**Chemical fluctuation theorem
governing *vibrant* reaction networks in living cells**

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To understand how accurately living cells can control their biological functions, it is essential to construct a rigorous mathematical description for chemical dynamics of intracellular networks interacting with complex and hidden cell environment. In this talk, we introduce a novel model and stochastic kinetics for intracellular networks interacting with cell environment, employing a complete description of cell state dynamics and its coupling to the system network. For a general model of intracellular birth-death processes, we present the chemical fluctuation theorem (CFT) that relates microscopic dynamics of the birth and death processes to the cell-to-cell variation in the product number. Combined with a new mathematical description of the gene expression network, CFT provides an excellent quantitative explanation of the cell-to-cell variation in the mRNA and protein levels for various recently investigated systems in a unified manner. Our analysis of mRNA counting statistics in *Escherichia coli* shows that the transcription of an active gene is a strongly non-Poisson process whose rate coefficient is a dynamic stochastic variable with either oscillatory or monotonically decaying time correlation function (TCF). The shape of the TCF of the rate coefficient has an important consequence for the cellular control over the transcriptional noise. This work demonstrates a promising, new approach in quantitative biology, attempting to make complex dynamics of chemical reactions in living cells and its biological consequence accessible to a rigorous mathematical description.