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DYNAMICAL SYSTEM ANALYSIS AND CONTROL MEASURES OF A WATERBORNE DISEASE MODEL WITH SOCIO-ECONOMIC CLASSES

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Abstract

Waterborne diseases are among the major health challenge facing the world today. We consider a 2-patch waterborne disease model with each patch representing a particular socio-economic class (SEC) formulated by Collins et al. [1]. We extend the model by introducing treatment of infected individuals as a control measure. To investigate the benefits of these control measure, we determine some of the important mathematical features of the model and analyze them accordingly. Particularly, we investigate the impact of the control measure in reducing the spread of waterborne disease for a situation where individuals belong to two different socio-economic classes (low socio-economic class and high socio-economic class). Our analytical predictions are supported by numerical simulations.

***Keywords*:** Waterborne disease, control measure, socio-economic class, basic reproduction number, disease dynamics

1. Introduction

Waterborne diseases such as Cholera, Cryptosporidium, Hepatitis A and E, Giardia and Rotavirus are among the major health challenge facing the world today. This particular health challenge is very common in developing countries where access to clean water is very limited. According to World Health Organization (WHO), unsafe water supply, poor sanitation and poor hygiene are major causes of waterborne diseases [2]. Available statistics revealed that approximately 1.1 billion people globally do not have access to sources of clean water [3]. Statistics also revealed that approximately 700,000 children die every year from diarrhoea caused by unsafe water and poor sanitation [4]. These death due to waterborne diseases could be reduced through access to clean water, provision of adequate sanitation facilities and better hygiene practices [2]. Control intervention strategies such as vaccination, quarantine, water purification and treatment of infected individuals are among the most effective methods of controlling the spread of these diseases [5-7].

Socio-economic status or socio-economic class can be defined as the position of an individual or group respectively within a hierarchical social structure [8]. Socio-economic status or socio-economic depends on income, occupation and education. Studies have shown that individuals in low socio-economic class (SEC) are characterized with poverty, malnutrition, poor sanitation, limited access to clean water and low standards of living. Consequently, these individuals are more exposed to waterborne disease. On the other hand, individuals in a high SEC are known for high standards of living, quality education, good jobs with higher income, clean living environments and access to clean water. Individuals in this group have less chances of contacting waterborne disease. Studies have also shown that socio-economic classes have impact in the spread of waterborne disease [1, 9, 10]. For instance, Collins et al [1] formulated a waterborne disease model with socio-economic classes and used the model to investigate the impact of socio-economic classes on the dynamics of waterborne disease. Hove-Musekwa et al [9] studied the effects of malnutrition in the spread of cholera using a mathematical model. Other mathematical models that have been used to explore the dynamics of waterborne diseases and other infectious diseases can be found [7, 9, 11-21]. There is no doubt that these studies have contributed immensely to the understanding of the dynamics and possible control strategies of waterborne disease. To the best of our knowledge, the impact of control measures on the spread of waterborne disease for a situation where individuals belong to different socio-economic classes

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have not yet been explored. The aim of this study is to fill this gap. Particularly, we will study the impact of control measure (treatment of infected individuals) on the spread of waterborne disease for a community where individuals belong to two different socio-economic classes.

2. Model development

In this section, we extended a two socioeconomic class model for waterborne disease proposed by Collins et al [1] by introducing treatment of infected individuals as a control measures to obtain

$$\frac{dS_1}{dt} = N_1\mu_1 - b_1S_1W_1 - (\mu_1 + \delta_{12})S_1 + \delta_{21}S_2$$
$$\frac{dI_1}{dt} = b_1S_1W_1 - (\gamma_1 + \mu_1 + l_{12} + \theta_1)I_1 + l_{21}I_2$$
$$\frac{dT_1}{dt} = \theta_1 I_1 - (\mu_1 + \xi_1)I_1$$
$$\frac{dW_1}{dt} = \nu_1 I_1 - (\sigma_1 + d_1)W_1$$
$$\frac{dR_1}{dt} = \gamma_1 I_1 - \mu_1 R_1$$
$$\frac{dS_2}{dt} = N_2\mu_2 - b_2S_2W_2 - (\mu_2 + \delta_{21})S_2 + \delta_{12}S_1 \quad (1)$$
$$\frac{dI_2}{dt} = b_2S_2W_2 - (\gamma_2 + \mu_2 + l_{21} + \theta_2)I_2 + l_{12}I_1$$
$$\frac{dT_2}{dt} = \theta_2 I_2 - (\mu_2 + \xi_2)I_2$$
$$\frac{dW_2}{dt} = \nu_2 I_2 - (\sigma_2 + d_2)W_2$$
$$\frac{dR_2}{dt} = \gamma_2 I_2 - \mu_2 R_2.$$

