

Analysis on SARS Models

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ABSTRACT

This work presents some stability analysis and numerical simulation results for a SARS (Severe Acute Respiratory Syndrome) model. We summarized some interesting results on sensitivity, uncertainty, and stability analyses and the effect of changing the values and/or the functions of model parameters, corresponding to different quarantine and isolation control methods, on the disease population dynamics. Numerical simulations have been developed to illustrate the effect of the quarantine and isolation control methods. The obtained results might be applicable to the study of the spreading of other diseases.

KEYWORDS: SARS Model, Stability Analysis, Differential Equations, Equilibrium, Reproductive Number.

1. INTRODUCTION

The SARS epidemic attacked Asia in 2003 leaving almost a thousand people dead and almost 2,000 sick. Before quarantine and isolation methods were put into place in late February of 2003, the disease spread quickly. However, once the quarantine and isolation methods, as well as more public awareness and stricter health precautions, were put into place then the disease started to die out.

In the articles [1, 5], a system of nonlinear ordinary differential equations was used to model the spread of the SARS disease. By dividing a population into six subpopulations, namely, susceptible (S), asymptotically infected (E), quarantined (Q), symptomatic (I), isolated (J) and recovered (R) individuals, the spread of SARS can be modeled into a system of nonlinear ordinary differential equations, using ratios and the probability of one subpopulation moving to the others.

We summarized some interesting results on different control methods that have been applied to the SARS model. Some sensitivity and uncertainty analyses have been done considering the effect of changing the values of different model parameters on the disease dynamics in [1, 2], and sufficient conditions under which the population of the disease groups can be put under control were given once different optimal quarantine and isolation control methods were applied [3 - 5]. Since the problem of putting the disease population under control is equivalent to stabilizing the disease-free equilibrium of the SARS model, analysis of the reproductive number has been done in [1] to obtain conditions under which the equilibrium is asymptotically stable or unstable. Thus, it can be determined when the disease can stop spreading and the disease can thus be put into control.

We have done numerical simulations of the SARS model under several different quarantine and isolation control methods. The effect of different control methods on the SARS population dynamics is discussed, based on the ideas in the articles [1- 6]. The obtained results might be applicable to study of the spreading of other diseases.

2. THE MODEL

By dividing a population into six subpopulations, namely, susceptible (S), asymptotically infected (E), quarantined (Q), symptomatic (I), isolated (J) and recovered (R) individuals, the spread of SARS can be modeled into the following system of differential equations:

$$\frac{dS}{dt} = \Pi - \frac{S(\beta I + \epsilon_E \beta E + \epsilon_Q \beta Q + \epsilon_J \beta J)}{N} - \mu S, \tag{1}$$

$$\frac{dE}{dt} = p + \frac{S(\beta I + \epsilon_E \beta E + \epsilon_Q \beta Q + \epsilon_J \beta J)}{N} - (\gamma_1 + \kappa_1 + \mu)E, \tag{2}$$

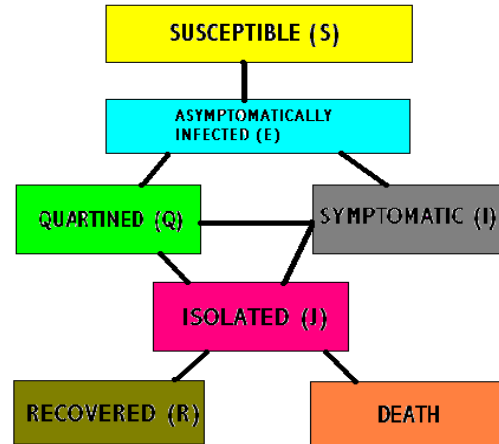
$$\frac{dQ}{dt} = \gamma_1 E - (\kappa_2 + \mu)Q, \tag{3}$$

$$\frac{dI}{dt} = \kappa_1 E - (\gamma_2 + \delta_1 + \sigma_1 + \mu)I, \tag{4}$$

$$\frac{dJ}{dt} = \gamma_2 I + \kappa_2 Q - (\sigma_2 + \delta_2 + \mu)J, \tag{5}$$

