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EVALUATING ENDEMIC EQUILIBRIUM IN EPIDEMIC MODELLING

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Abstract

An interesting application of a method of quantifier elimination in epidemiology was presented in this paper. The existence of the endemic equilibrium was investigated for several epidemic models, the SEIR, MSEIR and MSEIRS. Also, a value of the endemic equilibrium was calculated for these models. An interesting application of the SEIR model is that it was analyzed with the concrete values through the example of Ebola in three different countries. In order to complete the paper, a new virus covid-19 was considered and it was pointed out that the SIR and the SEIR model are not appropriate for it because of some unusual characteristics of covid-19. So, in the literature can be seen numerous different models applied to a new virus, such as SIQR, SVIR, their modifications and many others.

Keywords: epidemic model, quantifier elimination

1. Introduction

Mathematical models for epidemic diseases represent a very significant tool in epidemiology. A large number of models have been proposed, applied to the infection diseases and analysed. The important role have the compartmental models; a population is divided into compartments and the certain assumptions about the nature and time rate of transfer from one compartment to another are specified. Let us first mention a Kermack-McKendrick model that was presented in [3], a SIR model. A population of a size N is divided into three different groups, Susceptible, Infectious and Recovered in this model. Also, the following assumptions are given: a population is closed and all recovered individuals have complete immunity. So, a SIR model is convenient for modelling some diseases of childhood years, like chickenpox, smallpox, rubella and mumps. Considering the SEIR model, a population is divided into four different groups, Susceptible, Infectious, Exposed and Recovered. Note that one more group, Exposed, is added to the previous one so the SEIR model represents the extension of the SIR model. The next two defined models, the MSEIR and MSEIRS, represent generalizations of the SEIR and the SEIRS models which incorporate a group of the children that is protected by the maternal antibodies [12].

We can point out that mathematical modelling of infectious diseases has become important in the 1980s with the advent of the HIV epidemics. Also, since the appearance of the covid-19 pandemic numerous new epidemic models have been proposed. This makes the topic more and more significant and necessary in recent research.

A very important question that is posed in epidemiology is whether a disease currently present in a population will die out or it will reach an endemic stage. So, the question of the stability of a disease free equilibrium and of an endemic equilibrium has always been important. A notion of a basic reproduction number R_0 was used to answer it. We define R_0 as the number of secondary infections from each infected individual in the population that consists only of the susceptible individuals. This notion was first introduced by the author Dietz

[10] and it can be also applied to the stochastic models. Namely, if a value of R_0 exceeds one the disease will reach the endemic stage and will always be present in the population; in the opposite case, if the value of R_0 is less than one the disease will die out.

So, the models that we have been investigating in this paper are the SEIR, the MSEIR and the MSEIRS, respectively. The condition for the existence of an endemic equilibrium was calculated by the method of QE. A resulting condition is exactly the same as a resulting formula obtained in the epidemiological literature for these models, that is also obtained in the paper [5]. As a result of this paper, a value of the endemic equilibrium and the relation between this value and the reproduction number R_0 were calculated for these models. Note that the value of the endemic equilibrium was obtained directly by using QE. The MSEIRS model also has been investigating in the paper [5]; the algorithm for QE returned only a resulting formula without the value of an endemic equilibrium calculated [5]. The interesting application of the SEIR model was that it was analysed with the concrete values through the example of Ebola in three different countries, where the data were taken from [1]. The conclusion was that the reproduction number in Sierra Leone was significantly higher than in Guinea and Liberia.

Let us mention a new virus covid-19 and compare a reproduction number in Western Europe and in China in 2021. The average value of the parameter in Western Europe was 2.2 in the beginning of 2021, while a reported value in China was much higher, 3.32. The difference in numbers is a consequence of a different population density and social organization. Also, if we take measles for an example, a very large number of different values of R_0 ($range\ 5.4 - 18$) were reported in different study areas and periods [2]. Besides the value of the reproduction number, we can compare different epidemic models applied to the same infection. When we analyse a new virus covid-19, it is important to point out that the SIR and SEIR models are not convenient for it. The reason is that a new virus covid-19 has some unusual characteristics, such as transmission of a virus by the pre-symptomatic patients and the existence of the asymptomatic infectious patients. The exact number of the infected cannot be determined directly because of these characteristics and the other models should be used, such as the SIQR, the SVIR and their modifications.

