Some exact measures to quantify the potential transmission of an epidemic in a stochastic SVIS model with infection reintroduction and imperfect vaccine

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Abstract

This communication is oriented to the study of contagious disease dynamics under a Markovian approach within the area of epidemic modelling.
We consider infectious diseases that do not confer permanent immunity in constant size populations where individuals are homogeneous and uniformly mixed. Prior the start of the infectious process, a population proportion was vaccinated preventively to a communicable disease with an available vaccine that fails with a certain probability. This approach involves a stochastic SVIS model with infection reintroduction and imperfect vaccine. We represent the evolution of the epidemic, at each time point t, by the bi-dimensional CTMC, $X = \{(V(t), I(t)), t \geq 0\}$, where the random variables $V(t)$ and $I(t)$ count the number of vaccinated and infected individuals at time t, respectively.

The basic reproduction number, R_0, is probably the most used descriptor of disease transmission. Due to repeated contacts between the marked infective and previously infected individuals, R_0 overestimates the average number of secondary infections and leads to high immunization coverage. Our purpose is to describe alternative measures to R_0 to estimate the potential transmission of an infectious disease. In more detail, we define the exact and population reproduction numbers, R_{e0} and R_p, under the effect of vaccination. For these measures, we provide theoretical schemes involving their mass probability and generating functions and factorial moments. We illustrate theoretical and algorithmic results with several numerical examples.

The talk is based on the paper [1].

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References

[1] Gamboa, M., Lopez-Herrero, M.J. (2020). *Measuring Infection Transmission in a Stochastic SIV Model with Infection Reintroduction and Imperfect Vaccine.* Acta Biotheor, 68, 395-420. https://doi.org/10.1007/s10441-019-09373-9