Network Modeling of Coexistence of Virus Strains Admitting Chaotic Behavior

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Abstract

In the last months of 2020, there has been concern in society about the emergence and spread of a pandemic caused by the COVID-19 virus, as well as other viral infections in the aftermath of it. According to the WHO, the incidence of infectious diseases is expected to increase in the coming years, due to known environmental and socio-economic problems – low living standards and not always adequate medical care for a large part of the world's population. Thus, the study of the action of two strains of the virus is extremely important for society. The network model of interaction of two strains of the virus is considered in the paper. The nodes of the network model are described by the system of differential equations and take into account populations of susceptible, first–time and re–infected individuals across two strains. On the basis of numerical network modeling complex chaotic solutions of the model are obtained. The increasing the incubation period for the two strains of virus under consideration affects the complexity of the trajectories obtained. It should be noted that for small values of the incubation period, the obtained solutions tend to a certain melt value called the endemic solution. Conditions for the spread of infectious disease providing stable endemic conditions were obtained. The network model of coexistence of two strains of viruses is investigated. This model can be used to study the spread of infectious diseases. Subpopulations of individuals susceptible to the virus, given its two strains, are important in the model. According to the results of numerical studies, it is established that at certain values of the solution parameters large values of the periods are obtained. Such a network model can be used to investigate the spread of infectious diseases. Of great importance in the network model, there are the subpopulations of individuals susceptible to the virus, given its two strains. Numerical simulation of the interaction of two strains of the virus was performed in R package.

Keywords 1

Epidemiology, endemic state, stability, deterministic chaos, nonlinear analysis

1. Introduction

Vaccines are being developed for annual seasonal epidemics. Flu strains are mutated very quickly and the question of which most likely strain of influenza is invaded, is solved annually. Distributed vaccines protect against the three strains that are considered the most dangerous. However, if the strain is radically different from previously known strains, then the vaccine has little or no protection,

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which poses a threat of a pandemic. Since it takes at least 6 months to develop a vaccine that can protect against a new strain, there is no ready vaccine to protect against the attack of a new pandemic strain. There are antiviral drugs for the treatment of pandemic influenza, they also have some preventive effect, but this effect will only occur when providing antiviral treatment. Therefore, it is important to find ways of effective vaccination in the presence of different strains of the virus.

In previous studies [1–4], they have studied the use of models based on differential equation systems in the case of a single strain of the virus with a population of symptomatically and asymptomatically infected individuals, paying particular attention to endemic stability studies. For this purpose, linearization methods and the direct method of Lyapunov were used. At the same time, the model of interaction of subpopulations in the case of the spread of several virus strains and the question of nonlinear analysis of such models are of considerable interest [5–8].

Thus, the objective of the work is to offer and investigate the network model of coexistence of two virus strain from viewpoint of stability, periodicity and predictability of the epidemiological curves.

2. Theoretical results

The model is intended to describe the spread of various strains of the virus (such as pandemic and seasonal influenza). The model makes assumptions.

1. The compartments of latent persons are not considered.
2. It is believed that the course of the flu is necessarily accompanied by the presence of symptoms. That is, there is no compartment asymptomatically infected.
3. The total population size of N is considered constant.

So, a transition state diagram is considered (see Fig. 1):

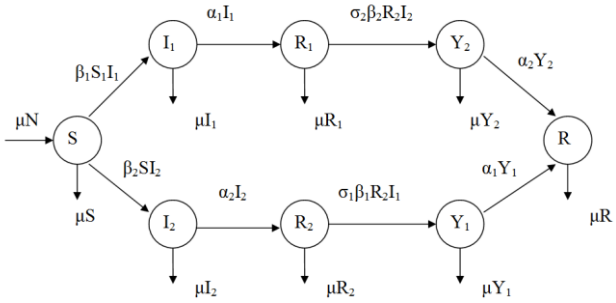


Figure 1: Network model for two virus strains

Here we have compartments that meet subpopulations S – susceptible, I_1 – infected with the 1st strain of the virus, I_2 – infected with the 2nd strain of the virus, R_1 – recovered after the 1st strain of the virus, R_2 – recovered after the 2nd strain of the virus, Y_1 – re-infected (but already the first strain), Y_2 – re-infected (but already the second strain of the virus), R – recovering after double infection of persons.

On its basis we have a system:

$$\begin{aligned} S' &= \mu(N - S) - (\beta_1 I_1 + \beta_2 I_2)S, \\ I' &= \beta_i S I_i - (\mu + \alpha_i) I_i, i = 1,2, \\ R_i' &= \alpha_i I_i - (\mu + \sigma_j \beta_j I_j) R_i; i, j = 1,2, i \neq j, \\ Y_i' &= \theta_i \beta_i R_j I_i - (\mu + \alpha_i) Y_i; i, j = 1,2, i \neq j, \\ R' &= \alpha_1 Y_1 + \alpha_2 Y_2 - \mu R. \end{aligned} \tag{1}$$

