Equilibrium Solutions of a Modified SIR Model with Vaccination and Several Levels of Immunity

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Abstract: We consider a system of ordinary differential equations which extends the well-known SIR model for the dynamics of an epidemic. The main feature is that the population is divided in several subgroups according to their immunity level, which has as a consequence different infection rates. The maximum level of immunity can be achieved either by recovering from an infection, or by possible vaccination. We consider the cases that the vaccination rate is independent on the size of infected population, or that it depends also on this value by a power law. In addition, we assume that the immunity level can decay in time. The goal of this paper is to analyze the existence and uniqueness of equilibrium solutions, which can be either a trivial (disease-free) equilibrium, with no infections, or an endemic equilibrium, with a certain amount of infected individuals. Moreover, we give conditions for the local asymptotic stability of the unique trivial equilibrium solution. It will turn out that, if this is the case, then there exists no endemic equilibrium, which means that the epidemic can be eradicated, by arriving at herd immunity. On the other hand, if the trivial equilibrium is unstable, then we prove the existence of an endemic equilibrium which, under natural conditions, turns out to be unique. The stability of the endemic equilibrium remains still an open problem.

Key-Words: ordinary differential equations, epidemic model, SIR, equilibrium solutions, waning immunity, vaccination

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1 Introduction

The SIR model is a standard system of ordinary differential equations used for the modeling of epidemies, see, [1], [2], [3]. It is a *compartmental model*, since the population is divided into several compartments: S - *susceptible*, I - *infected* and R - *recovered*. The dynamics can be described by transitions between different stages. Susceptible individuals can get the disease by contact with infected ones. The corresponding rate is directly proportional to the numbers S and I, while the transition from I to R occurs at a rate proportional to the number I of infected individuals. An individual in this last stage is already immune and cannot contribute anymore to the spread of the disease. By scaling the total population to 1, the system of ordinary equations corresponding to the SIR model is the following:

$$\begin{aligned} \frac{dS}{dt} &= -\beta \cdot I \cdot S \\ \frac{dI}{dt} &= \beta \cdot I \cdot S - \alpha \cdot I \\ \frac{dR}{dt} &= \alpha \cdot I \end{aligned} \tag{1}$$

The coefficients of the linear terms, i.e. the rates of passing from one state to another, are inversely proportional to the average time spent in the corresponding state. With T_{inf} the average time spent in the infectious state, we can therefore assume that $\alpha = T_{inf}^{-1}$, while for β we can consider the form $\beta = R(t) \cdot T_{inf}^{-1}$. The term $R(t)$ denotes the time dependent *effective reproduction number*, i.e. the average number of further infections produced by the contacts with one infectious individual. At the beginning of the epidemic its value is equal to R_0, the so called *basic reproduction number*, but after that it may vary due to restrictions, social distancing, increased frequency of testing, etc. Possible variations within this simplest framework are the SIRS and the SIS models, where in the first case the recovered individuals become again susceptible after some time, whereas in the latter situation an individual moves after infection directly into the susceptible state. In [3], it is shown that for these models the local asymptotic stability of the disease-free equilibrium holds if $R_0 < 1$, which means that the disease will die out due to arriving at herd immunity. If $R_0 > 1$ the disease will become endemic, reaching an endemic equilibrium which turns out to be asymptotically stable. In [4], the global stability of

equilibrium solutions of the SIR, SIRS and SIS models is proven by constructing appropriate Lyapunov functions.

The SIR model can be also extended to a SEIR model, by introducing the intermediate state E - *exposed*, or SVEIS with the state V - *vaccinated*, see, [5], where also the local stability of equilibrium solutions is analyzed. The stability of extensions of the classic SIR model is analyzed also in [3], where it is shown that in some cases there may be an asymptotically stable endemic equilibrium even if $R_0 < 1$ and other situations in which there is an endemic equilibrium that is unstable for certain values of $R_0 > 1$.

The phenomenon of waning immunity, where the rate of loss of immunity depends on the time since recovery, is modeled by delay differential equations like in [6], by systems of integro-differential equations like in [7], [8], or by coupling ordinary and partial differential equations like in [9], [10], the latter reference considering also vaccination, which is also considered in [11].

Other papers consider also age-structured populations, like: [12], with five levels of immunity and a discrete age structure, while, [13], considers the age and the immunity level as continuous variables and the dynamics is modeled by a system of integro-differential equations.

The paper, [14], considers a model which describes two competing diseases, influenza and COVID-19 and analyzes the dynamics of the corresponding non-linear system of differential equations under vaccination strategy and immunity waning.

In this paper we will modify the above SIR model by considering, besides the infected state I, several levels of immunity. The full immunity against infection can be obtained either by passing through the disease, or by vaccination. We further assume that the level of immunity decays with time. Therefore we introduce the states $S_0, \dots S_m$, $m \geq 2$, where S_0 describes the lowest possible level of immunity, while S_m stands for the maximum level, or full immunity. The system of ordinary differential equations corresponding to this model is the following:

$$\begin{aligned}
\frac{dS_k}{dt} &= -\beta_k \cdot I \cdot S_k - \gamma_k \cdot I^p \cdot S_k - \eta_k \cdot S_k \\
&\quad +\eta_{k+1} S_{k+1},\ 0 \leq k \leq m-1 \\
\frac{dS_m}{dt} &= \alpha \cdot I + \sum_{k=0}^{m-1} \gamma_k \cdot I^p \cdot S_k - \eta_m \cdot S_m \\
\frac{dI}{dt} &= \sum_{k=0}^{m-1} \beta_k \cdot I \cdot S_k - \alpha \cdot I
\end{aligned} \tag{2}$$

The assumption is that the total population remains constantly equal to 1, since birth and death phenomena are not considered. The infection mechanism is similar to that of the SIR model, but with different transmission rates $\beta_k \geq 0$, depending on the immunity level. We consider the assumption $\beta_m = 0$, that is, at the maximum level m there exists full immunity.

