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Epidemiological models have long been used to explore several aspects of vaccine-mediated infection control. In recent years, there has been a growing interest in mathematical modeling as a research tool for vaccine evaluation and development. Many models used for evaluating vaccine efficacy focus on the relationship between vaccine-induced immunity and transmission.

Mathematical models usually include many of the same assumptions used in empirical analyses. However, unlike empirical analyses, mathematical models are subject to uncertainty about the representation of model assumptions. In this paper, we have developed a number of mathematical models for predicting vaccine efficacy and selection in endemic settings. These models reflect the interaction between an infectious agent and hosts in a population, and use the concept of basic reproduction number ($R(o)$) to describe the nature of the transmission process. $R(o)$ is defined as the number of secondary infections that occur when a typical infected individual is introduced into a population that is completely susceptible. These models are developed to focus on the three-dimensional relationship between $R(o)$, efficacy and selection. One of these models estimates efficacy based on a "clinical hypothesis," i.e., the total fraction of vaccinated individuals that is immune to infection from natural infection with the same pathogen. The efficacy estimate obtained by this clinical hypothesis model is a function of the total number of vaccinations and the extent to which natural infection immunity increases with time since vaccination. The model estimates the relationship between herd immunity and vaccination coverage and predicts the reduction in force of infection that is associated with different vaccination strategies. The two other models are the "population-level" and "household" models and they use the concept of force of infection to estimate vaccination impact. The population-level model focuses on f678ea9f9e

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