Introduction of evolutionary mechanisms in the spread of epidemics

Pablo Yagüe Serrano[1], David Soriano Paños[2,3], and Jesús Gómez Gardeñes[1,3,4]

[1]Departament of Condensed Matter Physics, University of Zaragoza, 50009 Zaragoza (Spain).
[2]Instituto Gulbenkian de Ciência (IGC), 2780-156 Oeiras (Portugal).
[3]GOTHAM lab, Institute for Biocomputation and Physics of Complex Systems (BIFI), University of Zaragoza, 50018 Zaragoza (Spain).
[4]Center for Computational Social Science, University of Kobe, 657-8501 Kobe (Japan).

Contagious diseases cause millions of deaths worldwide every year. Epidemic models are compartmental models that allow us to predict their behaviour in order to take measures that help us to curb epidemic waves. In the last two years, we have suffered an historic pandemic caused by the SARS-CoV-2 virus, and in the last year variants of this virus have become very important, causing re-infections in the already recovered population. It is precisely in order to take into account the contribution of pathogen variants in the spread of an epidemic, that a new formalism has been developed.

Our equations are based on the formalism proposed in [1], in which a reinfection of the recovered individuals is included as a completely independent parameter of the system because of the social focus of the article. We adapt the reinfection mechanism proposed in that article to account for the evolutionary behaviour of a virus during an epidemic outbreak. On the one hand, that mechanism is governed in the system as a continuous variable x, which at each time step, for infected individuals, increases by a value of D, which is the parameter that models the mutation of the pathogen, the higher the value of D, the higher the mutation. On the other hand, we define the probability of reinfection of a recovered individual by contact with an infected individual as:

$$\lambda' = \lambda \left(1 - e^{-D(t-s)} \right) , \qquad (1)$$

where λ is the probability of a healthy individual becoming infected by contact with an infected individual and s is the time instant when he became infected. In this way, the more time goes by since the individual recovers, the higher the probability of reinfection tending asymptotically to λ.

After the proposal of the new formalism, a series of Monte Carlo simulations are made to compare them with the equations, as shown in the figure 1. In this graph we can see how there are 2 distinct phases, the first is a non-epidemic regime and the second leads to an endemic state
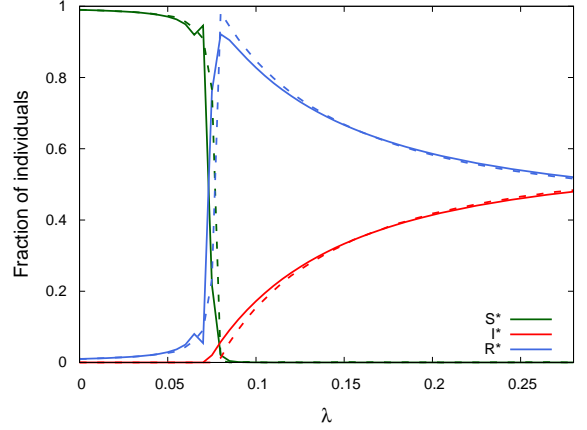

Fig. 1. In this figure, the solid lines represent the equations of our formalism, while the dashed lines represent the average of 40 Monte Carlo simulations. The parameters used are: $\mu = 0.8$ and an Erdös-Rényi lattice with $N = 10000$ and $\langle k \rangle = 10$.

in which there is a non-null fraction of infected individuals in the stationary regime.

The consequences of the endemic regime are very relevant, as the epidemic will not be curbed until external measures are introduced, such as vaccination, confinement, or other types of controls that we have seen in similar cases in the past.

[1] J. Gómez-Gardeñes, A. S. de Barros, S. T. Pinho, and R. F. Andrade, *Abrupt transitions from reinfections in social contagions*, EPL (Europhysics Letters) **110(5)**, 58006 (2015).

[2] R. M. Anderson, C. Vegvari, J. Truscott, and B. S. Collyer, *Challenges in creating herd immunity to SARS-CoV-2 infection by mass vaccination*, The Lancet **396**, 1614 (2020).