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An Empirically Calibrated Model of Cell Fate Decision Following Viral Infection. SETH COLEMAN, OLEG IGOSHIN, Center for Theoretical Biological Physics - Rice University, IDO GOLDING, Baylor College of Medicine; Center for Theoretical Biological Physics - Rice University — The life cycle of the virus (phage) lambda is an established paradigm for the way genetic networks drive cell fate decisions. But despite decades of interrogation, we are still unable to theoretically predict whether the infection of a given cell will result in cell death or viral dormancy. The poor predictive power of current models reflects the absence of quantitative experimental data describing the regulatory interactions between different lambda genes. To address this gap, we are constructing a theoretical model that captures the known interactions in the lambda network. Model assumptions and parameters are calibrated using new single-cell data from our lab, describing the activity of lambda genes at single-molecule resolution. We began with a mean-field model, aimed at exploring the population averaged gene-expression trajectories under different initial conditions. Next, we will develop a stochastic formulation, to capture the differences between individual cells within the population. The eventual goal is to identify how the post-infection decision is driven by the interplay between network topology, initial conditions, and stochastic effects. The insights gained here will inform our understanding of cell fate choices in more complex cellular systems.

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