The SIQR model is a compartmental model which represents a community divided by four compartments, assuming that the additional compartment of the quarantined people Q is added to the SIR model. In common epidemics, only symptomatic patients are infectious while for covid-19 a large number of pre-symptomatic or asymptomatic persons are also infectious and can be identified by PCR test. In the SIQR model a number of the quarantined patients is the variable and it is appropriate for covid-19. It was successfully applied in the analysis of the early stage of the outbreak of covid-19 in many different countries. Also, the modifications of a model were made; for example, the SIQR model was redefined to be more appropriate to the covid-19 and presented in the paper [23]. Note that a very large number of models were proposed for covid-19 and we have mentioned only some of them in this paper.

Now let us point out that a reproduction number has a crucial role in calculating a percent of a population that need to be vaccinated in order to eliminate a disease. We will first introduce the notion of herd immunity. A population is said to have herd immunity for a disease if enough people are immune so that the disease would not spread if it were suddenly introduced in the population. Herd immunity in a population is achieved by vaccination of the susceptibles in a population. In terms of a probability, we use a formula $1 - 1/R_0$ and say that the epidemic would die out when a proportion of immune (or vaccinated) persons would exceeds the value $1 - 1/R_0$. So, although the vaccines against covid-19 have been effective enough, achieving herd immunity is required to end the pandemic. In a research in a paper [6], a number of people that would be fully vaccinated

in June 2021 was predicted. The analysis was done for several different regions in the world for the same period of a time. The dataset used was a number of fully vaccinated people in May 2021; the considered regions were US, Asia, Europe, Africa and South America. The research results were the following: on June 1 the percentage of the fully vaccinated people would be 41.8% in the US, 17% in Europe, 8.8% in South America, and 0.6% in Africa. So, according to the obtained results, it could be seen that US would reach the highest level in the vaccination rate on June 1 2021. However, a conclusion was that the herd immunity would not be achieved in any of the considered regions.

Considering the mathematical methods used in this paper, a method for quantifier elimination presented in [24] was used. Historically, the first real quantifier elimination procedure was presented by Tarski. During the 1970s Collins developed the first elementary recursive real quantifier elimination procedure [7, 8], which was based on cylindrical algebraic decomposition (CAD). CAD has undergone many improvements. QE by partial cylindrical algebraic decomposition was developed by the author H. Hong [14]. The method of QE by real roots counting was published by the author V. Weispfenning in 1998 [28]. The improved version of this method is called Hermitian QE based on real roots counting and it has application in automated theorem proving in geometry. The method of QE based on virtual term *substitution* was developed by V. Weispfenning [26, 27] and implemented in REDLOG by Dolzmann and Sturm. Considering the systems that provide QE and formula simplification, REDLOG, QEPCAD and SLFQ were used.

Let us mention the application in control theory. A very large number of problems in the nonlinear control theory were formulated and solved in [16]. For example, the problems related to the stationary points of a dynamical system or an ability of a dynamic system to follow an algebraic curve were investigated. The application to the stability problems for the initial value problems and initial boundary value problems for partial differential equations is presented in [15]. The method based on CAD and the program QEPCAD developed by Hong were used [15]. A main difficulty is that a number of real variables in problem can be too large for solving by QEPCAD.

Generally, a difficulty can also represent a high degree of a quantified variable. A special case of QE (cubic case) was presented in [25]. Namely, a method that eliminates a quantified variable from a formula that represents a Boolean combination of polynomial inequalities of a degree less or equal three was presented. This method extends the virtual substitution of the parametrized test points already represented for the linear and quadratic case. A general problem for the previously mentioned methods can be a complexity of calculation; a resulting quantifier free formula can be very large. So, a simplification of a resulting formula can be necessary very often. A review of the simplification methods was presented by the authors A. Dolzmann and T. Sturm in paper [11]. The presented methods combine the elements of field theory and mathematical logic. These methods do not require a Boolean normal form computation.

Note that in this paper, we focus on the application of quantifier elimination in epidemiology. In the other papers related to both, QE and its applications, the completely different methods of QE were used. The approach that requires both quantifier elimination and simplification of a formula was used in [5] and the method is based on virtual term substitution. A resulting quantifier free equivalent formula consists of 54 atomic formulas for the MSEIRS model.