The meaning of the variables and parameters can be found in Tables (1) and (2) respectively. To carry out the qualitative analysis of model (1), it is advisable to rescale the model so that we can deal with non-dimensional variables. Hence, to non-dimensionalized the model, we rescale it as follows: $i_j =, s_j = \frac{S_j}{N},\ \tau_j = \frac{T_j}{N},\ r_j = \frac{R_j}{N}, w_j = \sigma_j\frac{W_j}{\nu_j N}$ and $\beta_j = \frac{b_j\nu_j N}{\sigma_j}$ for $j = 1,2$ and obtain the non-dimensionalized model given by

$$\frac{ds_1}{dt} = n_1\mu_1 - \beta_1 s_1 w_1 - (\mu_1 + \delta_{12})s_1 + \delta_{21}s_2$$
$$\frac{di_1}{dt} = \beta_1 s_1 w_1 - (\gamma_1 + \mu_1 + l_{12} + \theta_1)i_1 + l_{21}i_2$$
$$\frac{d\tau_1}{dt} = \theta_1 i_1 - (\mu_1 + \xi_1)i_1$$
$$\frac{dw_1}{dt} = \sigma_1\left(i_1 - \left(1 + \frac{d_1}{\sigma_1}\right)w_1\right)$$
$$\frac{dr_1}{dt} = \gamma_1 i_1 - \mu_1 r_1$$
$$\frac{ds_2}{dt} = n_2\beta_2 s_2 w_2 - (\mu_2 + \delta_{21})s_2 + \delta_{12}s_1 \quad (2)$$
$$\frac{di_2}{dt} = b_2S_2W_2 - (\gamma_2 + \mu_2 + l_{21} + \theta_2)i_2 + l_{12}i_1$$
$$\frac{d\tau_2}{dt} = \theta_2 I_2 - (\mu_2 + \xi_2)i_2$$
$$\frac{dw_2}{dt} = \sigma_2\left(i_2 - \left(1 + \frac{d_2}{\sigma_2}\right)w_2\right)$$
$$\frac{dr_2}{dt} = \gamma_2 i_2 - \mu_2 r_2,$$

where $s_j + i_j + \tau_j + r_j = n_j$ *and* $n_1 + n_2 = 1$. All parameters are assumed positive.

The initial conditions are assumed as follows:
$sj(0) > 0;\ ij(0) > 0; \tau_j(0) > 0;\ w_j(0) > 0;\ r_j(0) > 0$:
The subscript 1 is used to denote the lower SEC, or SEC 1, while the subscript 2 is used to denote the higher SEC, or SEC 2.

Table 1: Variables of the model (1) and their meanings

Variables	Meaning
N(t)	total human population
Sj(t)	susceptible individuals in the jth SEC
Ij(t)	infected individuals in the jth SEC
Tj(t)	treated individuals in the jth SEC
Rj(t)	recovered individuals in the jth SEC
Wj(t)	measure of pathogen concentration in water reservoir of the jth SEC

Table 2: Parameters of the model (1) and their meanings

Parameters	Meaning
b_j	transmission rate between Sj(t) and Wj(t)
β_j	scaled transmission rate between Sj(t) and Wj(t)
l_{jk}	rate at which individuals migrate from Sj(t) to Sk(t)
δ_{jk}	rate at which individuals migrate from Ij(t) to Ik(t)
γ_j	recovery rate of Ij(t)
ν_j	shedding rate of pathogens by Ij(t)
σ_j	net decay rate of pathogens in water source Wj
μ_j	natural death/birth rate in SEC j
ξ_j	recovery rate due to treatment in SEC j
θ_j	treatment rate in SEC j

3. Model analyses

In this section, we present a detail qualitative analysis of model (2). This is necessary for improving our understanding on the dynamics and control of waterborne disease for a community where this disease is endemic. Particularly, we will explore waterborne disease dynamics for a situation where individuals in the community belong to difference socio-economic classes.

