

Vaccination in a two-group epidemic model

Sebastian Aniţa, Malay Banerjee, Samiran Ghosh, Vitaly Volpert

▶ To cite this version:

Sebastian Aniţa, Malay Banerjee, Samiran Ghosh, Vitaly Volpert. Vaccination in a two-group epidemic model. Applied Mathematics Letters, 2021, 119, pp.1-7. 10.1016/j.aml.2021.107197 . hal-03379104

HAL Id: hal-03379104 https://hal.science/hal-03379104

Submitted on 15 Oct 2021

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers. L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Vaccination in a two-group epidemic model

Sebastian Anița^a, Malay Banerjee^b, Samiran Ghosh^b, Vitaly Volpert^{c,d,e,*}

 ^a Faculty of Mathematics, "Alexandru Ioan Cuza" University of Iasi, and "Octav Mayer" Institute of Mathematics of the Romanian Academy, Iasi 700506, Romania
 ^b Indian Institute of Technology Kanpur, kanpur - 208016, India
 ^c Institut Camille Jordan, UMR 5208 CNRS, University Lyon 1, 69622 Villeurbanne, France
 ^d INRIA Team Dracula, INRIA Lyon La Doua, 69603 Villeurbanne, France
 ^e Peoples Friendship University of Russia (RUDN University), 6 Miklukho-Maklaya St, Moscow, 117198, Russia

Abstract

Epidemic progression depends on the structure of the population. We study a two-group epidemic model with the difference between the groups determined by the rate of disease transmission. The basic reproduction number, the maximal and the total number of infected individuals are characterized by the proportion between the groups. We consider different vaccination strategies and determine the outcome of the vaccination campaign depending on the distribution of vaccinated individuals between the groups.

Keywords: Two-group epidemic model, vaccination, number of infected, optimization 2010 MSC: 92C60, 92D30

1. Introduction

Epidemic progression in a heterogeneous population depends on the proportion of different groups characterized by the rate of disease transmission [3, 4, 7, 8]. In this work we study the efficacy of vaccination campaign for different vaccination strategies. We consider the epidemic progression in a two-group population consisting of susceptible (S_1, S_2) and infected (I_1, I_2) compartments and described by the following model:

$$\frac{dS_{j}}{dt} = -\left(\beta_{j1}I_{1} + \beta_{j2}I_{2}\right)\frac{(S_{j} - V_{j})}{N},\tag{1.1}$$

$$\frac{dI_j}{dt} = \left(\beta_{j1}I_1 + \beta_{j2}I_2\right)\frac{(S_j - V_j)}{N} - \sigma_j I_j, \quad j = 1, 2,$$
(1.2)

where β_{ij} are the rates of disease transmissions, σ_j (j = 1, 2) are the clearance rates of infected individuals, and N is the total population. Here V_1 and V_2 denote the number of vaccinated in the first and second group, respectively. Let us note that the number of individuals in each class, which can be infected, is $S_j - V_j$, j = 1, 2. We suppose that vaccination is fully efficient in the

Preprint submitted to Applied Mathematics Letters

March 7, 2021

^{*}Corresponding author

Email address: volpert@math.univ-lyon1.fr (Vitaly Volpert)

sense that vaccinated individuals cannot become infected. Similar models without vaccination are considered in [5, 9].

In the next section we present analytical calculations of the basic reproduction number, the size of the epidemic, and study the effect of vaccination to arrest the disease progression. The last section is devoted to the discussion of different vaccination strategies.

2. Epidemic indicators

In this section we determine the basic reproduction number in the heterogeneous population, the total and the maximal number of infected individuals depending on the number of vaccinated individuals.

