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Quantifying noise modulation from coupling of stochastic expression to cellular growth: an analytical approach

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The overexpression of many proteins can often have a detrimental impact on cellular growth. This expression-growth coupling leads to positive feedback – any increase of intracellular protein concentration reduces the growth rate of cell size expansion that in turn enhances the concentration via reduced dilution. We investigate how such feedback amplifies intrinsic stochasticity in gene expression to drive a skewed distribution of the protein concentration. Our results provide an exact solution to this distribution by analytically solving the Chapman-Kolmogorov equation, and we use it to quantify the enhancement of noise/skewness as a function of expression-growth coupling. This analysis has important implications for the expression of stress factors, where high levels provide protection from stress, but come at the cost of reduced cellular proliferation. Finally, we connect these analytical results to the case of an actively degraded gene product, where the degradation machinery is working close to saturation.

Keywords: gene expression, Chapman-Kolmogorov equation, feedback in dilution, moment analysis

References

[1] I. Zabaikina, Z. Zhang, C. Nieto, P. Bokes, A. Singh, Quantifying noise modulation from coupling of stochastic expression to cellular growth: an analytical approach, accepted for publication in 2023 American Control Conference (ACC), bioRxiv, 2022.