

# Extinction Thresholds in Deterministic and Stochastic Models for Epidemics and Viral Dynamics

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**Abstract:** The basic reproduction number  $\mathcal{R}_0$  and type reproduction numbers  $\mathcal{T}_k$  are thresholds in deterministic epidemic theory that predict disease extinction when  $\mathcal{R}_0 < 1$  or  $\mathcal{T}_k < 1$ . In stochastic theory, there are also thresholds that predict disease extinction but are distinct from the deterministic theory. For example, in the case of a single infectious group in a continuous-time Markov chain epidemic model, if  $i$  infectious individuals are introduced into a susceptible population and  $\mathcal{R}_0 > 1$ , then the probability of disease extinction is  $(1/\mathcal{R}_0)^i$ . With multiple infectious groups from which the disease could emerge, the stochastic thresholds depend on the number of individuals within each group,  $i_j$ ,  $j = 1, \dots, n$  and on the probability of disease extinction for each group,  $q_j$ . It follows from multitype branching processes that the probability of disease extinction is approximately  $q_1^{i_1} \cdots q_n^{i_n}$ . We illustrate some relationships between the deterministic and stochastic thresholds derived from differential equation and continuous-time Markov chain models for vector-host, treatment, and within-host viral and cell dynamics.