2.1. Basic reproduction number

At the beginning of epidemic, let us assume that S_{10} and S_{20} denote the number of susceptible individuals in the two groups such that $S_{10} + S_{20} = N$, and we define $\frac{S_{10}}{N} = k$ and $\frac{S_{20}}{N} = 1 - k$, where $0 \le k \le 1$. The Jacobian matrix of the system (1.1) - (1.2) evaluated at the disease free equilibrium point is

$$J_1 = \begin{bmatrix} \theta_{2\times 2} & A \\ \theta_{2\times 2} & B \end{bmatrix}, \text{ with } A = \begin{bmatrix} -\beta_{11}a & -\beta_{12}a \\ -\beta_{21}b & -\beta_{22}b \end{bmatrix}, B = \begin{bmatrix} \beta_{11}a - \sigma_1 & \beta_{12}a \\ \beta_{21}b & \beta_{22}b - \sigma_2 \end{bmatrix}$$

with $a = k - \frac{V_1}{N}$ and $b = (1 - k) - \frac{V_2}{N}$. Clearly, two eigenvalues equal to zero, while the largest eigenvalue is given by

$$2\lambda = a\beta_{11} + b\beta_{22} - 2\sigma + \sqrt{(a+b)(a\beta_{11}^2 + b\beta_{22}^2)},$$

where we have assumed $\sigma_1 = \sigma_2 = \sigma$, $\beta_{12} = \beta_{21} = (\beta_{11} + \beta_{22})/2$ for simplicity of presentation. Since the basic reproduction number R_0 can be determined equating the largest eigenvalue to zero [6], we get:

$$\mathcal{R}_0 = \left(a\beta_{11} + b\beta_{22} + \sqrt{(a+b)\left(a\beta_{11}^2 + b\beta_{22}^2\right)}\right)/2\sigma.$$

2.2. Conditions of epidemic growth

Epidemic growth occurs for $\mathcal{R}_0 > 1$. Depending on the number of vaccinated individuals in the two classes, we can determine the regions in the (V_1, V_2) -parameter plane, where the epidemic progresses. Since the number of vaccinated in each group cannot be greater than the initial number of susceptible, then $V_1 \leq kN$ and $V_2 \leq (1 - k)N$. The boundary between the regions of epidemic growth and the region epidemic extinction can be obtained from the relation $\mathcal{R}_0 = 1$:

$$\Delta(V_1, V_2) \equiv ab(\beta_{11} - \beta_{22})^2 + 4\sigma(a\beta_{11} + b\beta_{22}) = 4\sigma^2$$

The epidemic extinction occurs in E_1 and the epidemic progresses in E_2 where:

$$E_1 = \{ (V_1, V_2) : \Delta(V_1, V_2) < 4\sigma^2, V_1 \le kN, V_2 \le (1 - k)N \},$$

$$E_2 = \{ (V_1, V_2) : \Delta(V_1, V_2) > 4\sigma^2, V_1 \le kN, V_2 \le (1 - k)N \}.$$

Thus, we obtain analytical conditions on the number of vaccinated individuals providing the epidemic arrest. Fig. 1 shows the regions with epidemic growth and extinction for different values of k.



Figure 1: Regions of epidemic growth and extinction are marked with deep and light colours, respectively. Parameter values are $\beta_{11} = 4$, $\beta_{22} = 1$, $\beta_{12} = \beta_{21} = 2.5$, $\sigma_1 = \sigma_2 = 1$ and k = 0.1 (green), k = 0.2 (red) and k = 0.3 (blue).

2.3. Final size of epidemic

Taking a sum of equations (1.1), (1.2), and then integrating between t = 0 and $t = \infty$, we obtain the equalities:

$$S_{10} - S_1^f = \sigma_1 \int_0^\infty I_1(t) dt, \ S_{20} - S_2^f = \sigma_2 \int_0^\infty I_2(t) dt$$
(2.1)

under the assumption that $I_j(0) = I_j(\infty) = 0$, j = 1, 2 and S_1^f , S_2^f are the final sizes of two susceptible groups. Next, we divide equation (1.1) by S_j , and integrate from 0 to ∞ :