Here for any t

$$S + I_1 + I_2 + R_1 + R_2 + Y_1 + Y_2 + R = N,$$

where biologically significant region is

$$\Omega = \left\{ (S, I_1, I_2, R_1, R_2, Y_1, Y_2) \in R_+^7 \middle| S + I_1 + I_2 + R_1 + R_2 + Y_1 + Y_2 \leq N \right\}.$$

Determine the equilibrium states of system (1) belonging to the boundary Ω from the system of algebraic equations:

$$\mu(N - S) - (\beta_1 I_1 + \beta_2 I_2)S = 0,$$
$$\beta_i S I_i - (\mu + \alpha_i) I_i = 0,$$
$$\alpha_i I_i - (\mu + \sigma_j \beta_j I_j) R_i = 0,$$
$$\theta_i \beta_i R_j I_i - (\mu + \alpha_i) Y_i = 0,$$
$$i, j = 1,2, i \neq j$$

We have three equilibrium states

$$E_0 = (N,0,0,0,0,0,0),$$
$$E_1 = (S_1^*, I_1^*, 0, R_1^*, 0,0,0),$$
$$E_2 = (S_2^*, 0, I_2^*, 0, R_2^*, 0,0).$$

Here:

$$S_1 = \frac{\mu + \alpha_1}{\beta_1}, I_1 = \frac{\mu(N\beta_1 - \mu - \alpha_1)}{\beta_1(\mu + \alpha_1)}, R_1 = \frac{\alpha_1(N\beta_1 - \mu - \alpha_1)}{\beta_1(\mu + \alpha_1)}.$$
$$S_2 = \frac{\mu + \alpha_2}{\beta_2}, I_2 = \frac{\mu(N\beta_2 - \mu - \alpha_2)}{\beta_2(\mu + \alpha_2)}, R_2 = \frac{\alpha_2(N\beta_2 - \mu - \alpha_2)}{\beta_2(\mu + \alpha_2)}.$$

We introduce the notions of the basic reproduction numbers

$$\Re_1 = \frac{\beta_1 N}{\mu + \alpha_1}, \Re_2 = \frac{\beta_2 N}{\mu + \alpha_2},$$

Hence,

$$S_1 = \frac{N}{R_1}, I_1 = \frac{\mu}{\beta_1}(R_1 - 1), R_1 = \frac{\alpha_1}{\beta_1}(R_1 - 1),$$
$$S_2 = \frac{N}{R_2}, I_2 = \frac{\mu}{\beta_2}(R_2 - 1), R_2 = \frac{\alpha_2}{\beta_2}(R_2 - 1).$$

Equilibrium states have the following epidemiological interpretation: E_0 – the state of absence of the disease; E_1 – the presence of strain 1 only; E_2 – the presence of strain 2 only.

Let us denote $\Re_0 = \max\{\Re_1, \Re_2\}$. If $\Re_0 \leq 1$ then it is the only equilibrium state in Ω. If $\Re_0 > 1$ then, either E_1, or E_2, or both belong Ω.

Fig. 2, 3 show the regions of existence and stability of equilibrium states E_i.

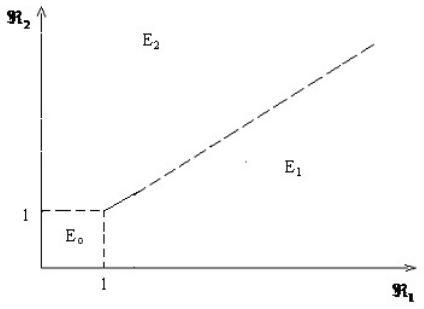


Figure 2: Stability regions in the case if $0 \leq \sigma_1, \sigma_2 \leq 2$

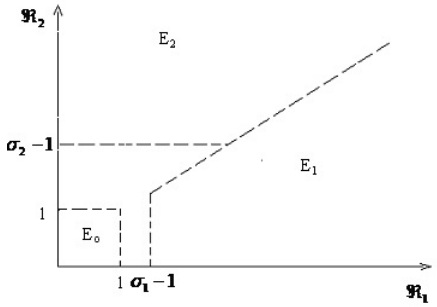


Figure 3: Stability regions in the case if $2 < \sigma_1 \leq \sigma_2$

When comparing the model described with the traditional SIR or SEIR model, here we show the way to take into account the interaction of two or more virus strains. Namely, adding to the network model the subpopulations of re-infected persons we are able to describe very complex interactions of various virus strains. The theoretical results presented can be generalized for any finite number of virus strains and an arbitrary amount of re-infectiousness. In the same way, the equilibrium states and basic reproduction numbers can be calculated.