This full immunity can be achieved either by passing through the disease, which means that infected individuals, which recover at rate $\alpha > 0$, change from state I to the state S_m, or by vaccination from any other level $0 \leq k \leq m-1$. The term which models this transition is considered to be of the form $\gamma_k \cdot I^p \cdot S_k$ with the vaccination rate $\gamma_k > 0$ (we assume that $\gamma_m = 0$, that is, the vaccination does not take place at the highest immunity level) and with the parameter $p \in [0, 1]$. This choice is motivated by the fact that the interest of individuals for vaccination might depend on the size of the infected population I through the factor of the form I^p. For $p = 0$ the corresponding term is considered as $\gamma_k \cdot S_k$, i.e. the vaccination rate is independent on the size of the infected population. We will consider also the situation of no vaccination at all, with $\gamma \equiv 0$.

The decay of immunity is modeled by the transition from state S_{k+1} to S_k with $0 \leq k \leq m-1$ at rate $\eta_k > 0$, while $\eta_0 = 0$ (the immunity cannot decay further at this lowest possible level).

Similarly to the SIR model we assume that $\alpha = T_{inf}^{-1}$ and $\beta_k = R_k \cdot \alpha$, with R_k being the basic reproduction number, that is, the average number of secondary infections generated from an infected individual on immunity level k. We consider the reproduction numbers corresponding to each immunity level to be constant in time.

We may consider natural monotonicity assumptions on the coefficients R_k, γ_k, which are decreasing with k (reproduction numbers and vaccination rate are lower at higher immunity levels, being =0 on the highest level), but in our mathematical model we will make use of them only if it is strictly necessary, otherwise we keep the assumptions as general as possible.

One such example is the assumption $R_k < 1$ for $k \geq 1$ (the values of $R_0 > 0$ can be arbitrary). This is no significant restriction, since we are free to choose the compartments of our model. By recalling the property of such epidemic models, which states that, if the basic reproduction number is < 1, then the disease will eventually die out, we can interpret the condition $R_k < 1$ for $k \geq 1$ in the sense that we can define the (partially) immune population groups in our model as those for which the epidemic vanishes, if the immunity would remain forever on that given level. This assumption is needed only for the uniqueness of the endemic equilibrium solution, otherwise we don't make use of it. Only for the basic reproduction number of the population without any immunity we will consider also the possibility that $R_0 > 1$.

The system (2) was introduced by the present author in [15], by using a stochastic approach based on Markov jump processes. A convergence result was proved and also numerical simulations were performed.

A related work is reported in [16], where the model is denoted as $SIR^{(k)}S$ model, corresponding to k levels of immunity. The decay of immunity follows a similar mechanism as described previously, but for the decay rates two possible specific assumptions are made: linear or exponential decay, while in [15], or in this paper, the rates are kept in a general form. In [16], there are considered two possible vaccination schemes: a general one, similar to the one considered in this paper with constant rates, but also a so called rational scheme, where only the susceptible population (with no immunity at all) and only one additional compartment with partial immunity are subjected to vaccination. The mathematical results of the mentioned paper are the following:

1. The existence of a unique trivial equilibrium is shown for $R_0 < 1$ (no other equilibrium exists in this case).
2. The model without vaccination has a unique endemic equilibrium if and only if $R_0 > 1$.
3. The model with vaccination for $m = 2$ has a unique endemic equilibrium if and only if $R^\eta > 1$, where R^η is a term which involves R_0 and the coefficients of the system of equations. It is conjectured that this result holds also for arbitrary $m > 2$.
4. The paper discusses also the connection between the ODE model and an ODE-PDE model for $m \to \infty$.

Compared to the aforementioned paper, which considered only a particular form of the immunity decay rates, the present work comes with new results from several points of view. First, we keep the vaccination and immunity decay rates as general as possible. Secondly, beyond constant vaccination rates, we consider also the scenario that the vaccination rates are proportional to some power I^p of the size of the infected population. This models the situation that if the incidence of the disease is low, the interest for vaccination is also low, and vice-versa.

Regarding the results of this paper, we show existence and uniqueness of the trivial and endemic equilibrium (for all m, not only for $m = 2$) under similar conditions as in [16], but in a more general setting and also in an additional scenario regarding the vaccination. Moreover, we analyze also the asymptotic stability properties of the disease-free (trivial) equilibrium, and show its stability for $R_0 < 1$ in the case that the vaccination rates depend on I^p and give also necessary and sufficient conditions for stability if the vaccination rates are independent on I, in the cases $m = 2$ and $m = 3$. We conjecture that this stability property holds for all k.

Concerning the endemic equilibrium, we show existence and uniqueness basically under the condition that ensures that the disease-free equilibrium in both scenarios regarding vaccination is unstable. Since we give only a general existence proof and cannot compute it by an exact formula as in the case of the trivial equilibrium, the question of stability of this endemic equilibrium is not addressed in this paper. The results are qualitatively similar to those corresponding to some extensions to the SIR model described in [3], since, in the case that the vaccination rates are independent on I, the disease-free equilibrium can be stable also if $R_0 > 1$, basically if the immunity does not decay too fast and if the vaccination rates are high enough. In the discussion section we will also point out some practical limitations of this mathematical result.

The present paper is structured as follows. In Section 2 we discuss the nonlinear system of equations corresponding to the equilibrium state, that is, the right hand sides of the ODE system (2) are set to be equal to 0. We also compute the corresponding Jacobian matrix, since the local asymptotic stability of an equilibrium solution is ensured by the negative sign of the real parts of the eigenvalues of the Jacobian matrix in this point. After describing this setup, in the next sections we present the main results of this paper. In Section 3 we discuss the existence, uniqueness and stability of the disease-free equilibrium, with no infections ($I = 0$) and in section 4 the existence and uniqueness of the endemic equilibrium. In each of these two sections we consider both scenarios regarding vaccination which are assumed in this paper. We conclude with a summary of the results given in Section 5 and with a discussion of their practical relevance which is presented in Section 6.

