STOCHASTIC MODELING OF THE BACTERICIDAL POTENCY

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We develop a stochastic model for bacterial growth, where the size of the bacterial population follows a Bienaymé–Galton–Watson branching process, and the offspring distribution depends on the concentration of the antibiotic.

For a fixed antibiotic concentration c > 0 we provide an estimator for the offspring mean m(c), and show that the estimator is weakly consistent and asymptotically normal. We provide a consistent estimator for the minimal inhibitory concentration (MIC), which is the smallest concentration preventing bacterial growth, an important parameter in microbiology.

As a real data we used measurements of *Chlamydia trachomatis* growth which was analyzed by a novel quantitative PCR method treated by 4 different antibiotics at 12 different antibiotic concentrations. We found that our model fits very well to this data.