Journal of Nonlinear Modeling and Analysis
Volume 6, Number 4, December 2024, 1046–1063
http://jnma-online.com
DOI:10.12150/jnma.2024.1046

Global Stability of an SIR Model Characterized by Vaccination and Treatment

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Abstract The global dynamics of a SIR model characterized by both vaccination and treatment are considered in the present paper. Global stability ensures convergence to an equilibrium solution irrespective of the initial state of infection. Various independent sets of sufficient conditions on parameters and functional relations are obtained through Lyapunov functionals for stability. It is also established how a disease-free environment can be provided by a proper combination of treatment and vaccination, which is a unique feature as far as SIR models are concerned, as many of the studies have ignored the influence of treatment. Results are illustrated with numerical examples and simulations are provided to visualize the illustrations.

Keywords Infectious disease model, vaccination and treatment, Lyapunov function, equilibrium, global stability

MSC(2010) 37L45, 37D35, 34D23.

1. Introduction

Infectious diseases are mainly caused due to disharmonious ecological interaction amongst microbial infectious agents (bacteria, fungi, parasites, or viruses) and a host. The disease dynamics are influenced by biological, social, behavioral, cultural and environmental changes. Intrinsic to the continuous process of globalization and urbanization, which can build up or ease the hosts exposure to the sources of disease and consequently its transmission in the population, there is a constant transformation in the interaction dynamics ([9]). A critical understanding of transmission dynamics and the connection between various influencing factors is important for the coherent development of an effective plan of action for prevention, control and health assistance. For a field scientist engaged in this activity, it is a difficult question in general, to appraise the rate of the spread of disease and the control of parameters. Also, the affordability of clinical trials and modification costs are another challenge. This situation demands methods/ strategies that have the potential to deal with the disease outbreak when it is in an active phase.

In this frame of reference, mathematical modelling is able to provide useful insights regarding transmission patterns and the detection of parameters to mitigate

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disease in the population. Mathematical models have the ability to translate biological, clinical, environmental, epidemiological and social data into mathematical equations and vice versa. This adaptive nature helps in developing models using collected information from experimental trials, which can be utilized to study the epidemiological behavior of the infectious disease and analyze the effectiveness of interventions taking into consideration several factors that could influence the dynamics of the disease transmission. The rational development of effective, low-cost strategies for prevention and control, health assistance and development of health policies are essential for guiding public health decision-making [18, 42]. One of the very popular models used to study infectious diseases is the susceptible, infected and recovered populations (SIR, for short) model. In this context, mathematical models have been developed to study about the dynamics of the disease such as Influenza A [6], Zika [29], Ebola [41], SARS [3, 25], MERS [1, 23], malaria [4, 7], yellow fever [28], cholera [38], chikungunya [11, 26], dengue [13, 27, 43] and COVID-19 [8, 10, 16, 21, 24, 30, 34, 40]. One may refer to [2, 5, 12, 14, 15, 17, 19, 20, 33, 37, 39] for some more models available in literature.

In this paper, we are going to make a detailed analysis of the global dynamics of an SIR model in which the roles of vaccination and treatment in controlling the spread of disease are the main focus. The model ([35]) is described by the following system of equations:

$$\begin{aligned} u^{'} &= a - bf(u,v) - du - cV(u) + \alpha w, \\ v^{'} &= b_1 f(u,v) - rP(v) - d_1 v, \\ w^{'} &= rP(v) - \alpha w. \end{aligned} \tag{1.1}$$

Here, $u(t)$, $v(t)$, and $w(t)$ represent susceptible, infected, and recovered (by treatment) populations at any time t respectively.

$' = \dfrac{d}{dt}$ denotes the time derivative of a function.

$a \geq 0$ is the rate of growth of the susceptible population, $b > 0$ denotes the interaction rate of infected with susceptible, d denotes the rate of susceptible individuals who are naturally immune to the infection and in no way get infected, $c > 0$ is the vaccination rate and the parameter $\alpha > 0$ is the rate at which a recovered person becomes susceptible again as he is not-vaccinated and re-exposed to infection. $0 < b_1 \leq b$ is the rate of conversion of susceptibles into infected, $d_1 > 0$ is the death rate of the infected population not at all treated or inadequately treated or beyond the treatment, $r > 0$ represents the treatment rate and also recovery rate. f denotes the infection function which shows how susceptible u are converted into infected v, $V(u)$ is the vaccination function (depends on susceptible population), and $P(v)$ is the recovery (by treatment) function of the infected individuals. All these functions are assumed to be continuous functions over the intervals of definitions.

It was claimed in [35] that several models on the SIR system become special cases of system (1.1). The model is quite general in this sense. System (1.1) includes a term that represents the treatment efforts in containing the spread of the disease (controlling the interaction of the infected population with the susceptible). This is a unique feature considering SIR models as most of the other studies concentrate on efforts of vaccination and ignore the influence of treatment. The reason could possibly be society worries more about epidemics than infectious diseases depending on the impacts they make. To elaborate, epidemics may not give enough time to treat, occur suddenly, and are impulsive in nature. On the other hand, infectious