2 The nonlinear system of equations at equilibrium

The considered dynamics, which involve only transitions between different states, but no changes in the population size, which is assumed to be equal to 1, is reflected also by the fact that the sum of the RHS in (2) is equal to 0, which means a conservation of the total population. Since the equations whose solutions are the equilibria which we are interested in are dependent, we replace the last equation with the assumed conservation property. The nonlinear system of equations which we consider is therefore the following:

$$\begin{aligned} -\beta_k \cdot I \cdot S_k - \gamma_k \cdot I^p \cdot S_k - \eta_k \cdot S_k + & \\ +\eta_{k+1} S_{k+1} &= 0 \\ \text{for } 0 \le k \le m-1 & \\ \alpha \cdot I + \sum_{k=0}^{m-1} \gamma_k \cdot I^p \cdot S_k - \eta_m \cdot S_m &= 0 \\ \sum_{k=0}^{m} S_k + I &= 1 \end{aligned} \quad (3)$$

We will also use the relation corresponding to the RHS of the equation for I in (2):

$$-\sum_{k=0}^{m-1} \beta_k \cdot I \cdot S_k + \alpha \cdot I = 0 \quad (4)$$

Note that equation (4) can be also obtained by summing up the first $m+1$ equations in system (3).

Since the sum of the components remains constant, for the stability analysis of the equilibrium points, which are the solutions of system (3), we disregard the equation for S_m and replace $S_m = 1 - \sum_{k=0}^{m-1} S_k - I$ in the equation for S_{m-1}.

For this reduced system, considering the variables in the order $S_0, S_1, \ldots S_{m-1}, I$, the Jacobian matrix, for which the signs the real parts of its eigenvalues determine the local stability property of the equilibrium points of the system (2), is given by:

$$J = \begin{pmatrix} -\beta_0 I - \gamma_0 I^p & \eta_1 & \ldots & 0 & -\beta_0 S_0 - \gamma_0 p I^{p-1} S_0 \\ 0 & -\beta_1 I - \gamma_1 I^p - \eta_1 & \ldots & 0 & -\beta_1 S_1 - \gamma_1 p I^{p-1} S_1 \\ \vdots & \vdots & & \vdots & \vdots \\ -\eta_m & -\eta_m & \ldots & -\beta_{m-1} I - \gamma_{m-1} I^p - \eta_{m-1} - \eta_m & -\beta_{m-1} S_{m-1} - \eta_m - \gamma_{m-1} p I^{p-1} S_{m-1} \\ \beta_0 I & \beta_1 I & \ldots & \beta_{m-1} I & \sum_{k=0}^{m-1} \beta_k S_k - \alpha \end{pmatrix} \quad (5)$$

When analyzing the existence and possible uniqueness of equilibrium solutions, we will consider separately the following situations regarding the dynamics of vaccination: either the form $\gamma_k \cdot I^p \cdot S_k$ with $p \in (0,1]$ where $\gamma_k \ge 0$ (the value $\gamma_k = 0$ for all k is also possible), or of the form $\gamma_k \cdot S_k$, where at least $\gamma_0 > 0$. That is, in this case the vaccination rates are independent on the size of the infected population. We will analyze the trivial equilibrium with $I = 0$ and also endemic equilibria with $I \neq 0$.

3 Equilibrium solutions with $I = 0$

We first discuss the equilibrium solutions with no infections under different assumptions regarding the vaccination.

3.1 The case $p > 0$ or $\gamma \equiv 0$

We consider first the case that the vaccination rate depends on the size of the infected population or that we have no vaccination at all. Under these assumptions, for $I = 0$ the system (3) reduces to:

$$\begin{aligned} -\eta_k \cdot S_k + \eta_{k+1} S_{k+1} &= 0, \ 0 \le k \le m-1 \\ -\eta_m \cdot S_m &= 0 \\ \sum_{k=0}^{m} S_k &= 1 \end{aligned} \quad (6)$$

Starting from the equation for S_m we obtain succesively $S_k = 0$ for $1 \le k \le m$ (since $\eta_k \neq 0$ if $k \ge 1$). By noting that $\eta_0 = 0$ and considering the conservation property, we obtain that the only equilibrium with $I = 0$ is given by $S_0 = 1, S_k = 0$ for $k \ge 1$. Under the assumption that $p = 0$ or $\gamma \equiv 0$ we replace all terms involving γ_k in the Jacobian (5) with 0, therefore the value of J taken in the current equilibrium point will be

$$J = \begin{pmatrix} 0 & \eta_1 & 0 & \ldots & 0 & -\beta_0 \\ 0 & -\eta_1 & \eta_2 & \ldots & 0 & 0 \\ \vdots & & & & & \\ -\eta_m & -\eta_m & -\eta_m & \ldots & -\eta_m - \eta_{m-1} & -\eta_m \\ 0 & 0 & 0 & \ldots & 0 & \beta_0 - \alpha \end{pmatrix} \quad (7)$$

Theorem 3.1. *Assume $p > 0$ or $\gamma \equiv 0$.*

If $R_0 < 1$, the unique solution $S_0 = 1, S_1 = \ldots = S_m = I = 0$ of (3) is an asymptotically stable equilibrium point of (2).

If $R_0 > 1$, this trivial equilibrium point is unstable.

Proof. From (7) can be easily seen (by expansion w.r.t the last row) that one eigenvalue of J is $\lambda_0 = \beta_0 - \alpha = \alpha(R_0 - 1)$ whose sign depends on the assumption on R_0. The other eigenvalues are the solutions of $p(\lambda) = 0$ with

$$p(\lambda) = \begin{vmatrix} -\lambda & \eta_1 & 0 & \ldots & 0 \\ 0 & -\eta_1 - \lambda & \eta_2 & \ldots & 0 \\ 0 & 0 & -\eta_2 - \lambda & \ldots & 0 \\ \vdots & & & & \vdots \\ 0 & 0 & 0 & \ldots & \eta_{m-1} \\ -\eta_m & -\eta_m & -\eta_m & \ldots & -\eta_m - \eta_{m-1} - \lambda \end{vmatrix}$$

Substracting the first column from all the others we

obtain

$$p(\lambda) = \begin{vmatrix} -\lambda & \eta_1+\lambda & \lambda & \dots & \lambda \\ 0 & -\eta_1-\lambda & \eta_2 & \dots & 0 \\ 0 & 0 & -\eta_2-\lambda & \dots & 0 \\ \vdots & \vdots & \vdots & & \vdots \\ 0 & 0 & 0 & \dots & \eta_{m-1} \\ -\eta_m & 0 & 0 & \dots & -\eta_{m-1}- \\ & & & & -\lambda \end{vmatrix}$$

We add next all other rows to row 1 and therefore we have

$$p(\lambda) = \begin{vmatrix} -\eta_m-\lambda & 0 & 0 & \dots & 0 \\ 0 & -\eta_1-\lambda & \eta_2 & \dots & 0 \\ 0 & 0 & -\eta_2-\lambda & \dots & 0 \\ \vdots & \vdots & \vdots & & \vdots \\ 0 & 0 & 0 & \dots & \eta_{m-1} \\ -\eta_m & 0 & 0 & \dots & -\eta_{m-1}- \\ & & & & -\lambda \end{vmatrix}$$

Expanding the determinant with respect to the first row and noting that the minor which arises has a triangular form, we conclude that the other eigenvalues of J are $\lambda_k = -\eta_k < 0,\ k = 1, \dots m$.

