On the stochastic engine of contagious diseases in exponentially growing populations

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The purpose of this paper is to analyze the mechanism for the interplay of deterministic and stochastic models for contagious diseases. Deterministic models for contagious diseases are prone to predict global stability. Small natural birth and death rates in comparison to disease parameters like the contact rate and the removal rate ensures that the globally stable endemic equilibrium corresponds to a tiny average proportion of infected individuals. Asymptotic equilibrium levels corresponding to low numbers of individuals invalidate the deterministic results.

Diffusion effects force probability mass functions of the stochastic model to possess similar stability properties as the deterministic model. Particular simulations of the stochastic model predict, however, oscillatory patterns. Small and isolated populations show longer periods, more violent oscillations, and larger probabilities of extinction.

We prove that evolution maximizes the infectiousness of the disease as measured by the ability to increase the proportion of infected individuals. This holds provided the stochastic oscillations are moderate enough to keep the proportion of susceptible individuals near a deterministic equilibrium.

We close our paper with a discussion of the herd-immunity concept and stress its close relation to vaccination-programs.

References

[1] T. Lindström, *On the stochastic engine of contagious diseases in exponentially growing populations*, Nonlinear Analysis: Real World Applications 77:104045 (2024)

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