Demographic and Environmental Variability in Stochastic Epidemic Models

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Demographic and environmental variability on births, deaths, transmission, or seasonality impact how a disease is propagated within a population. Accounting for demographic and environmental variability, we formulate stochastic epidemic models to investigate the probability of disease emergence. Stochastic models with demographic variability, such as continuous-time Markov chains and multi-type branching processes, provide insight into the effect of past exposure, vaccination history, or behavior on disease emergence. Models with demographic and environmental variability, such as non-homogeneous Markov processes and age-dependent branching processes, provide insight into the effects of seasonality on disease emergence. Some examples, including SARS, MERS and measles, are presented for stochastic multigroup models with groups for superspreaders or non-superspreaders, or groups with some or no prior pathogen exposure. In addition, stochastic epidemic models with seasonal transmission rates demonstrate the importance of the time at which infected hosts are introduced into the population. Public health implications for disease control are also discussed.