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Stochastic gene expression in cells undergoing division

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Stochasticity in gene expression is one of the most important problems of quantitative biology. It has been shown that, in the systems as small as living cells, production of proteins is strongly affected by random fluctuations coming from various sources. As a result, the biological noise is a meaningful factor influencing cellular processes and cell-fate decisions. The particular questions explored within the field of quantitative biology are, among others, the correct identification of noise sources and correct estimation of noise parameters, e.g., frequencies and sizes of the random bursts of protein production.

We propose a stochastic model of gene expression in cells undergoing division. The model combines a deterministic approximation of protein degradation and the two sources of noise: 1) Random bursts of protein production, and 2) more or less random duration of the cell cycle. Random partitioning of proteins between daughter cells is also possible as the third source of noise.

In the classical model proposed by the Xie group, the effect of cell division was tacitly identified with the effect protein degradation. We show that this may not be a correct assumption and the values of mean burst size and mean burst frequency inferred from the experiments using the classical model may be wrong. We show that our model provides more reasonable estimates for these quantities. Moreover, our model demonstrates that the "noise floor", observed in the experiments and previously ascribed to an unidentified extrinsic noise, may be the effect of cell division. Our model sets physical constraints, based on the degree of randomness in cell cycle duration, for the levels of noise in gene expression.

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