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**Applications of queueing theory to stochastic models of gene expression<sup>1</sup>**

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The intrinsic stochasticity of cellular processes implies that analysis of fluctuations ('noise') is often essential for quantitative modeling of gene expression. Recent single-cell experiments have carried out such analysis to characterize moments and entire probability distributions for quantities of interest, e.g. mRNA and protein levels across a population of cells. Correspondingly, there is a need to develop general analytical tools for modeling and interpretation of data obtained from such single-cell experiments. One such approach involves the mapping between models of stochastic gene expression and systems analyzed in queueing theory. The talk will provide an overview of this approach and discuss how theorems from queueing theory (e.g. Little's Law) can be used to derive exact results for general stochastic models of gene expression. In the limit that gene expression occurs in bursts, analytical results can be obtained which provide insight into the effects of different regulatory mechanisms on the noise in protein steady-state distributions. In particular, the approach can be used to analyze the effect of post-transcriptional regulation by non-coding RNAs leading to new insights and experimentally testable predictions.

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