If $R_0 < 1$, then all eigenvalues of the Jacobian at the equilibrium point are negative and we conclude that this equilibrium is asymptotically stable (locally). If $R_0 > 1$ then there exists a positive eigenvalue and therefore the trivial equilibrium is unstable. □

This result corresponds to the intuitive trivial expectation that, if $R_0 < 1$, that is, the reproduction number is less than 1 even for the lowest level of immunity, the disease will vanish and the components will approach the equilibrium state where all individuals are on the lowest immunity level. Moreover, since the vaccination terms have either the form $\gamma_k \cdot I^p \cdot S_k$ with $p \in (0, 1]$ or $\gamma \equiv 0$ (no vaccination), we conclude also that near this equilibrium the vaccination becomes irrelevant to its stability, which is always given. For $R_0 > 1$ however, we will see that the system has also at least one nontrivial (endemic) equilibrium with $I \neq 0$ which, under further additional conditions, is unique.

3.2 The case $p = 0$ (vaccination independent on I)

In this case, for $I = 0$ the system (3) reduces to:

$$\begin{aligned} -(\gamma_k+\eta_k)\cdot S_k + \eta_{k+1}S_{k+1} &= 0,\ 0 \le k \le m-1 \\ \sum_{k=0}^{m-1} \gamma_k \cdot S_k - \eta_m \cdot S_m &= 0 \\ \sum_{k=0}^{m} S_k &= 1 \end{aligned} \tag{8}$$

There are $m+2$ equations for the $m+1$ unknowns $S_0, \dots S_m$, but we note that summing up the first $m+1$ equations we obtain 0, so in fact we can consider only the equations for $0 \le k \le m-1$ and the conservation property defined by the last equation.

Since all coefficients which appear are > 0, we can express S_{k+1} in terms of S_k, that is, successively $S_1, S_2, \dots S_m$ in terms of S_0 in the form $S_k = \theta_k \cdot S_0$.

Taking into account that $\sum_{k=0}^{m} S_k = 1$, we obtain that the system (8) has a unique solution with all $S_k > 0$.

The interpretation is that, by vaccination at the given constant rates depending only on the immunity level, combined with immunity decay, the system has a trivial equilibrium. In this equilibrium point with no infections ($I = 0$) the Jacobian has the value

$$J = \begin{pmatrix} -\gamma_0 & \eta_1 & \dots & 0 \\ 0 & -\gamma_1-\eta_1 & \dots & 0 \\ \vdots & \vdots & & \vdots \\ -\eta_m & -\eta_m & \dots & -\gamma_{m-1}-\eta_{m-1}- \\ & & & -\eta_m \\ 0 & 0 & \dots & 0 \\ -\beta_0 S_0 & & & \\ -\beta_1 S_1 & & & \\ \vdots & & & \\ -\beta_{m-1}S_{m-1}-\eta_m & & & \\ \sum_{k=0}^{m-1}\beta_k S_k - \alpha & & & \end{pmatrix} \tag{9}$$

For a stability result we need a negative sign of the real parts of the eigenvalues of this matrix. Due to the structure of the last row we have that one eigenvalue is $\lambda_0 = \sum_{k=0}^{m-1}\beta_k S_k - \alpha = \alpha(\sum_{k=0}^{m-1} R_k S_k - 1)$. For the stability of the equilibrium given by the solution of (8) together with $I = 0$, it is therefore necessary that $\lambda_0 < 0$.

Remark 3.1. *The necessary condition $\sum_{k=0}^{m-1} R_k S_k < 1$ for the stability of the trivial equilibrium solution with $I = 0$ in the case $p = 0$ (vaccination rate independent on I) and $\gamma_0 > 0$ is equivalent to the inequality $\Psi(\bar{R}, \bar{\gamma}, \bar{\eta}) < 0$, where*

$$\begin{aligned} \Psi(\bar{R}, \bar{\gamma}, \bar{\eta}) &= (R_0-1)\gamma_0^{-1} + (R_1-1)\eta_1^{-1} + \\ &+ \sum_{k=2}^{m-1}(R_k-1)\eta_k^{-1}\prod_{j=1}^{k-1}\eta_j^{-1}(\gamma_j+\eta_j) - \\ &-\eta_m^{-1}\prod_{j=1}^{m-1}\eta_j^{-1}(\gamma_j+\eta_j). \end{aligned} \tag{10}$$

This inequality holds always if $R_k < 1$ for all k, but it can be also fulfilled even if this is not the case, if in addition the vaccination rates γ_k and the immunity decay rates η_k are chosen properly.

