Cooperative system analysis of the Ebola virus epidemic model

Karima Kabli [a], Soumia El Moujaddid [a], Khadija Niri [a], Abdessamad Tridane [b, *]

[a] Department of Mathematics and Computing, Ain Chock Science Faculty, Hassan II University, Casablanca, Morocco
[b] Department of Mathematical Sciences, United Arab Emirates University, P.O. Box 15551, Al Ain, United Arab Emirates

ARTICLE INFO

ABSTRACT

This paper aims to study the global stability of an Ebola virus epidemic model. Although this epidemic ended in September 2015, it devastated several West African countries and mobilized the international community. With the recent cases of Ebola in the Democratic Republic of the Congo (DRC), the threat of the reappearance of this fatal disease remains. Therefore, we are obligated to be prepared for a possible re-emerging of the disease. In this work, we investigate the global stability analysis via the theory of cooperative systems, and we determine the conditions that lead to global stability diseases free and endemic equilibrium.

1. Introduction

The Ebola Virus Disease (EVD) is a type of hemorrhagic fever caused by an infection from a virus of the filoviridae family. Since 1976, five species of this virus have been identified; the most recent virus that caused the 2014—2015 outbreak in West Africa is one of them. This recent epidemic has been the deadliest with 28514 cases and 11313 deaths (Center for Disease Contro, 2014). The case fatality rate of this outbreak has been different in different affected countries with Guinea (60%), Liberia (42%), and Sierra Leone (22%) (World Health Organization, 2017).

The natural host of the virus and how humans get infected by the virus, in the first place (World Health Organization, 2015), are among the many issues that have not yet been understood regarding this virus. The human-human infection, can happen in several ways such as via direct contact with body fluids of an infected person, contaminated needles, sexual contact (Johns Hopkins Medicine He), and direct contact with a dead person in funeral rites (Manguvo & Mafuvadze, 2015).

Mathematical modeling of the EVD has been the subject of many papers that attempted to study the epidemiological aspects of this disease or its dynamical aspects (Agusto, 2017; Althaus, 2014; Berge, Lubuma, Moremedi, Morris, & Kondera-Shava, 2017; Bodine, Cook, & Shorten, 2018; Browne, Gulbudak, & Webb, 2015; Chowell & Nishiura, 2014; Legrand, Freeman Grais, Boelle, Valleron, & Antoine, 2007; Vittoria Barbarossa et al., 2015; Webb & Browne, 2016; Weitz and Dushoff, 2015;

Wong, Bui, Chughtai, & Macintyre, 2017). From an epidemiological point of view, mathematical models were used to estimate the basic reproduction number $\mathscr{R}_0$ (Althaus, 2014; Bodine et al., 2018; Browne et al., 2015; Legrand et al., 2007; Wong et al., 2017), find the final epidemic size (Vittoria Barbarossa et al., 2015), estimate the effectiveness of interventions during the outbreak (Chowell & Nishiura, 2014), and finally to determine the control measure that stopped the spread from the dead bodies infected by the EVD (Weitz and Dushoff, 2015). On the other hand, the mathematical analysis the dynamic of the EVD models was investigated in (Agusto, 2017; Berge et al., 2017; Webb & Browne, 2016) by considering constant recruitment rate of the population (Agusto, 2017; Berge et al., 2017), where the standard Lyapunov approach was used to prove the global stability. The disease age density was also used to fit the data of the West African outbreak (Webb & Browne, 2016).

In this work, we propose a deterministic model to describe the spread the EVD that includes a non-constant recruitment of the population. The idea behind this assumption is the fact that the fertility rate in the African countries in general, and the countries which were infected by the recent outbreak in particular, is very high. Therefore, in order to have a better understanding of the dynamic of the disease in the coming years, we have to consider a non-constant recruitment of the population. With such an assumption, the considered model becomes a cooperative system.

The literature of cooperative dynamical systems is very rich. Muller (Müller, 1927) and Kamke (Kamke, 1932) were the first to apply monotone methods to differential equations. Later, Hirsch applied these results to dynamical systems and proved several results in this theory (Hirsch, 1982, 1983; Hirsch, 1990). The work of Smith and his collaborators (Smith & Thieme, 1990, 1991; Hirsch & Smith, 2005; Smith, 2008) improved the results of the Hirsch and used the theory of cooperative and irreducible systems in different types of ODEs with applications to biological systems. The application of the theory of cooperative systems in the epidemiological model is given in (Iggidr, Niri, & Moulay Ely, 2010), more recent works in (Niri, Kabli, & El moujaddid, 2015), and an epidemiological model with delay in (El Karkri & Niri, 2014; Niri & El Karkri, 2015).

We apply this theory to study the stability of the model of Ebola by showing that the theory of cooperative and irreducible systems could be an alternative to Lyapunov functions.

This paper is organized as follows: In the next section, section 2, we present the EVD model. The preliminary results of our analysis are in section 3, where we prove that the system is cooperative and irreducible, and we calculated the two disease thresholds, including the basic reproduction number. The local stability analysis is also given in this section. In section 4, we prove our main result: sufficient conditions of global stability for the endemic disease equilibrium. In Section 5, we present numerical simulations and support our results. Finally, the conclusion is given in Section 6, and Appendix is in Section A.

2. Introduction of the model

We adopted the model of Legrand et al. (Legrand et al., 2007) by ignoring the class of people that are dead but not yet buried. Ignoring such a class can be accepted as a modeling convention because the problem of the infection between people and the dead bodies before being buried was identified and controlled by the international community in their intervention to stop the spread of the disease via this route (Manguvo & Mafuvadze, 2015; WONG et al., 2017). Hence, our model described by the flow diagram in Fig. 1 is given by

$$
\begin{aligned}
\dot{S} &= \alpha N - \mu S - \frac{\beta_I SI}{N} - \frac{\beta_H SH}{N} \\
\dot{E} &= \frac{\beta_I SI}{N} + \frac{\beta_H SH}{N} - (\mu + \sigma)E \\
\dot{I} &= \sigma E - (\mu_H + \mu_Q + \mu + \mu_R)I \\
\dot{H} &= \mu_H I - (\mu' + \mu + \mu'_R)H \\
\dot{R} &= \mu_R I - \mu R + \mu'_R H,
\end{aligned}
\tag{1}
$$

where S is susceptible individuals, E is a class of exposed people by the close contacts with infectious individuals; and people in E could become infectious after an incubation period. Once people in E become infectious, they are moved to I. A proportion
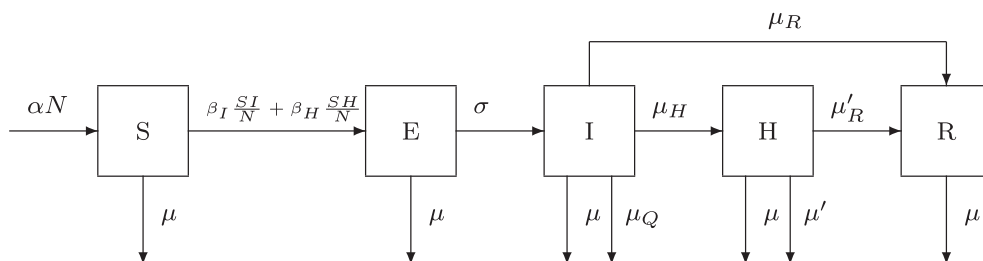

Fig. 1. An SEIHR model for Ebola virus disease.