A main result of this paper represents the obtained values of endemic equilibrium for the previously mentioned models by QE method. We can point out that there are no these values obtained by any method of QE in the existing literature.

2. Quantifier Elimination

The method that is used in this paper is the method of quantifier elimination.
Let us show the example of a formula with quantifiers which is equivalent to a formula without quantifiers. Suppose we are given a formula φ(a,b,c) in a set of real numbers **R**,

$$\exists x(ax^2+bx+c=0).$$

By the quadratic formula, we have the following equivalence:

$$\varphi\ (a,b,c)\leftrightarrow[(a\neq 0\wedge b^2-4ac\geq 0)\vee(a=0\wedge\ (b\neq 0\vee c=0))],$$

so φ is equivalent to a quantifier free formula.
Now let us introduce some basic definitions which are of importance for quantifier elimination.
The language L is recursive if the set of codes for symbols from L is recursive. The first order theory T is recursive if the set of codes for axioms for T is recursive. An L-theory T is complete if for every sentence φ in a language L the following holds:

$$T\vdash\varphi\ \text{ or }\ T\vdash\neg\varphi.$$

For each theory T arises question of its decidability, i.e. the existence of algorithm which for given $\varphi\in Sent_L$ gives an answer whether $T\vdash\varphi$ or $T\nvdash\varphi$. In the case of recursive complete theory in a recursive language, the answer is affirmative.
A theory T of a language L admits quantifier elimination if for every formula $\varphi(\bar{v})\in For_L$ there exist a quantifier free formula $\psi(\bar{v})\in For_L$ such that:

$$T\vdash\forall v(\varphi(\bar{v})\leftrightarrow\psi(\bar{v}))$$

Every logic formula is equivalent to its following prenex normal form:

$$Q_1x_1...Q_nx_n\varphi(x_1,...,x_n,y_1,...,y_m),$$

where $Q_i\in\{\forall,\exists\}$ and φ is a formula without quantifiers in DNF; formula of the form $\forall x\varphi$ is equivalent to $\neg\exists x\neg\varphi$; $\exists x(\varphi\vee\psi)\leftrightarrow\exists x\varphi\vee\exists x\psi$ is a valid formula. Using the previous we see that an L-theory T admits quantifier elimination if and only if for every L-formula of the form $\exists x\varphi(\bar{y},x)$, where φ is a conjunction of atomic formulas and negations of atomic formulas, exists equivalent quantifier free formula $\psi(\bar{y})$.

The original general algorithm for QE for any theory T was presented in [24]. Specially, the algorithm was applied to the theory of RCF.

2.1. Theories of ACF and RCF: The language of fields is L = {+, -,×,0,1, =}, where + and × are binary function symbols, - is unary function symbol, 0 and 1 are constant symbols and = is relational symbol.

We could axiomatize the class of algebraically closed fields by adding, to the axioms of fields (1), the axiom (2):

1. Axioms of field
2. for each n>1,

$$\forall x_0 \forall x_1 \cdots \forall x_{n-1} \exists x (x_0 + x_1 x + \cdots + x_{n-1} x^{n-1} + x^n = 0)$$

A set A = (1,2) is a set of axioms of algebraically closed fields; for any term *t* of a language L there exist a polynomial $p(x_1,...,x_n)$ with coefficients in **Z** such that $t = p(x_1,...,x_n)$ is a consequence of a set A. The set of axioms of algebraically closed fields allows quantifier elimination.

As example of ACF, we can take the field of complex numbers, which is the algebraic closure of the field of real numbers.

In order to know how to eliminate quantifiers in a theory of algebraically closed fields, it is sufficient to know how to eliminate the existential quantifier in the formula of the form:

$$\exists x (t_1 = 0 \wedge \cdots \wedge t_k = 0 \wedge t \neq 0),$$

where t_i represent an atomic formula of a language L. So, every t_i is polinomial by *x* whose coefficients are polynomials by the other variables with coefficients in **Z**.

The language of ordered fields is L = {+, -,×,0, 1, =, >}, where + and × are binary function symbols, - is unary function symbol, 0 and 1 are constant symbols and = and > are relational symbols.