Proof. From the system (8) we use the relations $S_{k+1} = \eta_{k+1}^{-1}(\gamma_k + \eta_k) \cdot S_k,\ k = 0, \ldots, m-1$. Since $\eta_0 = 0$, we obtain therefore $S_1 = \eta_1^{-1}\gamma_0 \cdot S_0$ and $S_k = \eta_k^{-1} \prod_{j=1}^{k-1} \eta_j^{-1}(\gamma_j + \eta_j) \cdot \gamma_0 \cdot S_0,\ k = 2, \ldots, m.$

The conservation property $\sum_{k=0}^{m} S_k = 1$ is thus equivalent to:

$$S_0 + \eta_1^{-1}\gamma_0 \cdot S_0 + \sum_{k=2}^{m} \eta_k^{-1} \prod_{j=1}^{k-1} \eta_j^{-1}(\gamma_j + \eta_j) \cdot \gamma_0 \cdot S_0 = 1$$

and from this we obtain:

$$S_0^{-1} = 1 + \eta_1^{-1}\gamma_0 + \sum_{k=2}^{m} \eta_k^{-1} \prod_{j=1}^{k-1} \eta_j^{-1}(\gamma_j + \eta_j) \cdot \gamma_0. \tag{11}$$

The condition $\sum_{k=0}^{m-1} R_k S_k < 1$ is therefore equivalent to $R_0 S_0 + R_1 \eta_1^{-1}\gamma_0 \cdot S_0 + \sum_{k=2}^{m-1} R_k \eta_k^{-1} \prod_{j=1}^{k-1} \eta_j^{-1}(\gamma_j + \eta_j) \cdot \gamma_0 \cdot S_0 < 1$. By multiplying with S_0^{-1} using (11), bringing all the terms on the LHS and dividing subsequently with γ_0, we obtain that a necessary condition for stability is given by

$$\begin{aligned} &(R_0 - 1)\gamma_0^{-1} + (R_1 - 1)\eta_1^{-1} + \\ &+ \sum_{k=2}^{m-1} (R_k - 1)\eta_k^{-1} \prod_{j=1}^{k-1} \eta_j^{-1}(\gamma_j + \eta_j) - \\ &- \eta_m^{-1} \prod_{j=1}^{m-1} \eta_j^{-1}(\gamma_j + \eta_j) < 0. \end{aligned}$$

It is clear that this inequality is fulfilled if one of the following conditions holds:

- $R_k < 1$ for all $k = 0, \ldots, m-1$.
- $R_0 \geq 1, R_k < 1,\ k = 1, \ldots, m-1$ (the partially immune individuals do not contribute to an exponential spread of the epidemic, which happens mainly due to the non-immune population). In this case the necessary condition for stability is fulfilled if $R_0 - 1 < \gamma_0 \cdot \eta_m^{-1} \prod_{j=1}^{m-1} (\eta_j^{-1}\gamma_j + 1)$. This global inequality involving all vaccination and immunity decay rates holds for example if the vaccination rates γ_j are sufficiently high, or if the immunity decay rates η_j are sufficiently small, a property which confirms also our intuition.
- $R_k \geq 1$ for $k = 0, \ldots, m-1$, (or basically no restriction on R_k's at all) if in addition the immunity decay rate η_m from the highest immunity level (full immunity) is sufficiently small. A larger threshold for this parameter can be considered for example if the vaccination rate γ_0 of individuals with no immunity is sufficiently large.

□

Expanding $det(J - \lambda I)$ with respect to the last row for J as in (9), one can see that the other eigenvalues than $\lambda_0 = \alpha(\sum_{k=0}^{m-1} R_k S_k - 1)$ depend only on $\gamma_i, \eta_i > 0$. We will show that for $m = 2$ and $m = 3$ these eigenvalues always have negative real parts.

Lemma 3.1. *If $m = 2$ or $m = 3$ the eigenvalues of the matrix*

$$J_1 = \begin{pmatrix} -\gamma_0 & \eta_1 & \ldots & 0 \\ 0 & -\gamma_1 - \eta_1 & \ldots & 0 \\ \vdots & \vdots & & \vdots \\ -\eta_m & -\eta_m & \ldots & -\gamma_{m-1} - \eta_{m-1} - \\ & & & -\eta_m \end{pmatrix}$$

have negative real parts, provided $\gamma_i, \eta_i > 0$.

Proof. For the moment we will keep $m \geq 2$ arbitrary. The characteristic polynomial of degree m is given by:

$$p_m(\lambda) = \begin{vmatrix} -\gamma_0 - \lambda & \eta_1 & \ldots & 0 \\ 0 & -\gamma_1 - \eta_1 - \lambda & \ldots & 0 \\ \vdots & \vdots & & \vdots \\ 0 & 0 & \ldots & \eta_{m-1} \\ -\eta_m & -\eta_m & \ldots & -\gamma_{m-1} - \eta_{m-1} - \\ & & & -\eta_m - \lambda \end{vmatrix}$$

Expanding with respect to the first row we obtain:

$$p_m(\lambda) = (-\gamma_0 - \lambda) \cdot p_{m-1}(\lambda) -$$

$$-\eta_1 \begin{vmatrix} 0 & \eta_2 & 0 & \ldots & 0 \\ 0 & -\gamma_2 - \eta_2 - \lambda & \eta_3 & \ldots & 0 \\ \vdots & & & & \vdots \\ 0 & 0 & 0 & \ldots & \eta_{m-1} \\ -\eta_m & -\eta_m & \ldots & & -\gamma_{m-1} - \eta_{m-1} \\ & & & & -\eta_m - \lambda \end{vmatrix}$$

where $p_{m-1}(\lambda)$ is the characteristic polynomial of a $(m-1) \times (m-1)$- submatrix and has the same structure as $p_m(\lambda)$.

The second determinant can be expanded with respect to the first column. By noting that eliminating

the first column and the last row we obtain the determinant of a lower triangular matrix with $\eta_2, \dots \eta_{m-1}$ on the diagonal, we therefore have:

$$\begin{aligned} p_m(\lambda) &= (-\gamma_0 - \lambda) \cdot p_{m-1}(\lambda) + (-1)^m \prod_{i=1}^{m} \eta_i \\ &= (-1)^m \cdot (\tilde{p}_m(\lambda) + \prod_{i=1}^{m} \eta_i) \end{aligned}$$

where the polynomial $\tilde{p}_m(\lambda)$ has positive coefficients and roots with negative real parts.

The stability property of this general polynomial is still an open problem, but we will show next that for $m = 2$ and $m = 3$ this polynomial has roots with negative real parts.

