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# The influence of assumptions on generation time distributions in epidemic models

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## Abstract

A simple class of stochastic models for epidemic spread in finite, but large, populations is studied. The purpose is to investigate how assumptions about the distribution of times between primary and secondary infections influences the outcome of the epidemic. Of particular interest is how assumptions of individual variability in infectiousness relates to variability of the epidemic curve. The main concern is the proportion of the population that finally are infected and the time scale at which the epidemic evolves. The theoretical results are illustrated by simulations.

**Keywords:** Epidemic models, Kermack-McKendrick-model, Epidemic curve, Generation time distribution, Basic reproduction number.