$$-\ln\left(\left(S_{j}^{f}-V_{j}\right)/\left(S_{j0}-V_{j}\right)\right) = \frac{\beta_{j1}}{N\sigma_{1}}\left(S_{10}-S_{1}^{f}\right) + \frac{\beta_{j2}}{N\sigma_{2}}\left(S_{20}-S_{2}^{f}\right), \ j=1,2$$

using the equalities in (2.1). Introducing four new quantities $x_1 = S_1^f / S_{10}$, $x_2 = S_2^f / S_{20}$, $v_1 = V_1 / S_{10}$, $v_2 = V_2 / S_{20}$, and assuming that $\sigma_1 = \sigma_2 = \sigma$, $\beta_{12} = \beta_{21} = (\beta_{11} + \beta_{22})/2$, we obtain the following equations

$$\beta_{j1}k(1-x_1) + \beta_{j2}(1-k)(1-x_2) = -\sigma \ln\left(\left(x_j - v_j\right) / \left(1 - v_j\right)\right), \ j = 1, 2,$$

with respect to x_1 and x_2 . The positive solution of this system, satisfying the restriction $0 < x_1, x_2 < 1$, determines the final size of susceptible populations (Fig. 2, left). We can now determine the number of infected individuals in each group at the end of epidemic and the total number of infected in both groups, $I_{tot} = N - V_1 - V_2 - S_1^f - S_2^f$.

2.4. Maximum number of infected

In order to find the maximal number of infected individuals in the heterogeneous population, we consider an approximation $t_m^1 = t_m^2$, where t_m^j is time at which the functions $I_j(t)$ reach their maxima (j = 1, 2). This approximation is justified since numerical simulations of system (1.1), (1.2) show that these two values of time are close to each other. Furthermore, the analytical



Figure 2: Left panel: the final sizes of epidemic for two groups S_1 (solid lines) and S_2 (dashed lines) for k = 0.1 (blue), k = 0.2 (green), k = 0.3 (red). Note that analytical and numerical results coincide. The finals sizes for S_1 and different values of k are very close to each other. Right panel: the maximal numbers of infected individuals for two groups S_1 (1a, 1b, 1c) and S_2 (2a, 2b, 2c) for k = 0.1 (blue), k = 0.2 (green), k = 0.3 (red). Each pair of close curves corresponds to the analytical and numerical results. Other parameter values are as follows: $\beta_{11} = 4$, $\beta_{22} = 1$, $\beta_{12} = \beta_{21} = 2.5$, $\sigma = 1$, $V_2 = 2.4 \cdot 10^6 - V_1$.

results for the maximal number of infected individuals obtained under the assumption $t_m^1 = t_m^2$ give a good approximation of the numerical results (Figure 2, right). Integrating equations $S'_1 + I'_1$, $S'_2 + I'_2$ from 0 to $t_m (= t_m^i)$, we obtain:

$$S_1^m - S_{10} + I_1^m = -\sigma_1 \int_0^{t_m} I_1(t) dt, \ S_2^m - S_{20} + I_2^m = -\sigma_2 \int_0^{t_m} I_2(t) dt,$$

where $I_j^m = I_j(t_m)$, j = 1, 2. Next, we divide equation (1.1) by S_j , and integrate over $[0, t_m]$ to find:

$$-\ln\left(\left(S_{j}^{m}-V_{j}\right)/\left(S_{j0}-V_{j}\right)\right) = \frac{\beta_{j1}}{N\sigma_{1}}(S_{10}-S_{1}^{m}-I_{1}^{m}) + \frac{\beta_{j2}}{N\sigma_{2}}(S_{20}-S_{2}^{m}-I_{2}^{m}), \ j=1,2.$$
(2.2)

Assuming that $I'_i(t_m) = 0$, we get from (1.2):

$$S_{j}^{m} = \sigma_{j} N I_{j}^{m} / \left(\beta_{j1} I_{1}^{m} + \beta_{j2} I_{2}^{m} \right) + V_{j}, \quad j = 1, 2.$$
(2.3)