For $m = 2$ we have

$$\begin{aligned} p_2(\lambda) &= \begin{vmatrix} -\gamma_0 - \lambda & \eta_1 \\ -\eta_2 & -\gamma_1 - \eta_1 - \eta_2 - \lambda \end{vmatrix} \\ &= \lambda^2 + (\gamma_0 + \gamma_1 + \eta_1 + \eta_2)\lambda + \eta_1\eta_2 \\ &\quad +\gamma_0(\gamma_1 + \eta_1 + \eta_2) \end{aligned}$$

Since all involved γ_i, η_j are > 0, the quadratic equation $p_2(\lambda) = 0$ has the form $\lambda^2 + a_1\lambda + a_0 = 0$ with $a_0, a_1 > 0$. This means that the sum of the roots $-a_1$ is negative, while the product a_0 is positive. If both roots are real (even if equal), they must be necessarily negative. In the case of complex conjugate roots of the form $x \pm iy$, their sum is equal with $2x = -a_1 < 0$ which means that both eigenvalues $\lambda_{1,2}$ have negative real part.

For $m = 3$ we have

$$\begin{aligned} p_3(\lambda) &= \begin{vmatrix} -\gamma_0 - \lambda & \eta_1 & 0 \\ 0 & -\gamma_1 - \eta_1 - \lambda & \eta_2 \\ -\eta_3 & -\eta_3 & -\gamma_2 - \eta_2 \\ & & -\eta_3 - \lambda \end{vmatrix} \\ &= -[\lambda^3 + (\gamma_0 + \gamma_1 + \eta_1 + \gamma 2 + \eta_2 + \eta_3)\lambda^2 \\ &\quad +[\gamma_0(\gamma_1 + \eta_1) + \gamma_0(\gamma_2 + \eta_2 + \eta_3) + \\ &\quad +(\gamma_1 + \eta_1)(\gamma_2 + \eta_2 + \eta_3) + \gamma_0\eta_2\eta_3]\lambda \\ &\quad +\gamma_0(\gamma 1 + \eta_1)(\gamma_2 + \eta_2 + \eta_3) + \eta_1\eta_2\eta_3] \end{aligned}$$

For the polynomial with positive coefficients $-p_3(\lambda) = \lambda^3 + a_2\lambda^2 + a_1\lambda + a_0$ we will use the Routh-Hurwitz criterion in order to show that its roots have negative real parts. According to Routh-Hurwitz, this property is equivalent to the fact that all principal minors of the following Hurwitz matrix are > 0:

$$H = \begin{pmatrix} a_2 & a_0 & 0 \\ 1 & a_1 & 0 \\ 0 & a_2 & a_0 \end{pmatrix}$$

This means that

$$a_2 > 0, \begin{vmatrix} a_2 & a_0 \\ 1 & a_1 \end{vmatrix} > 0,$$

$$\det H = a_0 \cdot \begin{vmatrix} a_2 & a_0 \\ 1 & a_1 \end{vmatrix} > 0.$$

Since all coefficients are positive, it is therefore sufficient to show that the principal minor of second order is positive, i.e. $a_1a_2 - a_0 > 0$. By computing this term from the above polynomial, it will turn out that all negative terms from $-a_0$ cancel with corresponding terms in a_1a_2 and that the remaining difference is positive. This proves the statement of the lemma. □

By summarizing the previous results we obtain the stability property in this case.

Theorem 3.2. *Let $p = 0$, $\beta_i, \gamma_i, \eta_i > 0$ and S_k the solution of (8) for $m = 2$ or $m = 3$. If the condition $\sum_{k=0}^{m-1} R_k S_k < 1$ holds, then these S_k together with $I = 0$ are an asymptotically stable equilibrium point of (2).*

4 Existence of an endemic equilibrium with $I \neq 0$

We will analyze now the equilibrium solutions of (2) with $I \neq 0$. The main result is the following:

Theorem 4.1. *Let $\alpha, \beta_k, \eta_k > 0$, $\gamma_k \geq 0$ for all k, except $\beta_m = \eta_0 = 0$.*

(i) If $p \in (0, 1]$ (vaccination dependent on I) or $\gamma_0 = 0$ (no vaccination for individuals on the lowest immunity level) and $\beta_0 > \alpha \Leftrightarrow R_0 > 1$, or

(ii) If $p = 0$ (vaccination independent on I), $\gamma_0 > 0$ and $\Psi(\bar{R}, \bar{\gamma}, \bar{\eta}) > 0$ with Ψ defined in (10),

then the system (3) has at least a solution $S_0, S_1, \dots, S_m, I$ with all components in $(0, 1)$ which corresponds to a nontrivial endemic equilibrium.

If in addition $R_k < 1$ for $k \geq 1$, then this solution is unique.

Proof. The basic outline of the proof can be described as follows. In order to compute the solution of the nonlinear system (3), we show first that we can express all S_k in terms of I. Inserting these terms into the conservation property, it will turn out that the existence of a solution is equivalent to the existence of a solution $I \in (0, 1)$ of this nonlinear equation. This can be ensured if there is a sign change of the values of this function between 0 and 1. In the case that this function can be proven to be monotone, then the solution, if it exists, turns out to be unique. Moreover, in the case of monotonicity without sign change, we will conclude that there exists no solution of the equation for I, which means that there exists no endemic equilibrium of the system of differential equations.

From the equations for $0 \leq k \leq m-1$ in (3) we obtain successively

$$S_{k+1} = \eta_{k+1}^{-1}(\beta_k I + \gamma_k I^p + \eta_k)S_k$$

and therefore $S_k = P_k(I) \cdot S_0$, where $P_k(I)$ is a generalized polynomial of degree k in I, that is, a finite linear combination of powers of I, the maximal exponent being equal to k (since $p \in [0,1]$). Moreover, all coefficients of P_k are positive and starting with $P_0(I) = 1$ and $P_1(I) = \eta_1^{-1}(\beta_0 I + \gamma_0 I^p)$ (since $\eta_0 = 0$) for $0 \leq k \leq m-1$ we have the recursion formula

$$P_{k+1}(I) = \eta_{k+1}^{-1}(\beta_k I + \gamma_k I^p + \eta_k) \cdot P_k(I) \quad (12)$$

Dividing (4) by $I \neq 0$ we obtain $\sum_{k=0}^{m-1} \beta_k S_k = \alpha \Leftrightarrow \sum_{k=0}^{m-1} \beta_k P_k(I) \cdot S_0 = \alpha \Leftrightarrow S_0 = \alpha / Q_{m-1}(I)$, where $Q_{m-1}(I) = \sum_{k=0}^{m-1} \beta_k P_k(I)$ is a generalized polynomial of degree $m-1$ in I.