We could axiomatize the class of real closed fields by adding, to the axioms of ordered fields (1), the axioms (2), (3):

1. Axioms of ordered field
2. $\forall x \exists y (x = y^2 \vee -x = y^2)$
3. $\forall x_0 \forall x_1 \cdots \forall x_{2n} \exists x (x_0 + x_1 x + \cdots + x_{2n} x^{2n} + x^{2n+1} = 0)$, for any n ≥1

Models of a set of axioms A = (1, 2, 3) are real closed fields. The set A allows quantifier elimination; for any term *t* of a language L there exist a polynomial $p(x_1,...,x_n)$ with coefficients in **Z** such that $t = p(x_1,...,x_n)$ is a consequence of a set A.

The basic examples of a model of real closed fields are set of real numbers **R** and real closure of a set **Q**. The set A allows quantifier elimination.

In order to know how to eliminate quantifiers in a theory of real closed fields, it is sufficient to know how to eliminate the existential quantifier in the formula of the form:

$\exists x\left(p_1 = 0 \wedge \cdots \wedge p_k = 0 \wedge q_1 > 0 \wedge \cdots \wedge q_m > 0\right)$,
where p_i, q_j are polinomials by x whose coefficients are polynomials by the other variables with coefficients in **Z**.

3. Applications of QE in Epidemiology

The mathematical models have become the important tool in analysing the spread and control of the infectious diseases. Let us first mention a Kermack-McKendrick model that is presented in [3], a SIR model. The population of a size N is divided into three groups, Susceptible, Infectious and Recovered in this model. The Susceptible (S(t)) population contains the individuals who are at risk of becoming infected. The Infectious (I(t)) class represent the individuals who have been infected. The Recovered (R(t)) class represent the individuals who have been recovered. Notice that recovered individuals are permanently recovered and cannot be infected again in this model and a total size of population remains constant. A number of individuals in each of these classes changes with time, meaning that S(t), I(t) and R(t) are functions of time t. Since a total size of a population is equal N it holds:

N = S(t) + I(t) + R(t).

Generally, mathematical models consist of the systems of differential equations that describe the dynamics in each class.

3.1. SEIR model: In the SEIR model defined in [3] a population is divided into four groups, Susceptible, Infectious, Exposed and Recovered. So, comparing it with the previously described SIR model, one more group, Exposed, was added. The Exposed (E(t)) class represent the individuals who have been infected but yet not infectious (this means that they do not show any symptoms and are not able to infect the others). In the further analysis of this model, we assume that birth rates and death rates are equal. Also, we assume that the new born children have no inherited immunity.

The SEIR model for the transmission of infectious diseases is presented by the system of four differential equations:

$$\frac{d}{dt}S = \mu - \beta IS - \mu S$$
$$\frac{d}{dt}E = \beta IS - (\mu + \sigma)E$$
$$\frac{d}{dt}I = \sigma E - (\mu + \gamma)I$$
$$\frac{d}{dt}R = \gamma I - \mu R$$

where the meaning of the variables and parameters is the following: S susceptibles, E exposed, I infectious, R recovered, β transmission parameter, μ birth rate = mortality rate, σ rate of a change from exposed to infectious, γ recovery rate.

A point in SEIR-space is an equilibrium point if it holds:

$$\mu - \beta IS - \mu S = 0 \wedge \beta IS - (\mu + \sigma)E = 0 \wedge$$
$$\wedge \sigma E - (\mu + \gamma)I = 0 \wedge \gamma I - \mu R = 0,$$

(where it holds: $I + S + E + R = 1$) and represents an endemic state if

$$S > 0 \wedge E > 0 \wedge I > 0 \wedge R > 0.$$

(note that a disease free equilibrium, that is obtained by setting $I = 0$, always exist and has the value (1, 0, 0, 0)).