As before, we assume that $\sigma_1 = \sigma_2 = \sigma$ and set $\gamma_{ij} = \beta_{ij}/\sigma$, $u_1 = I_1^m/N$, $u_2 = I_2^m/N$, and v_1, v_2 as defined in the previous subsection. Using (2.3), we can rewrite equation (2.2) as follows:

$$\ln\left(\lambda_{j}\frac{\gamma_{j1}u_{1}+\gamma_{j2}u_{2}}{u_{j}}\right) = (\lambda_{1}-u_{1})\gamma_{j1} + (\lambda_{2}-u_{2})\gamma_{j2} - \frac{\gamma_{j1}u_{1}}{\gamma_{11}u_{1}+\gamma_{12}u_{2}} - \frac{\gamma_{j2}u_{2}}{\gamma_{21}u_{1}+\gamma_{22}u_{2}}$$

where $\lambda_j = ((j-1) + (3-2j)k)(1-v_j)$, j = 1, 2. Solving this system of equations, we find u_j and, consequently, I_j^m , j = 1, 2 (Fig. 2, right). We then use formulas (2.3) to determine S_j^m , j = 1, 2.

3. Optimization of vaccination strategies

Since there is a cost related to vaccination, an optimal control problem (optimal vaccination) is proposed:

$$\min_{0 \le V_1 \le \overline{V}_1, 0 \le V_2 \le \overline{V}_2} \int_0^T (I_1(t; V) + I_2(t; V)) dt + \gamma (V_1 + V_2) dt$$



Figure 3: Left panel: various vaccination strategies shown as lines in the (V_1, V_2) -plane. Right panel: plots of $I_1(t) + I_2(t)$ for four vaccination strategies shown in the left figure. The colours of the curves correspond to the colours of respective dots in the left panel. Scaling of the black curve is shown at the right vertical axis and of other curves the left vertical axis. Parameter values are the same as in Fig. 2.

meaning that we are interested to minimize total damage of the epidemics, which includes the cost related to the total number of infected individuals and the cost of the vaccine. Here, $(S_1(t; V), S_2(t; V), I_1(t; V), I_2(t; V))$ is the solution to (1.1)-(1.2) which satisfies the initial conditions $S_j(0; V) = S_{j0}, I_j(0; V) = I_{j0}, j \in \{1, 2\}$, where $V = (V_1, V_2) \in [0, \overline{V}_1] \times [0, \overline{V}_2]$ is the control/vaccination strategy. Since, due to certain constraints, not all individuals may be vaccinated we have imposed the constraints on $V_1, V_2: 0 \leq \overline{V}_j \leq S_{j0}, j = 1, 2$, and γ is a positive constant. Let

$$\mathcal{J}(V) = \int_0^T (I_1(t; V) + I_2(t; V)) dt + \gamma(V_1 + V_2).$$

Consider the following adjoint problem

$$\frac{dQ}{dt} = -A_V^{\tau}Q + (0, 0, 1, 1)^{\tau}, \quad Q(T) = (0, 0, 0, 0)^{\tau}, \quad (3.1)$$

where the superscript τ denotes the transposition,

$$A_{V} = \begin{pmatrix} -\frac{\beta_{11}}{N}I_{1} - \frac{\beta_{12}}{N}I_{2} & 0 & -\frac{\beta_{11}}{N}(S_{1} - V_{1}) & -\frac{\beta_{12}}{N}(S_{1} - V_{1}) \\ 0 & -\frac{\beta_{21}}{N}I_{1} - \frac{\beta_{22}}{N}I_{2} & -\frac{\beta_{21}}{N}(S_{2} - V_{2}) & -\frac{\beta_{22}}{N}(S_{2} - V_{2}) \\ \frac{\beta_{11}}{N}I_{1} + \frac{\beta_{12}}{N}I_{2} & 0 & \frac{\beta_{11}}{N}(S_{1} - V_{1}) - \sigma_{1} & \frac{\beta_{12}}{N}(S_{1} - V_{1}) \\ 0 & \frac{\beta_{21}}{N}I_{1} + \frac{\beta_{22}}{N}I_{2} & \frac{\beta_{21}}{N}(S_{2} - V_{2}) & \frac{\beta_{22}}{N}(S_{2} - V_{2}) - \sigma_{2} \end{pmatrix},$$

