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The Stochastic Signature of Mixed Promoter States LEONARDO SEPULVEDA, Department of Biochemistry and Molecular Biology, Baylor College of Medicine and Center for Theoretical Biological Physics, Rice University, IDO GOLDING, Department of Physics and Center for the Physics of Living Cells, University of Illinois at Urbana-Champaign — Gene promoters typically contain multiple binding sites for transcription factors. This allows for distinct transcription-factor binding configurations, each characterized by a different transcriptional activity of the regulated gene. However, at a given transcription-factor concentration, the promoter is not expected to exhibit a single configuration, but, instead, a "mixed state" with fractional probabilities for the different configurations. What is the nature of these mixed promoter states at the single-cell level? We investigate this question by measuring simultaneously, in individual cells, the concentration of the CI transcription factor and the transcriptional output of the regulated promoter, P_{RM}, in *E. coli*. We use the mRNA copy-number statistics to reconstruct the stochastic kinetics of the different promoter configurations and calculate their probabilities at each CI concentration. We find that the mRNA distribution for cells in a mixed state can be described as a convolution of the pure-state distributions, indicating rapid switching between the pure promoter states. Thus, mixed promoter states do not result in different cell populations but instead appear as a new, well-defined promoter activity.

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