

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

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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.

$$\begin{aligned} \frac{dS}{dt} &= \mu N - \sum_{i=1}^{n} \beta_{i} I_{i} S - \mu S; \\ \frac{dI_{1}}{dt} &= \beta_{1} I_{1} S + \sum_{j=2}^{n} \epsilon_{1j} \beta_{1} I_{1} I_{j} - \sigma_{1} I_{1} - \rho_{1} I_{1} - \mu I_{1}; \\ \frac{dI_{i}}{dt} &= \beta_{i} I_{i} S + \sum_{j=i+1}^{n} \epsilon_{ij} \beta_{i} I_{i} I_{j} - \sum_{j=1}^{i-1} \epsilon_{ji} \beta_{j} I_{j} I_{i} - \sigma_{i} I_{i} - \rho_{i} I_{i} - \mu I_{i} \qquad (1 < i < n); \\ \frac{dI_{n}}{dt} &= \beta_{n} I_{n} S - \sum_{j=1}^{n} \epsilon_{jn} \beta_{j} I_{j} I_{n} - \sigma_{n} I_{n} - \rho_{n} I_{n} - \mu I_{n}; \\ \frac{dQ_{i}}{dt} &= \sigma_{i} I_{i} - \alpha_{i} Q_{i} - \mu Q_{i}; \\ \frac{dR}{dt} &= \sum_{i=1}^{n} \rho_{i} I_{i} + \sum_{i=1}^{n} \alpha_{i} Q_{i} - \mu R, \end{aligned}$$

where *S*, I_i , Q_i , and *R* are population densities of susceptibles, infectives who hold strain *i*, corresponding isolated and recovered individuals, respectively. The total population size is constant and given by $N = S + \sum_{i=1}^{n} I_i + \sum_{i=1}^{n} Q_i + R$. $\beta_i I_i$ gives the infection force of strain *i* for the susceptible with the coefficient β_i , and $\epsilon_{ij}\beta_i I_i$ gives that for the infective with strain *j* of the lower dominance, where i > j. Parameter σ_i is the quarantine rate for the infective who holds strain *i*, which reflects the detectability of the infection by strain *i*. Parameters α_i and ρ_i are the recovery rates for the infective with strain *i* respectively under and out of the isolation. Parameter μ is the natural death rate. We are focusing on the dependence of the endemic/epidemic size on the difference of strains in the detectability, and trying to discuss the influence of superinfection on the endemic/epidemic size by the analysis on our model.