and $S_i = S_i(t; V), I_i = I_i(t; V)$ for brevity. Let Q(t; V) be a solution of problem (3.1), $V \in [0, \overline{V}_1] \times [0, \overline{V}_2]$ and $Q(t; V) = (Q_1(t, V), Q_2(t; V), Q_3(t; V), Q_4(t; V))^{\tau}$. Following the method presented in [1, 2], we can prove that for any $\theta \in \mathbb{R}^2$ such that $V + \epsilon \theta \in [0, \overline{V}_1] \times [0, \overline{V}_2]$ for any sufficiently small $\epsilon > 0$.

$$d\mathcal{J}(V)(\theta) = \sum_{j=1,2} \theta_j \left[\gamma - \int_0^T \left(\frac{\beta_{j1}}{N} I_1(t;V) + \frac{\beta_{j2}}{N} I_2(t;V) \right) (Q_j(t;V) - Q_{j+2}(t;V)) dt \right].$$

The evaluation of directional derivative of \mathcal{J} allows us to derive a conceptual iterative algorithm (gradient type) which improves at each step the control $V = (V_1, V_2)$. On the other hand, we can

prove as in [1] that there exists at least one optimal control $V^* = (V_1^*, V_2^*) \in [0, \overline{V}_1] \times [0, \overline{V}_2]$ (optimal vaccination strategy), *i.e.*, $\mathcal{J}(V^*) \leq \mathcal{J}(V)$, $\forall V \in [0, \overline{V}_1] \times [0, \overline{V}_2]$. Using the form of the directional derivative of \mathcal{J} we deduce that

$$V_{j}^{*} = \begin{cases} 0, & \int_{0}^{T} \left(\frac{\beta_{j1}}{N} I_{1}(t; V^{*}) + \frac{\beta_{j2}}{N} I_{2}(t; V^{*})\right) \left(Q_{j}(t; V^{*}) - Q_{j+2}(t; V^{*})\right) dt < \gamma \\ \overline{V}_{j}, & \int_{0}^{T} \left(\frac{\beta_{j1}}{N} I_{1}(t; V^{*}) + \frac{\beta_{j2}}{N} I_{2}(t; V^{*})\right) \left(Q_{j}(t; V^{*}) - Q_{j+2}(t; V^{*})\right) dt > \gamma, \end{cases}, \ j = 1, 2.$$

This allows us to improve the above mentioned gradient-type algorithm. More detailed analysis and applications of this approach will be presented elsewhere.

The optimal control problem in the beginning of this section is considered for a single vaccination at time t=0. We now consider the case of several consecutive vaccinations after some given time intervals with the same total number of vaccines distributed between the two groups. The corresponding optimal control problem will be considered in further studies. Here we restrict ourselves to some numerical results. Different vaccination strategies are illustrated in Fig. 3. Each point on the (V_1, V_2) -plane shows one vaccination with the corresponding numbers of vaccinated individuals in each class. As such, for the first vaccination we have $V_1 + V_2 = 10^6$ for all vaccination strategies but the proportion between the two groups are different. Similarly, the total number of vaccinated individuals equals $2 \cdot 10^6$ after the second vaccination stage with different proportions between the classes in different vaccination strategies.

The curve with black dots in the left panel of Fig. 3 corresponds to a random choice of vaccinated individuals. Since for k = 0.2 we have $S_2/S_1 = (1 - k)/k = 4$, then setting $V_2 = 4V_1$ we obtain the same proportion of vaccinated individuals in each class as the proportion between the classes of susceptible individuals. We neglect here the change of S_2/S_1 during the epidemic progression. Though this vaccination strategy is quite natural, it is less efficient compared to the other strategies where more individuals from S_1 are vaccinated.

