SIQR model on the disease spread by multiple strains with a 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 the host and for the reproduction in the host. Moreover, even when an individual is infected by a hardly detectable novel or mutant strain, the superinfection of another detectable strain could serve the infected individual to be diagnosed and quarantined, which in turn may help to suppress the disease spread.

In this work, we consider an SIQR model on the epidemic dynamics of a disease transmission with n strains which follows an order of competitive dominance according to the invasion success in the host.

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

where S, I_k , Q_k , and R are population densities of susceptibles, infectives who hold strain k, corresponding isolated and recovered individuals, respectively. The total population size is denoted 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 , and $\epsilon \beta I_j$ gives that for the infective with strain j of the lower dominance $(0 \le \epsilon \le 1)$. Parameter σ_k is the quarantine rate for the infective who holds strain k, which reflects the detectability of strain k. Parameters α_k and ρ_k are the recovery rates for the infective with strain k under and out of the isolation, respectively. μ is the natural death rate.

In the absence of superinfection, the system approaches either the disease-free equilibrium or the single strain endemic equilibrium consisting of infectives who hold the strain with the largest strain-specific reproduction number. In the presence of superinfection, the analysis on our model shows that it is possible to have infectives holding different strains at the endemic state. We are going to discuss the influence of superinfection and the distribution of the strain-basic reproduction number to the endemicity in the disease spread.