

The Micro-Epidemic Dynamics of Pneumococcal Transmission in Day Care Groups and Families

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*Streptococcus pneumoniae* (pneumococcus) is a normal part of the human nasopharyngeal flora. At the same time, nasopharyngeal colonisation (carriage) of the bacterium is a prerequisite to severe diseases caused by pneumococcus (e.g. sepsis, meningitis, and pneumonia), and it causes over one million annual deaths in children worldwide. The epidemiology of pneumococcal carriage has become a key question in the development and introduction of new cost effective vaccines against pneumococcal disease, because these vaccines protect also against carriage, thus reducing transmission. Understanding pneumococcal carriage is complicated by the fact that there exist over 90 different serotypes, based on the polysaccharide capsule of the bacterium, leading to a situation where different serotypes interact in competing to colonise human hosts. The prevalence of carriage reaches as high as 80% in some populations. However, monitoring carriage status is only achieved through active sampling.

In this work our goal is to assess the effect of exposure within day care centres and families on pneumococcal transmission. We use a longitudinal data set consisting of monthly samples (serotype-specific status of carriage) from attendees and their family members in three day care centres in Finland. We model the dynamics of transmission with a continuous-time event history model of acquisition and clearance of carriage. The model parameters are estimated in a Bayesian framework using a Markov chain Monte Carlo algorithm, which utilizes latent processes because of incomplete data from panel observations. In particular, we include into parameter estimation the unobserved exposure due to the non-participating day care attendees.