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Unravelling the transmission dynamics of streptococcus pneumoniae with approximate bayesian computation

Approximate Bayesian computation (ABC) provides an appealing method for connecting stochastic models to observed data. With the help of ABC, it is possible to distinguish probabilistically, given the data, between different model candidates, and finally learn the distributions of model parameters. Furthermore, having posterior distributions for models and model parameters, one can calculate posterior means, and perform prediction.

Streprococcus pneumoniae is a bacteria colonizing especially children. After introduction of vaccine against the most common strains, what has been observed is a fast serotype replacement, after which the prevalence of streptococcus pneumonia strains in general remains unchanged. Large carriage studies from children were conducted during these years. To understand the transmission dynamics of streprococcus pneumonia, as well as the observed diversity and fast serotype replacement, we aim to conduct ABC model selection and parameter learning. This could help to say whether there exists fittness differences between different strains, and what the ultimate effects of vaccination will be.