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Listening to the Noise: Random Fluctuations Reveal Gene Network Parameters BRIAN MUNSKY, Los Alamos National Laboratory, BROOKE TRINH, MUSTAFA KHAMMASH, University of California at Santa Barbara — The cellular environment is abuzz with noise originating from the inherent random motion of reacting molecules in the living cell. In this noisy environment, clonal cell populations exhibit cell-to-cell variability that can manifest significant prototypical differences. Noise induced stochastic fluctuations in cellular constituents can be measured and their statistics quantified using flow cytometry, single molecule fluorescence *in situ* hybridization, time lapse fluorescence microscopy and other single cell and single molecule measurement techniques. We show that these random fluctuations carry within them valuable information about the underlying genetic network. Far from being a nuisance, the ever-present cellular noise acts as a rich source of excitation that, when processed through a gene network, carries its distinctive fingerprint that encodes a wealth of information about that network. We demonstrate that in some cases the analysis of these random fluctuations enables the full identification of network parameters, including those that may otherwise be difficult to measure. We use theoretical investigations to establish experimental guidelines for the identification of gene regulatory networks, and we apply these guideline to experimentally identify predictive models for different regulatory mechanisms in bacteria and yeast.

Brian Munsky
Los Alamos National Laboratory

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