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Evaulating average MIC over time using a Baysian latent class mixture model: examples from a Salmonella enterica serovar Typhimurium and S. enterica serovar 4,[5],12:i:-

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The minimum inhibitory concentration is a measure of resistance to an antibiotic that is used commonly to describe the resistance of an isolate. As these data arise from a serial dilution experiment, the average MIC cannot be calculated using the standard average formula. As a consequence, MIC data often dichotomized based on a threshold that splits the population into two (resistant and non-resistant) or three categories (susceptible, resistant, intermediate) and the changes the proportion of bacteria in the population evaluated. This approach although valid can result in a less complete picture of the patterns of MIC seen in the bacterial communities, in particular, gradual increases (MIC creep) and decreases (MIC decline) below the threshold of resistance. We used data from MIC results from 15 antibiotic and two Salmonella: Salmonella enterica serovar Typhimurium and S. enterica serovar 4,[5],12:i: to evaluate patterns of mean MIC and the proportion of the population in the resistant population using the Bayesian latent class mixture model.The results of the analysis demonstrated that for some antibiotic there appears to be evidence of MIC creep in the non-resistant population which would otherwise go undetected, as no significant changes in the proportion of the bacterial community in the resistant population are detected. Also, the results document that when the serial dilutions are severely truncated, that application of the Bayesian latent class mixture model might be unsuitable. The use of Bayesian latent class model has the potential to add an additional dimension to the analysis of MIC data obtained from surveillance programs. However, a limited the spectrum of MIC dilutions is also discussed can limit the application for some antibiotic.