Inserting the S_k's computed above into the conservation property $\sum_{k=0}^{m} S_k + I = 1$ we obtain

$$\sum_{k=0}^{m} \frac{\alpha}{Q_{m-1}(I)} \cdot P_k(I) + I = 1 \Leftrightarrow$$
$$\alpha \sum_{k=0}^{m} P_k(I) + I \cdot Q_{m-1}(I) - Q_{m-1}(I) = 0 \Leftrightarrow$$
$$\alpha \sum_{k=0}^{m} P_k(I) + (I-1) \sum_{k=0}^{m-1} \beta_k P_k(I) = 0 \Leftrightarrow$$
$$R_m(I) = 0$$

where $R_m(I)$ defined as above is a generalized polynomial of degree m in I.

We have that $R_m(1) = \alpha \sum_{k=0}^{m} P_k(1) > 0$ since all coefficients of P_k are > 0.

We further have $R_m(0) = \sum_{k=0}^{m-1}(\alpha - \beta_k)P_k(0) + \alpha P_m(0) = \alpha(\sum_{k=0}^{m-1}(1-R_k)P_k(0) + P_m(0))$.

Assuming first that $p \in (0,1]$ or $\gamma_0 = 0$, we have that $P_1(0) = 0$ and therefore $P_k(0) = 0$ for all $1 \leq k \leq m$. We thus have $R_m(0) = \alpha(1 - R_0) < 0$ if $R_0 > 1$.

Due to the sign change of R_m between 0 and 1, we conclude that there exists at least a nontrivial solution I of the equation $R_m(I) = 0$.

If $p = 0$ then we have to consider system (8) and for computing $R_m(0)$ we need to compute the terms $P_k(0)$ which, by adapting (12) for the case $p = 0$ can be computed by $P_{k+1}(0) = \eta_{k+1}^{-1}(\gamma_k + \eta_k)P_k(0)$. Since $P_0 \equiv 1$, this is exactly the recursion for the S_k from Remark 3.1. We therefore have $P_1(0) = \eta_1^{-1}\gamma_0$ and $P_k(0) = \eta_k^{-1}\prod_{j=1}^{k-1}\eta_j^{-1}(\gamma_j + \eta_j) \cdot \gamma_0$ for $k = 2, \ldots, m$. Using the form

$$R_m(0) = \alpha(\sum_{k=0}^{m-1}(1-R_k)P_k(0) + P_m(0))$$

we thus have

$$\alpha^{-1}R_m(0) = 1 - R_0 + (1-R_1)\eta_1^{-1}\gamma_0 +$$
$$+ \sum_{k=2}^{m-1}(1-R_k)\eta_k^{-1}\prod_{j=1}^{k-1}\eta_j^{-1}(\gamma_j + \eta_j) \cdot \gamma_0 +$$
$$+\eta_m^{-1}\prod_{j=1}^{m-1}\eta_j^{-1}(\gamma_j + \eta_j) \cdot \gamma_0$$

The condition $R_m(0) < 0$ is therefore equivalent to $\Psi(\bar{R}, \bar{\gamma}, \bar{\eta}) > 0$ with Ψ defined in (10). In this case, due to the sign change of R_m, we have at least a nonzero solution of the equation $R_m(I) = 0$.

Once the existence of a solution I of the equation $R_m(I) = 0$ is established, the corresponding values S_k can be computed as follows: $\sum_{k=0}^{m} S_k + I = 1 \Leftrightarrow \sum_{k=0}^{m} P_k(I)S_0 + I = 1$ and from this we obtain $S_0 = (1-I)/\sum_{k=0}^{m} P_k(I)$. The other values can be computed then recursively by $S_{k+1} = \eta_{k+1}^{-1}(\beta_k I + \gamma_k I^p + \eta_k)S_k$.

We will analyze next sufficient conditions for the monotonicity of R_m, which implies the uniqueness of this solution.

Indeed, deriving the function

$$R_m(I) = \alpha \sum_{k=0}^{m} P_k(I) + (I-1) \sum_{k=0}^{m-1} \beta_k P_k(I) \quad (13)$$

and taking into account that $P_0(I) \equiv 1$ and thus $P_0'(I) = 0$, we obtain

$$\begin{aligned} R_m'(I) &= \alpha \sum_{k=0}^{m} P_k'(I) + \sum_{k=0}^{m-1} \beta_k P_k(I) + \\ &\quad + (I-1) \sum_{k=0}^{m-1} \beta_k P_k'(I) \\ &= \alpha P_m'(I) + \sum_{k=0}^{m-1} \beta_k P_k(I) + \\ &\quad + \sum_{k=1}^{m-1} (\alpha + (I-1)\beta_k) P_k'(I) \\ &= \alpha \left(P_m'(I) + \sum_{k=0}^{m-1} R_k P_k(I) + \right. \\ &\quad \left. + \sum_{k=1}^{m-1} (1 - R_k + IR_k) P_k'(I) \right) \end{aligned}$$

Since $P_k(I), P_k'(I) > 0$ for $I > 0$, we note that $R_k < 1$ for $k = 1, \ldots, m-1$ is a sufficient condition for $R_m'(I) > 0$, i.e. for the uniqueness of the endemic equilibrium. □

Note that, if $R_m(0) > 0$ and $R_m(I)$ is increasing (for example if $R_k < 1$ for $k \geq 1$), then there exists no endemic equilibrium, but only the trivial one. In the case $p > 0$ or $\gamma \equiv 0$ we have $R_m(0) > 0$ if $R_0 < 1$, while if $p = 0, \gamma_0 > 0$ this is equivalent to the inequality $\Psi(\bar{R}, \bar{\gamma}, \bar{\eta}) < 0$ with Ψ defined in (10). In both cases we can thus say that, if the local stability condition for the trivial equilibrium with $I = 0$ is fulfilled, then this is the unique equilibrium state.

