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Observer design for a schistosomiasis model

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ABSTRACT

This paper deals with the state estimation for a schistosomiasis infection dynamical model described by a continuous nonlinear system when only the infected human population is measured. The central idea is studied following two major angles. On the one hand, when all the parameters of the model are supposed to be well known, we construct a simple observer and a high-gain Luenberger observer based on a canonical controller form and conceived for the nonlinear dynamics where it is implemented.

On the other hand, when the nonlinear uncertain continuous-time system is in a bounded-error context, we introduce a method for designing a guaranteed interval observer. Numerical simulations are included in order to test the behavior and the performance of the given observers.

1. Introduction

Human schistosomiasis is a behavioral and occupational disease associated with poor human hygiene, insanitary animal husbandry and economic activities. Among human parasitic diseases, schistosomiasis ranks second behind malaria as far as the socio-economic and public health importance in tropical and subtropical areas are concerned. Urinary schistosomiasis, caused by the species Schistosoma haematobium, is common in Africa and the Middle East. The main clinical sign of schistosomiasis infection is haematuria itself caused by the depositions of eggs by an adult female's worms through the bladder by urinary intermediary [1].

The most effective form of treatment for infected individuals is the use of the drug praziquantel a drug that kills the worms with high efficiency. Control programs often consist on mass chemotherapy possibly supplemented by snail (intermediate host) control. Since school-age children are the heaviest infected group that suffer the most from morbidity and by that are major sources of infection for the community, school targeted chemotherapy can be then an adequate effective approach to control that morbidity [1,2].

Schistosomiasis have one of the most complex host-parasite process to model mathematically because of the different steps of growth of larval assumed by the parasite and the requirement of two host elements (definitive human host and intermediate snail hosts) during their life cycle.

Current world-wide interest in the control of schistosomiasis has focused attention upon the intermediate hosts of the causative parasite, since there is general agreement that the most promising method of controlling the disease is to eliminate or greatly reduce the numbers of these vector snails. It is necessary to obtain information about snail populations, whether the information is used for snail-control evaluation, for ecological research, or for the study of transmission potential.

In epidemiology, mathematical models are very often used to describe the dynamic evolution of the diseases. Deterministic Ordinary differential Equations (ODEs) are one of the major modeling tools and are used in our case.

In this paper, we are interested in the estimation problem of the unknown snails population state of a schistosomiasis model whose dynamics are modeled by a continuous time system.

Symbolically, we can write a dynamical system as:

$$\begin{cases} \dot{X}(t) = F(X(t)), \\ Y(t) = h(X(t)), \end{cases} \tag{1}$$

with $X(t) \in \mathbb{R}^n$, $Y(t) \in \mathbb{R}^p$, $p < n$.

If it is possible to have the value of the state at some time t_0 then it is possible to compute $X(t)$ for all $t \geq t_0$ by integrating the differential equation with the initial condition $X(t_0)$. Unfortunately, it is not often possible to measure the whole state at a given time and by the same way to integrate the differential equation because one does not know the initial condition. One can only have a partial information on the state and this partial information is precisely given by $Y(t)$ the

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output of the system. Therefore we shall show how to use this partial information $Y(t)$ together with the given model in order to have a reliable estimation of the unmeasurable state variables. A state observer is usually employed, in order to accurately reconstruct the state variables of the dynamical system. In the case of linear systems, the observer design theory developed by Luenberger [3], offers a complete and comprehensive answer to the problem. In the field of nonlinear systems, the nonlinear observer design problem is much more challenging and has received a considerable amount of attention in the literature.

An observer for (1) is a dynamical system

$$\begin{cases} \dot{\hat{Z}}(t) = \hat{F}(Z(t), Y(t)), \\ \hat{X}(t) = L(Z(t), Y(t)) \end{cases} \tag{2}$$

whose task is state estimation. It is expected to provide a dynamical estimate $\hat{X}(t)$ of the state $X(t)$ of the original system. The output is in general a function of the state variable, that is, $Y(t) = h(X(t))$.

One usually requires at least that $|\hat{X}(t) - X(t)|$ goes to zero as $t \to \infty$. When the convergence of $\hat{X}(t)$ towards $X(t)$ is exponential, the system (1) is an "exponential observer". More precisely, system (2) is an exponential observer for system (1) if there exists $\lambda > 0$ and $c_0 \geq 0$ such that, for all $t \geq 0$ and for all initial conditions $(X(0), \hat{X}(0))$, the corresponding solutions of (1) and (2) satisfy

$$|\hat{X}(t) - X(t)| \leq e^{-\lambda t}(|\hat{X}(0) - X(0)| + c_0).$$

The best situation corresponds to the case where $c_0 = 0$. In this situation a good estimate of the real unmeasured state is rapidly obtained. One must notice that we do not need to care about the initial condition of the observer since the convergence of $\hat{X}(t)$ towards the real state $X(t)$ does not depend on this choice.

