization of the dynamics of the malware.

Analysis of the model

The *feasibility region* of (1) is defined to be the following set:

$$
\Lambda = \Big\{(M,S,E,I,Q,R) \in \mathbb{R}^6_+ : M + S + E + I + Q + R \le \frac{\beta + \pi}{\mu - b}\Big\}, \tag{2}
$$

with initial conditions,

$$
M(0) > 0,\ \ S(0) > 0,\ \ E(0) \ge 0,\ \ I(0) \ge 0,\ \ Q(0) \ge 0,\ \ R(0) \ge 0. \tag{3}
$$

Theorem. *The feasible region in eqn* (2) *subject to eqn* (3) *is positively invariant.*

- The theorem assures that the solutions to (1) belong in the feasible region.

A *malware free equilibrium state* is given by

$$
MFE = \left(\frac{\beta}{\eta + \mu}, \frac{\pi}{\mu} + \frac{\eta\beta}{\mu(\eta + \mu)}, 0, 0, 0, 0\right). \tag{4}
$$

- In the paper, we show that the MFE exists for $\Gamma_0 \le 1$, where Γ_0 is the reproduction number. The importance of reproduction number is presented on the block below.
- We also show that the existence of endemic equilibrium state for $\Gamma_0 > 1$.

The importance of the reproduction number

If $\Gamma_0 < 1$, then a few infected individuals introduced into a completely susceptible population will on average fail to replicate themselves, and the disease will not spread. On the other hand, if $\Gamma_0 > 1$, the number of infected individuals will increase with each generation and the disease will spread.

Numerical results

Some results obtained after implementing the piecewise pseudospectral relaxation method.

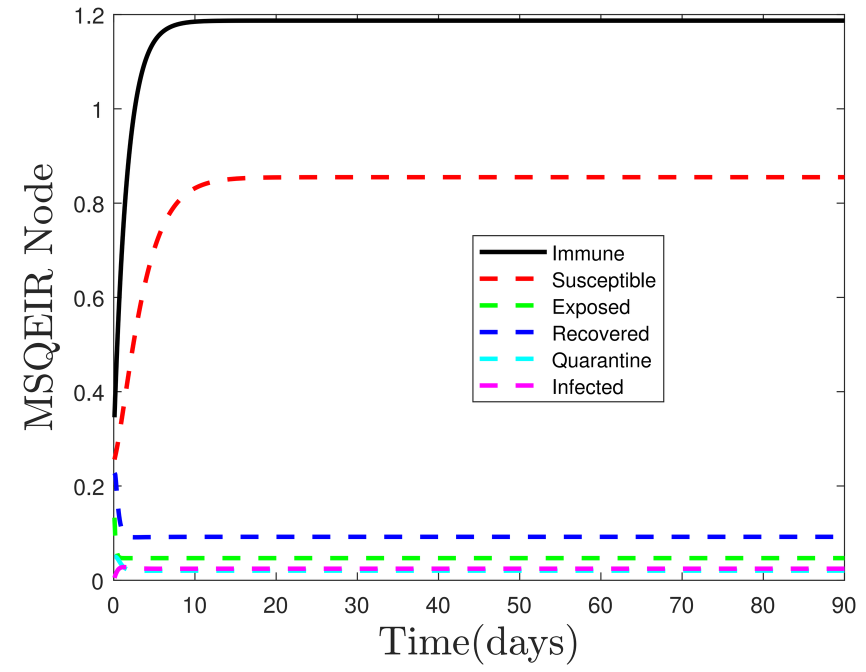

Figure: Time series solution

Numerical results

- Validation of the piecewise pseudospectral relaxation method against ode45.

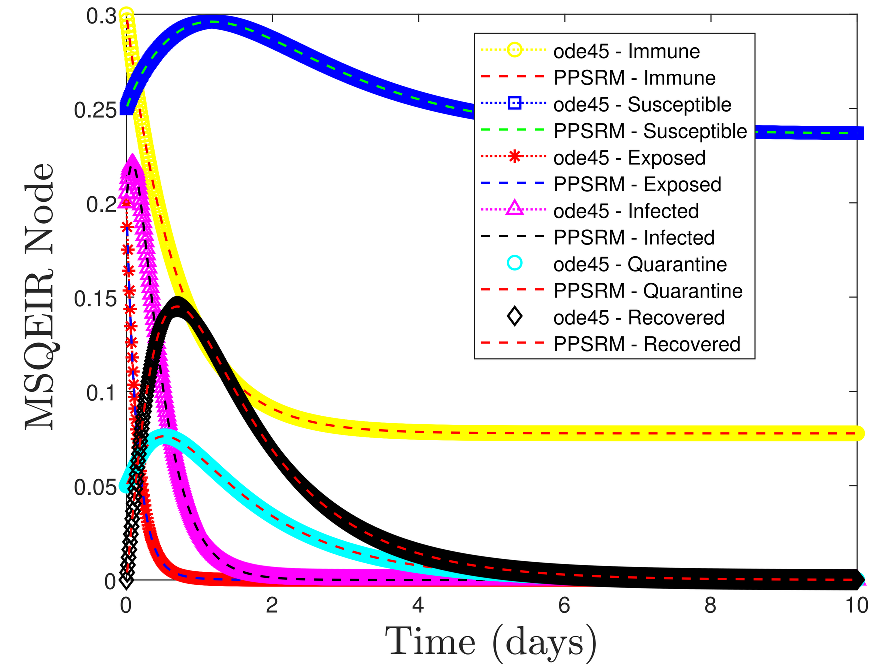

Figure: Time series solution

Conclusions and Outlook

In this article, we developed a model for understanding dynamics of a virulent code. A detailed analysis of the model was presented. In the analysis, the meaningfulness of the model, the reproduction number, and the equilibria stability were presented in detail. The model was solved using the pseudo spectral method and MATLAB's ode45. The results from both methods were in excellent agreement. Effects of the recovery rate on the time series solution are presented graphically and we concluded that increasing the recovery rate contains the spread of the virus and the infectious node decreases dramatically. Phase portraits graphs were presented and the effect of the removal rate of the various populations is presented in graphical form. Increasing the removal rate affects the node dynamics of the model. In particular, the infectious class and the quarantined class.

For Further Information

For the details of our work:

- V.M. Magagula, S.N. Mungwe, Stability analysis of a virulent code in a network of computers, Math Comput Simul, 182 (2021), pp. 296 – 315.

Original article can be downloaded from:

- www.sciencedirect.com

References

[1] P. van de Driessche, J. Watmough, Reproduction number and sub-threshold endemic equilibria for compartmental models of disease transmission, Math. Biosci., 180 (2002), pp. 29 – 48.

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