5 Summary of the results

Consider the system (2) of ordinary differential equations modeling the spread of an epidemic into a population subjected to possible vaccination, with several levels of immunity which can decay in time. The basic reproduction numbers on these levels are given by $R_k = \alpha\beta_k$ and the vaccination rates are either of the form $\gamma_k I^p$ with $p \in (0, 1]$ or constant γ_k, i.e. independent on the size of the infected population. The results of this paper regarding existence, uniqueness and stability of the equilibrium solutions can be summarized as follows.

5.1 The case $p > 0$ or $\gamma \equiv 0$ (vaccination dependent on I or no vaccination)

In this case we have a unique trivial equilibrium solution with $I = 0$, with $S_0 = 1, S_1 = \ldots, S_m = 0$. If $R_0 < 1$, this is the only equilibrium solution at all and it is locally asymptotically stable. Note however that this situation has no practical relevance, since the reproduction numbers R_k should logically decay with increasing level of immunity k, therefore an epidemic with such values of the spreading paremeters would vanish by its natural dynamics, even without vaccination.

The relevant situation is therefore when we have $R_0 > 1$. In this case there exists at least one nontrivial solution corresponding to an endemic equilibrium with $I \in (0, 1)$. If additionally $R_k < 1$ for $k \geq 1$, then this nontrivial equilibrium solution is unique. This assumption on the basic reproduction numbers for higher levels of immunity is a natural one, since we can define our compartments in a convenient way and can therefore consider that on any immunity level larger than 0 the basic reproduction number corresponds to a value for which the epidemic will eventually die out.

Since we cannot compute explicitly the endemic equilibrium solution, its stability under the conditions considered in this paper can be only conjectured.

5.2 The case $p = 0$ (vaccination independent on I)

In this case, which assumes implicitely that at least $\gamma_0 > 0$, there exists a unique trivial equilibrium solution with $I = 0$ and $S_k > 0$ for all k. A necessary (and at least for $m = 2, 3$ also sufficient) condition for the local asymptotic stability of this solution is $\sum_{k=0}^{m-1} R_k S_k < 1$ or, equivalently, $\Psi(\bar{R}, \bar{\gamma}, \bar{\eta}) < 0$, with

$$\Psi(\bar{R}, \bar{\gamma}, \bar{\eta}) = (R_0 - 1)\gamma_0^{-1} + (R_1 - 1)\eta_1^{-1} + \\ + \sum_{k=2}^{m-1} (R_k - 1)\eta_k^{-1} \prod_{j=1}^{k-1} \eta_j^{-1}(\gamma_j + \eta_j) - \\ -\eta_m^{-1} \prod_{j=1}^{m-1} \eta_j^{-1}(\gamma_j + \eta_j). \quad (14)$$

In this case, if in addition the property $R_k < 1$ for $k \geq 1$ holds, by the proof of Theorem 4.1 and the afterward remark, we conclude that there exists no endemic equilibrium with $I > 0$.

By neglecting the negative terms with factors $R_k - 1 < 0$ for $k \geq 1$, we have that a sufficient condition such that the only equilibrium solution is the trivial one with $I = 0$ is given by $R_0 - 1 < \gamma_0 \cdot \eta_m^{-1} \prod_{j=1}^{m-1} (\eta_j^{-1}\gamma_j + 1)$, together with $R_k < 1$ for $k \geq 1$.

Note that the RHS of the former inequality is monotone increasing in the vaccination rates γ_j and monotone decreasing in the immunity decay rates η_j. Assuming the natural condition $R_0 > 1$, we obtain that the unique equilibrium is the trivial one (which implies the vanishing of the epidemic) if the vaccination rates are sufficiently high and/or the immunity decay rates are sufficiently low.

If, however, $\Psi(\bar{R}, \bar{\gamma}, \bar{\eta}) > 0$, then we have at least one nontrivial (endemic) equilibrium with $I > 0$. The uniqeness of this equilibrium is implied by the condition $R_k < 1$ for $k \geq 1$. The stability of such nontrivial equilibria is still an open problem.

6 Discussion

In this final section we discuss the possible practical relevance of the mathematical results of this paper. In any epidemic model one is basically interested if the epidemic can be eradicated, that is, if herd immunity can be achieved by a suitable vaccination strategy, or if its dynamics will allways stabilize in an endemic state. The practical relevant case is $R_0 > 1$, since otherwise the disease will vanish by itself. We also consider the assumption $R_k < 1$ for $k \geq 1$, which was already explained in this paper.

Consider first the case that the vaccination rates depend also on I^p. In this situation the interest for vaccination is high only if the number of infections is high and vice-versa. The case that we have no vaccination can be also considered within the same framework. In this situation the disease-free equilibrium

turns out to be unstable and there exists a unique endemic equilibrium. This means that herd immunity cannot be achieved under these assumptions on the vaccination strategy.

However, in the case that the vaccination rates are constant, independent on I, the picture turns out to be different. We give a necessaray condition for stability of the disease-free equilibrium which can be fulfilled also if $R_0 > 1$, if the vaccination rates are sufficiently high and the immunity decay rates sufficiently low. We proved that this condition is also sufficient in the cases $m = 2$ and $m = 3$, which correspond to the classes 'no immunity', 'partial immunity', 'full immunity' and 'no immunity', 'low immunity', 'high immunity', 'full immunity', respectively. Moreover, if the necessary condition for this trivial equilibrium is fulfilled, then in turns out that that there exists no endemic equilibrium. That is, if stability is given, which in our paper is shown for $m \leq 3$, then one can arrive at herd immunity and therefore the disease can be eradicated.

Nevertheless, this theoretical result has some practical limitations. The immunity decay rates are basically given, so they can not be changed, while the vaccination rates cannot be increased arbitrarily, due to medical and logistic reasons. So, depending on the particular parameters of the model which correspond to a given disease and on the values of the vaccination rates that can be assumed as realistic, in practice both outcomes are possible: either herd immunity is achieved, according to the theoretical result, or one arrives at an endemic equilibrium. This outcome appears if the necessary condition for stability of the disease-free equilibrium is not fulfilled, due to fast decay of immunity and low vaccination rates, the last fact being possible due to several reasons, also of practical nature.

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