SIQR Model on the Disease Spread by Multiple Strains with Competitive Dominance

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Numerous studies have provided evidences of the superinfection with multiple strains about various infectious diseases such as malaria, SARS-CoV-2, dengue, and HIV. Such strains are clearly under the exploitative competition for hosts and for the reproduction within host. Even if an individual is infected by a hardly detectable strain, the superinfection of another detectable strain may serve to detect the infection and quarantine the individual. Therefore, a superinfection may help to suppress the disease spread. In this work, we consider an Susceptible-Infective-Quarantined-Recovered (SIQR) model on the epidemic dynamics of a disease transmission with n strains. We assume an order of competitive dominance among strains according to the infection success.

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\begin{aligned}
\frac{dS}{dt} &= \mu N - \sum_{k=1}^{n} \beta I_k S - \mu S; \\
\frac{dI_1}{dt} &= \beta I_1 S + \sum_{k=2}^{n} \epsilon\beta I_1 I_k - \sigma_1 I_1 - \rho_1 I_1 - \mu I_1; \\
\frac{dI_j}{dt} &= \beta I_j S - \sum_{k=1}^{j-1} \epsilon\beta I_j I_k + \sum_{k=j+1}^{n} \epsilon\beta I_k I_j - \sigma_j I_j - \rho_j I_j - \mu I_j \quad (1 < j < n); \\
\frac{dI_n}{dt} &= \beta I_n S - \sum_{k=1}^{n-1} \epsilon\beta I_k I_n - \sigma_n I_n - \rho_n I_n - \mu I_n; \\
\frac{dQ_k}{dt} &= \sigma_k I_k - \alpha_k Q_k - \mu Q_k \quad (k = 1, 2, \ldots, n); \\
\frac{dR}{dt} &= \sum_{k=1}^{n} \rho_k I_k + \sum_{k=1}^{n} \alpha_k Q_k - \mu R,
\end{aligned}
$$

where S, I_k, Q_k, and R are population densities of susceptibles, infectives who hold strain k, corresponding quarantined and recovered individuals, respectively. In our modeling, the quarantined state follows the isolation with which infectives cannot transmit the disease to anyone. The total population size is given by $N = S + \sum_{k=1}^{n} I_k + \sum_{k=1}^{n} Q_k + R$. βI_k gives the infection force of strain k for the susceptible with the coefficient β. $\epsilon\beta I_k$ gives the superinfection force of strain k for the infectives with strain j of the lower dominance ($0 \leq \epsilon \leq 1$). Superinfection for the infectives with strain of the higher dominance always fails. The subscript k indicates the dominance of strain in infectives I_k. Parameter σ_k is the detectability of strain k by the quarantine. Parameters α_k and ρ_k are the recovery rates for the infectives with strain k under and out of the isolation, respectively. μ is the natural death rate.

We focus on the dependence of the endemic/epidemic size on the detectabilities of multiple strains, and discuss the influence of superinfection on the endemic/epidemic size.