$$\frac{dR}{dt} = \sigma_1 I + \sigma_2 J - \mu R. \tag{6}$$

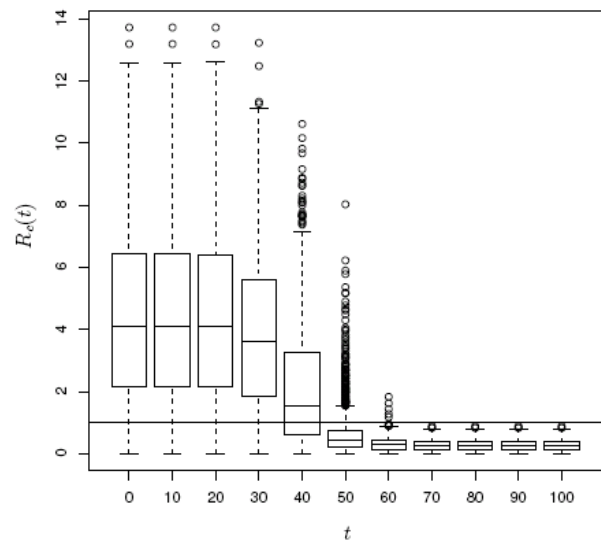
The following flow chat shows the direction of changes among different subpopulation groups.



3. STABILITY RESULT

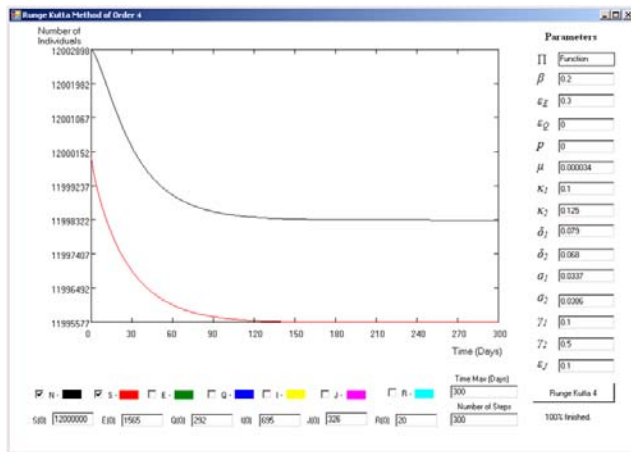
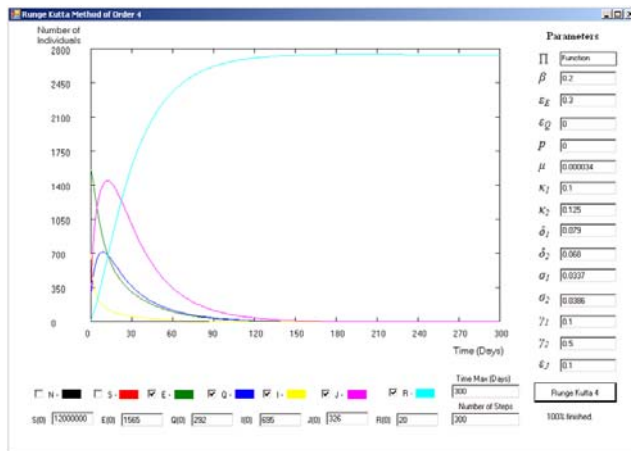
Lemma 1: The Disease-free equilibrium of the system of differential equations $(S^*, E^*, Q^*, I^*, J^*, R^*) = (\pi/\mu, 0, 0, 0, 0, 0)$ is locally asymptotically stable if $R_c < 1$ and unstable if $R_c > 1$, where R_c is the reproductive number and defined to be $R_c = \frac{\epsilon E \beta}{D1} + \frac{\beta \kappa_1}{D1 D2 D3} + \frac{\epsilon Q \beta \gamma_1}{D1 D4} + \frac{\epsilon J \beta \kappa_1 \gamma_2}{D1 D3 D4}$, where $D1 = \gamma_1 + \kappa_1 + \mu$, $D2 = \gamma_2 + \delta_1 + \sigma_1 + \mu$, $D3 = \sigma_2 + \delta_2 + \mu$, $D4 = \kappa_2 + \mu$.

4. GRAPH of $R_c(t)$



5. COMPUTER SIMULATION

By using the aid of a computer, graphs are obtained of the six different subpopulations at time t . It also provides a graphical solution of the total population N at time t . The computer analysis makes playing with the various parameters easier. It can also represent the parameters as a function of time or as a piece wise continuous function.



6. REFERENCES

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