3. Experimental results

Consider the system (1) for the values of parameters

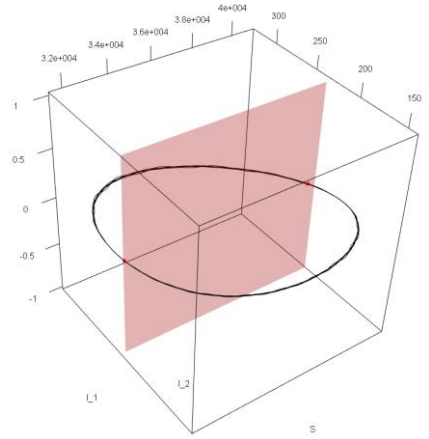
$$N = 10^5,\ \mu = 0.005,\ \beta_1 = 0.4*10^{-5},\ \beta_2 = 0.3*10^{-5},\ \alpha_2 = 0.1428,\ \sigma_1 = 1,\ \sigma_2 = 1.$$

Note that we get

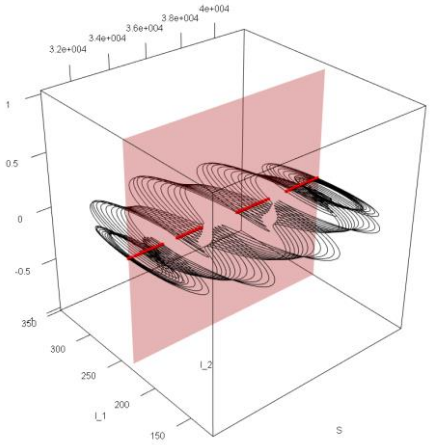
$$\Re_1 = \frac{\beta_1 N}{\mu + \alpha_1} = \frac{4 \cdot 10^{-6} \cdot 10^5}{5 \cdot 10^{-3} + 0{,}1428} = \frac{0{,}4}{0{,}1478} = 2{,}706,$$

$$\Re_2 = \frac{\beta_2 N}{\mu + \alpha_2} = \frac{3 \cdot 10^{-6} \cdot 10^5}{5 \cdot 10^{-3} + 0{,}1428} = \frac{0{,}3}{0{,}1478} = 2{,}0298.$$

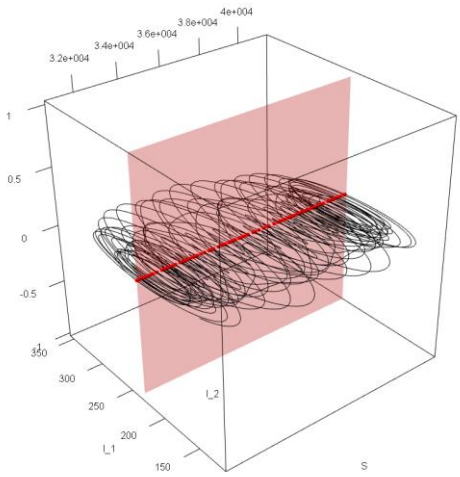
That is $\Re_1 > \Re_2$ and all the conditions, which were mentioned above, hold. Computational modeling of (1) has been implemented (see Fig. 4).



a)



b)



c)

Figure 4: Phase plot of S (a), I_1 (b), and I_2 (c) during 8000 days

We see a complex nonlinear behavior of the system trajectory. Such nonlinear behavior is caused by a change in a number of model parameters. The figure 4 shows the effect of changes in the incubation period on the trajectory and solutions of the equation system.

We see that increasing the incubation period for the two strains of virus under consideration affects the complexity of the trajectories obtained. It should be noted that for small values of the incubation period, the obtained solutions tend to a certain melt value called the endemic solution. At the same time, an increase in the incubation period leads to a periodic solution of the system. Such phenomena in the theory of dynamical systems have been called bifurcation, which occurs when the values of the system parameters change and affect the change in the qualitative behavior of the whole model.

In this case, we transform from a steady endemic focus to a limit cycle. Such a limit cycle corresponds to the situation of periodic epidemics. The impact of other parameters on the change in the qualitative behavior of system trajectories should also be investigated. A further change in the incubation period affects the complexity of such a periodic solution. From a certain value of the incubation periods corresponding to different strains of the virus, there is a doubling of the period, then the period increases 4 times, 8 times and so on.

4. Conclusion

Therefore, the network model of coexistence of two strains of viruses was investigated. Such a model can be used to investigate the spread of infectious diseases. Of great importance in the model are the subpopulations of individuals susceptible to the virus, given its two strains.

It is clear that the model can be developed for the cases of three strains, four, etc. In this case, a system of seven ordinary differential equations was proposed as a mathematical object. At the same time, more sophisticated models based on delayed differential equations, stochastic differential equations, partial differential derivative equations can be used in the study of the spatial spread of the epidemic. Of great importance in all these cases is a qualitative study of the nonlinear behavior of the model. We see from numerical studies that at certain values of the parameters of the solution, large values of periods are obtained. Such solutions are called quasi-periodic and correspond to a situation called in the theory of dynamical systems as “deterministic chaos”.

The obtained solution trajectories of the proposed model in Figure 4 also indicate the complexity of epidemic prediction. Even in the simplest case of describing a model based on deterministic equations, we get chaotic solutions. This is due to the complexity of nonlinear interaction between subpopulations of the epidemiological model. It is undoubted that further studies should address the use of a seasonal spread of epidemiologically relevant disease that is consistent with the use of non-stationary dynamic models. Also, of great importance is the inclusion in the model of populations of symptomatically and asymptotically infected persons.

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