3.1 Basic reproduction number

Model (2) has a unique disease free equilibrium (DFE) given by

$$(s_1^*,\ i_1^*,\ \tau_1^*,\ w_1^*,\ s_2^*,\ i_2^*,\ \tau_2^*,\ w_2^*) = \left(\frac{\delta_{21}}{\delta_{12}+\delta_{21}},\quad 0,\quad 0,\quad 0,\quad \frac{\delta_{12}}{\delta_{12}+\delta_{21}},\quad 0,\quad 0,\quad 0\right).$$

Obviously, the DFE depends on the migration rates of susceptible individuals across the SECs.

Epidemiologically, the basic reproduction number is the average number of secondary infections that result from introducing a single typical infected individual into a completely susceptible population. We determine the basic reproduction number of model (2) using the next generation matrix approach of van den Driessche and Watmough (2002) [22]and is given by

$$R_0^c = \frac{R_{11}^c + R_{22}^c + \sqrt{\left(R_{11}^c + R_{22}^c\right)^2 + 4(R_{12}^c R_{21}^c - R_{11}^c R_{22}^c)}}{2} \qquad (3)$$

where

$$R_{11}^c = \frac{\beta_1 s_1^* \sigma_1 (k_2-\theta_2)}{\sigma_1\big((k_1-\theta_1)(k_2-\theta_2) - l_{12}l_{21}\big)},\quad R_{12}^c = \frac{\beta_1 s_1^* \sigma_1 l_{21}}{\sigma_1\big((k_1-\theta_1)(k_2-\theta_2) - l_{12}l_{21}\big)},$$

$$R_{22}^c = \frac{\beta_2 s_2^* \sigma_2 (k_1-\theta_1)}{\sigma_1\big((k_1-\theta_1)(k_2-\theta_2) - l_{12}l_{21}\big)},\quad R_{21}^c = \frac{\beta_2 s_2^* \sigma_2 l_{12}}{\sigma_1\big((k_1-\theta_1)(k_2-\theta_2) - l_{12}l_{21}\big)},$$

and $k_1 = \mu_1 + \gamma_1 + l_{12}$, $k_2 = \mu_2 + \gamma_2 + l_{21}$.

In the absence of treatment, the basic reproduction number becomes

$$R_0 = \frac{R_{11} + R_{22} + \sqrt{(R_{11} + R_{22})^2 + 4(R_{21}R_{12} - R_{11}R_{22})}}{2} \qquad (4)$$

where

$$R_{11} = \frac{\beta_1 s_1^* k_2}{k_1k_2 - l_{12}l_{21}},\quad R_{22} = \frac{\beta_1 s_1^* \sigma_1 l_{21}}{k_1k_2 - l_{12}l_{21}},$$

$$R_{22}^c = \frac{\beta_2 s_2^* k_1}{k_1k_2 - l_{12}l_{21}},\quad R_{21}^c = \frac{\beta_2 s_2^* l_{12}}{k_1k_2 - l_{12}l_{21}},$$

and$k_1 = \mu_1 + \gamma_1 + l_{12}$, $k_2 = \mu_2 + \gamma_2 + l_{21}$.

By elementary algebraic manipulations we have that

$$R_0^c \le R_0. \qquad (5)$$

This shows that introduction of treatment of infected individuals (control measure) has some influence in reducing the number of secondary infections across the two socio-economic classes in the community.

