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# INCORPORATING EVOLUTIONARY DYNAMICS INTO INFECTION MODELS WITH ANTIBIOTIC TREATMENT

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In this study we explore the within-host evolutionary dynamics of bacteria under antibiotics and the pressure by the immune system. To describe a typical infection, we use a mathematical model based on ordinary differential equations, combined with a stochastic component for pathogen evolution in a 2-dimensional trait space: fitness cost and fitness advantage of resistance mutations. Exploring different mechanisms of drug action, dosage and duration of treatment, we examine the heterogeneous bacterial trait combinations that emerge and are selected under different regimes. We find that the speed of bacterial escape during treatment depends critically on population size, mutation rate, and local distribution of fitness effects.