A total number $5 \cdot 10^6$ of individuals are vaccinated in five times with 10^6 vaccines each one. The first vaccination is effectuated at the beginning of the (t = 0) and the remaining vaccinations after every five time units. For various vaccination strategies shown in Fig. 3 (left), the corresponding functions $I(t) = I_1(t) + I_2(t)$ are shown in Fig. 3 (right). We can characterize the vaccination strategies by the functions $V_2(t) = f_i(V_1(t))$, i = 1, 2, 3, 4. We conclude that for any two vaccination strategies f_1 and f_2 such that $f_1(V_1) < f_2(V_1)$, the corresponding functions (sum of infected individuals in both classes) satisfy the inequality $I^1(t) < I^2(t)$ for all t > 0. A similar relation holds for the total number of infected individuals at the end of epidemic.

Thus, vaccination of the first class of susceptible individuals is more efficient from the point of view of minimizing the number of infected individuals. This conclusion can be expected because the rate of disease transmission by this group is faster. However, this conclusion may not hold true if we minimize the number of deaths taking into account different mortality rates in the two groups. Let us consider an example with two groups: S_1 corresponds to people less than 60 years old, S_2 to people more than 60. Assume that k = 0.8, that is, $S_{10} = 0.8N$ and $S_{20} = 0.2N$. Consider the vaccination strategies where V_1/V_2 =const and let us vary this ratio. The total numbers of infected individuals in each group at the end of epidemic are presented in the following table.

V_1/V_2	$V_1/V_2 = 8$	$V_1/V_2 = 4$	$V_1/V_2 = 1.5$
I_1^{tot}	5 476 432	5 707 105	6 209 094
I_2^{tot}	1 364 707	1 227 671	908 982
6			

The ratio $V_1/V_2 = 4$ corresponds to a random choice of vaccinees. As before, increase of the proportion of the first group decreases the total number of infected $I_1^{tot} + I_2^{tot}$. However, the total number of deaths depends on the mortality rate in each group. In the application to the Covid-19, we assume that the mortality rate of infected individuals in the second group is of the order of magnitude 10 times larger than in the first group. In this case, the total number of deaths decreases for a larger proportion of vaccinees in the second group.

Acknowledgements

The last author has been supported by the RUDN University Strategic Academic Leadership Program.

References

- S. Aniţa, V. Arnăutu, V. Capasso, An Introduction to Optimal Control Problems in Life Sciences and Economics, Birkhasuer, New York, 2011.
- [2] V. Barbu, Mathematical Methods in Optimization of Differential Systems, Kluwer, Dordrecht, 1994.
- [3] F. Brauer, C. Castillo-Chavez, Z. Feng, *Mathematical Models in Epidemiology*, Springer, New York, 2019.
 [4] O. Diekmann, H. Heesterbeek, T. Britton, *Mathematical Tools for Understanding Infectious Disease Dynamics*, Princeton University Press, New Jercy, 2013.
- [5] J. Dolbeault, G. Turinici, Heterogeneous social interactions and the Covid-19 lockdown outcome in a multi-group SEIR model, Math. Model. Nat. Phenom., 15 (2020), 36.
- [6] P. van den Driessche, J. Watmough, Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission, Math. Biosci., Vol 180 (1–2), 2002, 29 – 48.
- [7] M. J. Keeling, P. Rohani, Modeling Infectious Diseases in Humans and Animals,
- [8] M. Martcheva, An Introduction to Mathematical Epidemiology, Springer, New York, 2015.
- S. Sharma, V. Volpert, M. Banerjee, Extended SEIQR type model for COVID-19 epidemic and data analysis, *Math. Biosci. Eng.*, 17(6) (2020), 7562 7604.