Therefore, there is an endemic equilibrium for the SEIR model if the following formula holds:

$$(\exists E)(\exists R)(\exists I)(\exists S)(\mu - \beta IS - \mu S = 0 \wedge \beta IS - (\mu + \sigma)E = 0 \wedge$$
$$\wedge \sigma E - (\mu + \gamma)I = 0 \wedge \gamma I - \mu R = 0 \wedge S > 0 \wedge E > 0 \wedge I > 0 \wedge R > 0)$$

(note that $I + S + E + R = 1$). (1)

Let us rewrite the system first. We will combine a substitution method and QE method presented in [24]. We can express the values of E and R from the third and fourth equation, respectively:

$$E = \frac{(\mu + \gamma)I}{\sigma}, R = \frac{\gamma I}{\mu + \gamma}. \quad (2)$$

Now we will substitute the values from (2) into the second equation and a formula (1). So, we have the following system:

$$\beta IS - (\mu + \sigma)\frac{(\mu + \gamma)I}{\sigma} = 0$$
$$I + S + \frac{(\mu + \gamma)I}{\sigma} + \frac{\gamma I}{\mu} - 1 = 0$$

So, we will apply QE algorithm to the inner quantified subformula of our formula:

$$(\exists I)(\exists S)\left(\beta IS - (\mu + \sigma)\frac{(\mu + \gamma)I}{\sigma} = 0 \wedge I + S + \frac{(\mu + \gamma)I}{\sigma} + \frac{\gamma I}{\mu} - 1 = 0 \wedge S > 0 \wedge I > 0\right)$$

More precisely, we will apply the algorithm to a formula

$$(\exists S)\left(\beta IS - (\mu + \sigma)\frac{(\mu + \gamma)I}{\sigma} = 0 \wedge I + S + \frac{(\mu + \gamma)I}{\sigma} + \frac{\gamma I}{\mu} - 1 = 0 \wedge S > 0 \wedge I > 0\right)$$

By the method for QE we have
$T_1 = A_2 t_1 - A_1 t_2$,

where $t_1 \equiv \beta IS - (\mu + \sigma)\frac{(\mu+\gamma)I}{\alpha}$, $t_2 \equiv I + S + \frac{(\mu+\gamma)I}{\sigma} + \frac{\gamma I}{\mu} - 1$ and the coefficients are equal $A_1 = \beta I$, $A_2 = 1$. Our formula is equivalent to:

$$A_2 \neq 0 \wedge (\exists S)(T_1 = 0 \wedge t_2 = 0 \wedge S > 0 \wedge I > 0).$$

When we rewrite the equality $T_1 = 0$ we get the following one:

$$(\mu + \sigma)\frac{(\mu + \gamma)}{\sigma} + \beta I + \beta\frac{(\mu + \gamma)I}{\sigma} + \frac{\beta\gamma I}{\mu} - \beta = 0$$

The previous equation represents a linear equality by a variable *I* and we can express a value of *I* from it. So, we have the equality:

$$I = \frac{\sigma\beta - (\mu + \sigma)(\mu + \gamma)}{\sigma\beta(1 + \frac{\mu + \gamma}{\sigma} + \frac{\gamma}{\mu})}$$

Since we have a condition $I > 0$ we get the following:

$$\frac{(\mu + \sigma)(\mu + \gamma)}{\sigma\beta} < 1 \qquad (3)$$

An obtained condition (3) is the same as a condition that can be find in epidemiological literature. More precisely, the most often a formula for a reproduction number is used in epidemiological literature:

$$R_0 = \frac{\beta\sigma}{(\mu + \gamma)(\mu + \sigma)}.$$

It is known that if it holds $R_0 > 1$, then a disease will reach an endemic stage.
Now let us find a value of the endemic equilibrium. When we set all the derivatives of a given system equal to zero and solve it, we get a value of $S^* = \frac{(\mu+\sigma)(\mu+\gamma)}{\sigma\beta}$. According to the previous, we can express a value of S^*as a function of R_0:

$$S^* = \frac{1}{R_0}.$$

Also, we can express a value of the endemic equilibrium as a function of R_0. It follows:

$$(S^*, E^*, I^*, R^*) = \left(\frac{1}{R_0}, \frac{(\mu + \gamma)\mu}{\sigma\beta}(R_0 - 1), \frac{\mu}{\beta}(R_0 - 1), \frac{\gamma}{\beta}(R_0 - 1)\right)$$

