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Collective decisions among bacterial viruses RICHARD JOH, School of Physics, Georgia Institute of Technology, YURIY MILEYKO, Department of Mathematics, Duke University, EBERHARD VOIT, Department of Biomedical Engineering, Georgia Institute of Technology, JOSHUA WEITZ, School of Biology, Georgia Institute of Technology — For many temperate bacteriophages, the decision of whether to kill hosts or enter a latent state depends on the multiplicity of infection. In this talk, I present a quantitative model of gene regulatory dynamics to describe how phages make collective decisions within host cells. Unlike most previous studies, the copy number of viral genomes is treated as a variable. In the absence of feedback loops, viral mRNA transcription is expected to be proportional to the viral copy number. However, when there are nonlinear feedback loops in viral gene regulation, our model shows that gene expression patterns are sensitive to changes in viral copy number and there can be a domain of copy number where the system becomes bistable. Hence, the viral copy number is a key control parameter determining host cell fates. This suggests that bacterial viruses can respond adaptively to changes in population dynamics, and can make alternative decisions as a bet-hedging strategy. Finally, I present a stochastic version of viral gene regulation and discuss speed-accuracy trade-offs in the context of cell fate determination by viruses.

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