

OPTIMAL VACCINATION STRATEGIES FOR STOCHASTIC EPIDEMICS AMONG A POPULATION OF HOUSEHOLDS

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Many models of infectious diseases assume that the population among which the disease is spreading is locally as well as globally large. By locally large, it is meant that if the population is split into several groups, eg by age, sex and/or geographical location, then each of these groups (and not just the total population) is also large. However, this assumption is unrealistic for many human and animal epidemics, since such populations are usually partitioned into small groups or households, and there is a growing interest in models for epidemics among populations whose structure remains locally finite as the population becomes large. One class of such non-locally-large models assumes that the population is partitioned into households, with different contact rates for within- and between-household infection. This mixing structure has important implications for the threshold behaviour of the epidemic and consequently for optimal vaccination strategies.

In this talk, I will give a brief introduction to models for epidemics among a population of households. In particular, I will describe a reproduction number that determines whether or not a major epidemic can occur and then consider optimal vaccination strategies, which reduce the reproduction number to its threshold value of one with minimum vaccination coverage.