3.2. Numerical analysis of the SEIR model: In order to analyse the SEIR model we have taken the data for Ebola in three different countries, Guinea, Sierra Leone and Liberia [1]. We have calculated a reproduction

number for SEIR model We used the values $\sigma = 0.188$ and $\gamma = 0.178$ from [1]. Since a value of a mortality rate is very small we have taken $\mu = 0.000034$. When we use a formula for R_0 for the SEIR model:

$$R_0 = \frac{\beta\sigma}{(\mu+\gamma)(\mu+\sigma)},$$

we get the following values presented in the Table I:

Parameter	Guinea	Sierra Leone	Liberia
β	0.27	0.45	0.28
f	0.74	0.48	0.71
R_0	1.49	2.53	1.57
β^*	0.178	0.178	0.178

Table I. Values of parameters and a reproduction number

Note that the values are very close to those presented in [1] obtained by the formula $R_0 = \beta/\gamma$. More precisely, the two values for Sierra Leone are the same, while the difference for both countries, Guinea and Liberia is equal 0.02. Since it holds $R_0 > 1$, a conclusion is that the Endemic Equilibrium is stable for all three countries. However, we can see that a value of R_0 (=2.53) in Sierra Leone is significantly higher than in the other two countries. This number depends on a population structure, human mobility, etc.
Notice that a value of a transmission rate β is constant in the absence of any control measures or interventions. When the control measures such as quarantine or isolation are applied, a value of a parameter β decreases.
Now we will analyse the sensitivity of Endemic Equilibrium of the SEIR model. We can notice that in cases when a value of transmission rate β decreases and the values of the other parameters are fixed, then a value of R_0 decreases. In cases when a value of R_0 becomes less than one, the Endemic Equilibrium becomes unstable.
Now let us find the critical value of a transmission rate for all three countries. In order to find a critical value of transmission rate, we set up the equality $R_0 = 1$, where the values of the other parameters are constant. Since these values of parameters are the same for all three countries, we get the same resulting value of $\beta^* = 0.178$. So, we can conclude that when we keep the values of three parameters constant, a disease will spread out if a value of transmission rate is greater than a critical value $\beta^* = 0.178$, while the disease will be controlled if a value of β is less than $\beta^* = 0.178$.
Since the vaccine against Ebola was approved in 2020, a quarantine and isolation were the only control measures for a long period of time. The aim of these measures was to decrease a value of a reproduction number and control a disease. The values of a reproduction number for Guinea and Liberia are not high so mathematically it would not be difficult to achieve. However, in the practice a disease did not die out because of a phenomenon called superspreading. Namely, the superspreading is the transmission of the infectious disease to a very large number of uninfected persons by a relatively small number of highly contagious persons. The documented outbreaks of Ebola were sporadic, unpredictable and localized in Western Africa.

3.3. MSEIRS model: It is known that the newborn children of the mothers who are immune to the specific disease are passively protected by maternal antibodies for a certain period of time. The MSEIR and MSEIRS models represent generalizations of the SEIR and SEIRS models that incorporate a group of children being protected by maternal antibodies. They are presented by the author Hethcote in [12].
The MSEIRS model for the transmission of infectious diseases is presented by the system of five differential equations:

$$\frac{d}{dt}M = \mu(1-S) - (\xi+\mu)M$$
$$\frac{d}{dt}S = \mu S + \xi M + \gamma R - \mu S - \beta IS$$
$$\frac{d}{dt}E = \beta IS - (\mu+\sigma)E$$
$$\frac{d}{dt}I = \sigma E - (\nu+\mu)I$$
$$\frac{d}{dt}R = \nu I - (\mu+\gamma)R$$

where the meaning of the variables and parameters is the following: M newborns protected by the maternal antibodies, S susceptibles, E exposed, I infectious, R recovered, β transmission rate, μ birth rate = mortality rate, ξ rate of loss of protection by maternal antibodies, σ rate of change from exposed to infectious, γ rate of loss of immunity, ν rate of loss of infectiousness.

