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A general kinetic model for the spread of infectious diseases in continuously structured compartments

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We propose a general kinetic compartmental model for the spread of infectious diseases, wherein each compartment is structured by a continuous variable that captures inter-individual phenotypic variability [1, 2, 3].

The model comprises a system of integro-differential equations for the dynamics of the population density functions (i.e. the phenotype distributions) of the different compartments. First, we formally derive this model from an underlying stochastic model, which describes the evolutionary dynamics of single individuals. Then, we explore the connections between this general model and specific compartmental models employed in epidemiology [4, 5, 6].

We derive the classical threshold quantity R_0, the Basic Reproduction Number, after some simplifying assumptions on our general model. Finally, we discuss possible applications of the model in different epidemiological scenarios and compare simulations of the microscopic (Monte Carlo) and macroscopic (ODEs) layers of our construction.

References

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