3.2 The type reproduction number

The type reproduction number T_0^ci for the control model represents the average number of secondary infections produced by an infected individual in a susceptible patch i over his/her lifetime in the resence of treatment [12]. To determine the proper control effort needed to eradicate the spread of the infection while targeting control at one particular socio-economic class (patch), and having no control over reducing the spread of the disease in other socio-economic class (patches), it is necessary that we consider the type reproduction number [23,24]. The type reproduction number T_1^c for SEC 1 of the treatment model (2) is given by

$$T_1^c = R_{11}^c + \frac{R_{12}^c R_{21}^c}{1-R_{22}^c}, \quad (6)$$

provided that $R_{22}^c \neq 0$.

Similarly, the type reproduction number T_2^c for SEC 2 is given by

$$T_2^c = R_{22}^c + \frac{R_{11}^c R_{21}^c}{1-R_{11}^c}, \quad (7)$$

provided that $R_{11}^c \neq 0$.

In the absence of treatment of infected individuals, the type reproduction number T_1 and T_2 for SEC 1 and SEC 2 respectively is given by

$$T_1 = R_{11} + \frac{R_{12}R_{21}}{1-R_{22}}, \quad (8)$$

$$T_2 = R_{22} + \frac{R_{12}R_{21}}{1-R_{11}}. \quad (9)$$

Obviously,

$$T_1^c \leq T_1, \qquad T_2^c \leq T_2. \quad (10)$$

The inequality (10) shows that the treatment of infected individual has the capacity of reducing the number of secondary infections in each of the socio-economic class (sub populations) in the community to a certain level.

4. Numerical simulations

Here, we carry out numerical simulations to support our analytical results. The parameter values used for our numerical simulation are given in Table 3.

Table 3: Parameter values used for numerical simulations

Symbols	Parameters values
β_1	10.00
β_2	$0.5\beta_1$
μ_1	0.0000557
μ_2	0.0000557
γ_1	0.250
γ_2	0.750
σ_1	0.0333
σ_2	$1.8\sigma_1$
δ_{12}	0.10
δ_{21}	0.05
l_{12}	0.10
l_{21}	0.05
θ_1	0.35
θ_2	0.39
ξ_1	$0.5\,\gamma_1$
ξ_2	$0.5\,\gamma_2$

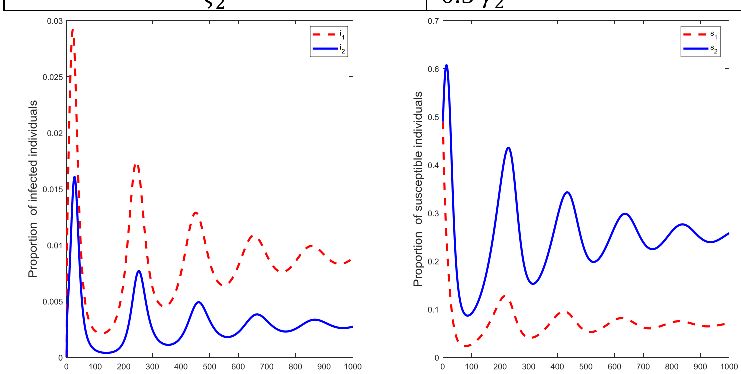

Figure 1. Plot illustrating the differences in the dynamics of SEC 1 and SEC 2 for both infected and susceptible individual

Figure 1 illustrates the possible differences in the dynamics of SEC 1 and SEC 2 for both infected and susceptible individual. From the figure we discovered that individuals in the lower SEC 1 have more chances of contacting waterborne disease than individuals in higher SEC 2.This results agree with our analytical predictions and other findings in the literature. Therefore, our model can be used to study and make predictions for a real life situations where waterborne disease is endemic.

