

Abstract Submitted  
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**Complex kinetics of the  $\lambda$  Bacteriophage genetic switch**<sup>1</sup> LAURA FINZI, Emory University, CARLO MANZO, Institute of BioEngineering of Catalugna, CHIARA ZURLA, Georgia Institute of Technology, DAVID DUNLAP, Emory university — The kinetics of the  $\lambda$  bacteriophage repressor-mediated DNA loop formation and breakdown were characterized by Tethered Particle Microscopy (TPM). A generalized likelihood ratio test was first applied to determine the location of change points (cp) in the TPM trace. Expectation-maximization (EM) clustering and the Bayesian information criterion were then used for accurate determination of the number of states accessible to the system. This procedure (cp-EM) allows objective and quantitative determination of TPM change points without the artificial time resolution limitations that arise from filtering and thresholding. Only two states were identified, which corresponded to the looped to the unlooped DNA configurations. The probability distribution function of the looped and unlooped DNA state dwell times revealed a complex kinetics. In particular, it was found that a stretched exponential provided a satisfactory fitting for the probability distribution of the unlooped state dwell times, while the dwell time distribution for the looped DNA state could not be fitted with a standard pdf; we observed, however, that a power law decay fits well the long dwell times. A mechanism is proposed to explain this kinetic behavior, where  $\lambda$  repressor non-specific binding to DNA may play an important physiological role.

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