

SIR modeling for the disease transmission: Application of the QSSA idea

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Abstract

In this work, we consider an SIR model of infectious disease transmission through the outside environment of host individual, for example, like an aerial infection. The pathogen population around the host population is assumed to be reproduced by the infective hosts themselves. Furthermore the dispersal of pathogen individuals outside of the host is assumed to be passive, and sufficiently fast outside of the host. Susceptible individual becomes infective with the successful disease transmission, and then comes to have an infectivity. With these assumptions, we construct an SIR model of susceptible, infective and removed subpopulations in the host population, around which the pathogen population is dispersing. Assuming the representative time scale for the reproduction and dispersal of pathogen population is very small compared to that for the host state transition, we can apply the quasi stationary state approximation (QSSA) for the model, and get a SIR model, which includes the well-known Kermack–McKendrick model as the simplest case. Then we can find a flexibility of the model to discuss the characteristics of disease transmission with some different natures, including the basic reproduction number R_0 . Further we can show a potential way of the rational extension of SIR modeling for a variety of epidemic diseases.

Keywords: (*Mathematical biology, Population dynamics, SIR model, ODE, QSSA*)

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