A point in MSEIR-space is an equilibrium point if

$$\mu(1-S) - (\xi+\mu)M = 0 \wedge \mu S + \xi M + \gamma R - \mu S - \beta IS = 0 \wedge$$
$$\wedge \beta IS - (\mu+\sigma)E = 0 \wedge \sigma E - (\nu+\mu)I = 0 \wedge \nu I - (\mu+\gamma)R = 0,$$

(where it holds: $I + S + E + R + M = 1$) and represents an endemic state if

$$S > 0 \wedge E > 0 \wedge I > 0 \wedge R > 0 \wedge M > 0.$$

Therefore, there is an endemic equilibrium for the MSEIRS model if the following formula holds:

$$(\exists E)(\exists R)(\exists I)(\exists S)(\exists M)(\mu(1-S) - (\xi+\mu)M = 0 \wedge \mu S + \xi M + \gamma R - \mu S - \beta IS = 0 \wedge$$
$$\wedge \beta IS - (\mu+\sigma)E = 0 \wedge \sigma E - (\nu+\mu)I = 0 \wedge \nu I - (\mu+\gamma)R = 0 \wedge$$
$$\wedge S > 0 \wedge E > 0 \wedge I > 0 \wedge R > 0)$$

(note that $I + S + E + R + M = 1$). (4)

Let us rewrite the system first. We will use a substitution method first and express the values of E and R from the fourth and fifth equation, respectively:

$$E = \frac{(\nu + \mu)I}{\sigma}, R = \frac{\nu I}{\mu + \gamma}. \quad (5)$$

Now we will substitute the previous values into the third equation and a formula (4). So, we have the following system:

$$\beta IS - (\mu + \sigma)\frac{(\nu + \mu)I}{\sigma} = 0$$
$$I + S + \frac{(\nu + \mu)I}{\sigma} + \frac{\nu I}{\mu + \gamma} + M - 1 = 0$$

So, we will apply QE algorithm to the most inner quantified subformula of a formula:

$$(\exists M)(\exists I)(\exists S)\left(\beta IS - (\mu + \sigma)\frac{(\nu + \mu)I}{\sigma} = 0 \wedge I + S + \frac{(\nu + \mu)I}{\sigma} + \frac{\nu I}{\mu + \gamma} + M - 1 = 0\right)$$

where it holds $M > 0, I > 0, S > 0$.

More precisely, we will apply the algorithm to a formula:

$$(\exists S)\left(\beta IS - (\mu + \sigma)\frac{(\nu + \mu)I}{\sigma} = 0 \wedge I + S + \frac{(\nu + \mu)I}{\sigma} + \frac{\nu I}{\mu + \gamma} + M - 1 = 0\right)$$

By the method for QE we have
$T_1 = A_2 t_1 - A_1 t_2$,

where $t_1 \equiv \beta IS - (\mu + \sigma)\frac{(\nu+\mu)I}{\sigma}$, $t_2 \equiv I + S + \frac{(\nu+\mu)I}{\sigma} + \frac{\nu I}{\mu+\gamma} + M - 1$ and the coefficients are equal $A_1 = \beta I$, $A_2 = 1$ (notation is analogous to the previous one). Our formula is equivalent to:

$$A_2 \neq 0 \wedge (\exists S)(T_1 = 0 \wedge t_2 = 0),$$

where it holds $M > 0, S > 0, I > 0$.

When we rewrite the equality $T_1 = 0$ we get the following one:

$$(\mu + \sigma)\frac{(\nu + \mu)}{\sigma} + \beta I + \beta\frac{(\nu + \mu)I}{\sigma} + \frac{\beta\nu I}{\mu + \gamma} + \beta M - \beta = 0$$

Now we substitute values from (5) into the previous formula. A formula is equivalent to:

$$(\mu + \sigma)\frac{(\nu + \mu)}{\sigma} + \beta I + \beta E + \beta R + \beta M - \beta = 0$$

If we express a value of S from (5) and substitute it into the previous formula we get:

$$(\mu + \sigma)\frac{(\nu + \mu)}{\sigma} + \beta - \beta S - \beta = 0$$

Now we can express a value of S as a function of parameters:

$$S = \frac{(\mu + \sigma)(\nu + \mu)}{\sigma\beta} \tag{6}$$

Similarly as for the SEIR model, after some basic calculation using (6) and $t_2 = 0$, we get a resulting condition:

$$\frac{(\mu + \sigma)(\nu + \mu)}{\sigma\beta} < 1 \tag{7}$$

If we would compare the resulting conditions for the SEIRS and MSEIRS model, we would see that a value of the reproduction number is the same. Notice that the resulting condition for the MSEIRS model does not contain all the given parameters. The same result (7) was obtained in [5] by using different method, QE based on virtual term substitution.

