

Inference on Extended-Spectrum Beta-Lactamase *Escherichia coli* and *Klebsiella pneumoniae* data through $SMC^{\wedge}2$

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We propose a novel stochastic model and parameters inference procedure for the spread of antimicrobial-resistant (AMR) bacteria in a population. The epidemic is treated as a hidden Markov model (HMM) with the latent process given by the individuals' state and the observed process given by the detected infected. The transmission rate of the epidemic takes into account both individuals' locations and covariates, while the recovery rate is the same across the population. The data are sparse in both space and time with a likelihood formulation that includes the sensitivity and specificity of the test. The spatial sparsity in the observation is tackled with synthetic data derived from previous geographical studies on the area of interest. The parameters of the disease are inferred via $SMC^{\wedge}2$, which represents a novel approach in disease modelling. In contrast with competitors methods, $SMC^{\wedge}2$ sequentially targets the posterior over both parameters and latent process and it can explore the sample space more efficiently. The overall work is based on a case study on Extended-Spectrum Beta-Lactamase(ESBL)-producing bacteria: ESBL-producing *Escherichia coli* (*E. coli*) and ESBL-producing *Klebsiella pneumoniae* (*K. pneumoniae*). The data were collected in Malawi as part of the Drivers of Resistance in Uganda and Malawi (DRUM) project. The main findings of our work include: transmission parameters estimates with related connection on within household transmission and across households transmission; spatial decay of the epidemic; estimates of the effective R; spatial location of the epidemics; sensitivity to the parameters.