There are numerous means to deal with the synthesis of nonlinear observers. The most general method to tackle it is to use a "high-gain method observer " when the functions of the variables are perfectly known in the dynamical model. This means is much more general than "the output injection model " developed in [4–7], which is applied to a very special class of systems only.

If it happens that some functions of the variables are partially known in the dynamical model but bounded with a priori known bounds, we can define a bounded error observer giving $\hat{X}(t)$ with $|\hat{X}(t) - X(t)|$ bounded by a "reasonable" positive real constant (depending on the uncertainty), "reasonable" meaning that this constant is small with respect to the measurement errors as developed in [8].

This paper shows out first a high-gain observer for a reduced nonlinear model of schistosomiasis as proposed by Allen [9]. This high-gain observer method, has been initiated in [10–12]. However, the convergence of this kind of observers is difficult to prove (because of the global Lipshitz condition). So, we propose a simpler observer whose convergence analysis is studied. This nonlinear observer design does not require Lipschitz extension of functions and change of coordinates for the system contrary to the high-gain observer.

In the second part, we will present an interval observer design to handle the already mentioned uncertainties of the model parameters. The methodology of interval observers has already been studied using a theoretical framework [13,14], and interval observers have been developed for particular models [15,16], and have been validated experimentally [14]. In these works the authors address conditions for stability of the interval observer.

The construction of an observer requires some properties of observability and requires essentially the existence of globally defined and globally Lipschitzian change of coordinates.

The paper is organized as follows: In Section 2 we present the biological assumptions that guided the model's structure and the model's equations. In Section 3 we perform a high-gain observer design. Section 4 will point out a simple observer design. Section 5 tackles the guaranteed interval observer construction. Finally Sections 6 and 7 will respectively be constituted of the different estimator simulations and the conclusion.

2. Model and assumptions

In this section, the model proposed is a modified version of Allen's model [9]. The main point in the model presented in Allen in a relatively isolated community, based on the model presented in Allen [9] is to take into account an additional mammalian host as well as a competitor snails. The model assumes that hosts population and infection rates are independent of environmental factors. The totality of simplifying assumptions lead one to question the quantitative predictions of the model. However, the qualitative features of the results are in themselves of considerable interest [9]. Here, we ignore competitor snails population. Thus, the total human population size, denoted by $N_H(t)$, is split into susceptible individuals $(X_1(t))$ and infected individuals $(X_2(t))$ so that $N_H(t) = X_1(t) + X_2(t)$, and the total mammal population size, denoted by $N_M(t)$, is also subdivided into susceptible mammals $(X_6(t))$ and infected mammals $(X_7(t))$ so that $N_M(t) = X_6(t) + X_7(t)$. Whereas, the total snails population, denoted by $N_S(t)$, is subdivided into susceptible snail host $(X_3(t))$, infected snails which are not yet shedding cercariae $(X_4(t))$ and infected and shedding snail $(X_5(t))$. Thus $N_S(t) = X_3(t) + X_4(t) + X_5(t)$. We assume that the total time interval considered, T, is not too large so that the infection in the definitive hosts (e.g. human) does not result death. Further, it is assumed that infected snails and infected mammals do not recover from schistosomiasis as their life spans are short in comparison to that for humans. For simplicity, assume that births in each population group (human, snail and alternate host) were allowed to enter only the uninfected populations. Another assumption made is that the latent periods can be ignored in both definitive and intermediate hosts. This means that we disregard the time period between the moment when a cercaria penetrates a definitive host and the moment when the cercaria has grown to a sexually mature parasite. Other assumptions are that the recovery rate of infected intermediate hosts is independent of the length of the infectious period, and that the rate of output of cercariae from an infected intermediate host is constant throughout the period when it remains infected. We furthermore assume that births and deaths were considered to be proportionate to population size.

Thus, the differential equations which govern the disease are:

$$\begin{cases} \dfrac{dX_1}{dt} = -t_{15} X_5 X_1 + r_{12} X_2, \\ \dfrac{dX_2}{dt} = t_{15} X_5 X_1 - r_{12} X_2, \\ \dfrac{dX_3}{dt} = b_3 (X_3 + X_4 + X_5) - t_{32} X_2 X_3 - d_3 X_3 - t_{37} X_3 X_7, \\ \dfrac{dX_4}{dt} = t_{32} X_2 X_3 + t_{37} X_3 X_7 - d_4 X_4 - r_{54} X_4, \\ \dfrac{dX_5}{dt} = r_{54} X_4 - d_5 X_5, \\ \dfrac{dX_6}{dt} = b_6 (X_6 + X_7) - t_{65} X_5 X_6 - d_6 X_6, \\ \dfrac{dX_7}{dt} = t_{65} X_5 X_6 - d_7 X_7. \end{cases} \tag{3}$$

where:

- t_{15} = transmission rate from infected snails to uninfected humans,
- t_{32} = transmission rate from infected humans to uninfected snails,
- t_{37} = transmission rate from infected mammals to susceptible snail,