Now let us find a value of the endemic equilibrium. Notice that we have already calculated a value of S^* by the method of QE directly and that is obtained in (7):

$$S^* = \frac{(\mu + \sigma)(\nu + \mu)}{\sigma\beta}.$$

Now we can substitute the previous value into the system in which derivatives are equal to zero and evaluate the endemic equilibrium. Since it holds: $S^* = \frac{1}{R_0}$, we will present the obtained value as a function of R_0:

$$(M^*, S^*, E^*, I^*, R^*) = \left(\frac{\mu}{(\xi + \mu)R_0}(R_0 - 1), \frac{1}{R_0}, \frac{\mu + \nu}{\sigma}I^*, I^*, \frac{\nu}{\mu + \gamma}I^*\right),$$

where the value of $I^*$is the following:

$$\frac{\xi\mu(R_0 - 1)(\mu + \gamma)}{\beta(\mu + \gamma)(\xi + \mu) - \gamma\nu(\xi + \mu)R_0}$$

So, we can point out that a value of endemic equilibrium was calculated by QE method. Note that in paper [5] the value of EE was not calculated and only the resulting condition for the existence of EE was presented.

Now let us compare the obtained results with the results for the MSEIR model that also has been presented in [12]. A value of the reproduction number is the same for both MSEIR and MSEIRS model:

$$R_0 = \frac{\beta\sigma}{(\mu+\nu)(\mu+\sigma)},$$

but a value of endemic equilibrium is different. More precisely, we have calculated a value of the EE for the MSEIR model and it is equal

$$M^* = \frac{\mu}{\xi+\mu}\left(1-\frac{1}{R_0}\right), S^* = \frac{1}{R_0}, E^* = \frac{\xi\mu}{(\mu+\sigma)(\mu+\xi)}\left(1-\frac{1}{R_0}\right)$$

$$I^* = \frac{\sigma\xi\mu}{(\mu+\nu)(\mu+\sigma)(\mu+\xi)}\left(1-\frac{1}{R_0}\right), R^* = \frac{\sigma\xi\nu}{(\mu+\nu)(\mu+\sigma)(\mu+\xi)}\left(1-\frac{1}{R_0}\right)$$

4. Discussion and Conclusion

Quantifier elimination has an application in many areas, including epidemiology. In this paper, we have shown an interesting application of QE for the SEIR, the MSEIR and MSEIRS model. This method for QE for a theory of RCF was first presented in [24]. Additionally, one concrete example of evaluation and analysis of the reproduction number for Ebola was presented. It was concluded that if government would apply control measures as quarantine and isolation (some mechanisms like closing the schools, preventing mass gathering and similar), according to the calculations a disease would die out. However, it did not happen in the practice because of one specific phenomenon called superspreading. The outbreaks of Ebola that were documented were sporadic, unpredictable and localized in Western Africa.

Considering the methods used in the other papers with the same topic, QE based on virtual term substitution was applied in [5] and the algorithm for the existence of endemic equilibrium was presented. Namely, a resulting quantifier free equivalent formula consists of 25 atomic formulas for the SEIRS and 54 atomic formulas for the MSEIRS model, respectively [5]. So, a simplification of these formulas was necessary. In order to illustrate the complexity of their result, we can point out a resulting formula presented for the SIS model [5]. More generally, the approach to QE in the theory of RCF is completely different in the other literature; QE based on virtual term substitution, Hermitian QE based on real roots counting and QE by cylindrical algebraic decomposition were used.

A main result of this paper represent the obtained values of endemic equilibrium for the previously mentioned models by QE method. We can point out that there are no these values obtained by any method of QE in the existing literature. Since the author H. W. Hethcote introduced the MSEIR and the MSEIRS model, the values of a reproduction number and endemic equilibrium for these models can be seen in his papers [12,13].

To conclude this paper, let us consider a new virus covid-19. The numerous new epidemic models have been proposed for it. Since covid-19 has the unusual characteristics such as the existence of asymptomatic infectious patients, the SIR and SEIR model are not appropriate for a new virus. For example, the SIQR model was suitable in the analysis of the early stage of the outbreak in Italy [22] and some other countries. Also, the SIQR model was reformulated such that the compartments for infected and quarantined were redefined to be appropriate for covid-19 [23].

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