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Stochastic de novo emergence of antibiotic resistance

Bacterial evolution of resistance to antibiotics is a major public health concern. Once prevalent, resistant strains can transmit among patients and become difficult to eradicate. However, ultimately, the resistant strains must originate from a *de novo* mutation or horizontal gene transfer event in a single bacterial cell. Using high-replicate experiments with *Pseudomonas aeruginosa* facing streptomycin as a model system, we quantified the probability that a single resistant cell establishes a large surviving lineage. Strikingly, this probability drops to near zero well below the standardly measured minimum inhibitory concentration (MIC) of the antibiotic. We show that this result can be explained by a simple model in which the antibiotic has partial inhibitory effects below the MIC, and each cell has an independent chance of establishment.

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