Stochastic fluctuations can cause identical cells or individual molecules to exhibit wildly different behaviors. Often labeled "noise," these fluctuations are frequently considered a nuisance that compromises cellular responses, complicates modeling, makes predictive understanding and control all but impossible. However, if we examine fluctuations more closely and match them to discrete stochastic analyses, we discover virtually untapped, yet powerful sources of information and opportunities. In this talk, I will present our collaborative endeavors to integrate single-cell and single-molecule experiments with precise stochastic analyses to gain new insight and quantitatively predictive understanding for signal-activated gene regulation. I will explain how we experimentally quantify transcription dynamics at high temporal and spatial resolutions; how we use precise computational analyses to model this data and efficiently infer biological mechanisms and parameters; how we predict and evaluate the extent to which model constraints (i.e., data) and uncertainty (i.e., model complexity) contribute to our understanding. I will finish with the discussion of new opportunities in which noise analysis not only helps us to better understand gene regulation phenomena, but where it actually introduces new opportunities to precisely control these phenomena.