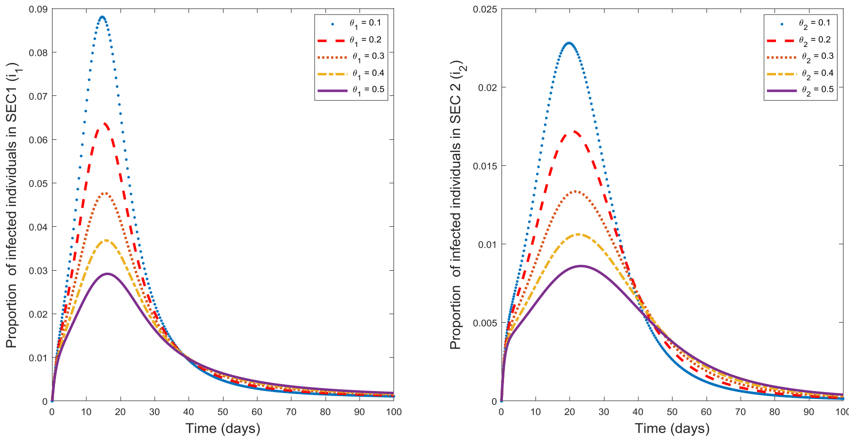

Figure 2: Plot illustrating the effectiveness of treatment rates on infected individuals on SEC 1 and SEC 2.

The impact of treatment in reducing the spread of waterborne disease across the two socio-economic classes is explored here by plotting the infected class for various values of treatment rate (see Figure 3). First, we discover from the figure that increase in treatment rate decreases the infections across the two socio-economic classes. To compare the impact of treatment on the two socio-economic classes, we consider equal treatment rate for the two socio-economic classes. From the figure we also discover that introducing equal treatment rate across the two socio-economic classes will result in lower infections population on the socio-economic class 2. This shows that the two socio-economic class will require different treatment effort to completely eradicate the infections. Particularly, the socio-economic class 1 will require more treatment effort to eradicate the disease.

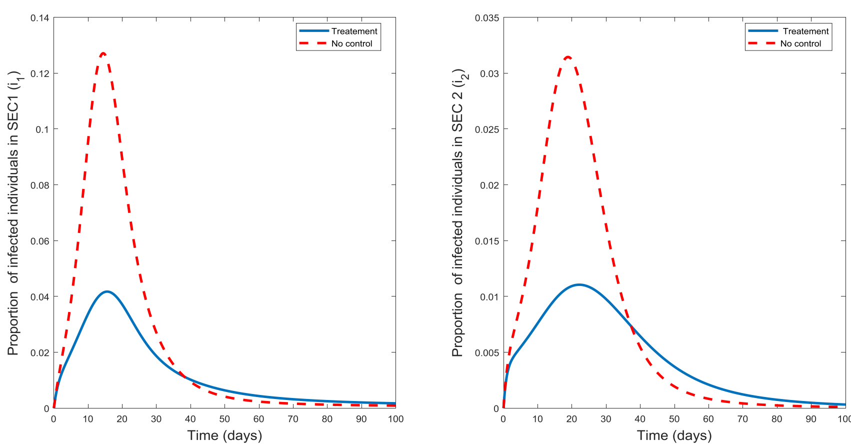

Figure 3: Plot illustrating the impact of treatment on infected individuals on SEC 1 and SEC 2.

In Figure 3 we present a numerical simulation illustrating the impact of treatment on infected individuals by comparing the numerical solutions of infected individuals when treatment is considered and when no control in considered. The results shows that introducing treatment can reduce the infection population by over 50% across both socio-economic classes. Therefore, introducing treatment is highly recommended for reducing the spread of infection in both socio-economic classes.

5. Discussion

The study is motivated by the need to understand the impact of control measure (treatment of infected individuals) in reducing the spread of waterborne disease for a community where individuals belong to two different socio-economic classes (low socio-economic class and high socio-economic class). We considered a socio-economic class model for waterborne disease formulated by Collins et al [1] and extended it by introducing control measure (treatment of infected individuals). The possible benefits of the control measure were investigated analytically. Our findings revealed that introducing treatment have great impact in reducing the spread of waterborne disease for any of the two socio-economic classes. Further analysis using numerical simulation revealed that introducing treatment can reduce the infection population by over 50% across both socio-economic classes.

The possible differences in the dynamics of SEC 1 and SEC 2 for both infected and susceptible individual was explored numerically. Particularly, we discovered that individuals in the lower SEC 1 have more chances of contacting waterborne disease than individuals in higher SEC 2. This results agree with our analytical predictions and other findings in the literature [9]. Overall, our model agree with real life expectation for waterborne disease dynamics. Therefore, we can use this model to study and make prediction for waterborne disease epidemic for a community that comprises different socio-economic classes of individuals.

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