Transmission dynamics of measles in a vaccinated population

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The statistical testing of mechanistic models to observed time series of infectious disease cases has been problematic because the dynamics of susceptible hosts is incompletely observed. Previously we have proposed a method for reconstructing the dynamics of numbers of susceptible hosts from information on case reports and serological data **??**. Here, we propose a method to test various mechanistic transmission models against the reconstructed time series of infections and susceptible hosts. The various transmission models embody different hypothesis about the clustering of infected and susceptibles in the population, and identification of the most parsimonious transmission model informs us about the (unobserved) transmission dynamics. The proposed method is applied to data on measles outbreaks in a highly vaccinated human host population. We identify the most parsimonious transmission model, and estimate the values of several parameters of interest, such as the basic reproduction number.

References

[1] Wallinga J., P. Teunis & M. Kretzschmar, 2003, Reconstruction of measles dynamics in a vaccinated population, *Vaccine* ,(in press).

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