

SIMULATING DETERMINISTIC AND STOCHASTIC SVEIR MODELS TO DETERMINE THE DISEASE ELIMINATION TIME FOR DIFFERENT VACCINATION RATES

Luiz S. Freitas ^{1*}, Hyun Mo Yang ¹ and Carlos A. Braumann ^{2,3}

¹Laboratório de Epidemiologia e Fisiologia Matemáticas, Universidade Estadual de Campinas

²Centro de Investigação em Matemática e Aplicações, Instituto de Investigação e Formação
Avançada, Universidade de Évora

³Departamento de Matemática, Escola de Ciências e Tecnologia, Universidade de Évora

luizsf28@gmail.com(*corresponding author), hyunyang@ime.unicamp.br, braumann@uevora.pt

ABSTRACT

We consider a SVEIR model with constant population size N and with compartments X, H, Y, V, Z (number of susceptibles, exposed, infectious, vaccinated and recovered, respectively). Let ν be the vaccination rate of susceptibles. From [1], we know that there is a critical value of the vaccination rate, ν_c , such that, when $\nu > \nu_c$, the system converges to a disease-free equilibrium (in which $H = Y = 0$) and, when $\nu < \nu_c$, the system converges to an endemic equilibrium. We consider the situation where we start with no vaccination (so the initial population will be at the endemic equilibrium corresponding to $\nu = 0$) and we introduce vaccinating at rate $\nu > 0$. We also assume that we are not able to distinguish among susceptible, exposed and recovered individuals, so that we will vaccinate all these categories of individuals.

We then consider the more realistic stochastic case in which the transitions between compartments occur randomly according to a Markov chain with transition rates equal to the deterministic rates. We study this system through Monte Carlo simulations using the Gillespie algorithm (see [2]).

Contrary to the deterministic system, in the stochastic case a disease-free state will be reached whatever the value of ν is. So, the issue for public health policy decision will be to determine the

minimum value of ν that will give a high probability (say 95% or 99% probability) of reaching a disease-free state before some prescribed time horizon T . That is the purpose of this paper. We will also compare with the value of ν that will lead the deterministic system in the same time horizon to $H(T) + Y(T) < 1$, which for practical purposes can be considered a disease-free state.

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References

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