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**The effect of extrinsic noise on the dynamics of simple gene network motifs**

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Cellular processes do not follow deterministic rules; even in identical environments genetically identical cells can make random choices leading to different phenotypes. This randomness originates from fluctuations present in the biomolecular interaction networks. Most previous work has been focused on the intrinsic noise of these networks. Yet, especially for high-copy-number biomolecules, extrinsic or environmental noise has been experimentally shown to dominate the variation. Here we develop an analytical formalism that allows for calculation of the combined effect of intrinsic and extrinsic noise on gene expression motifs. We introduce a new and generic method for modeling bounded extrinsic noise as an auxiliary species in the master equation. We focus our study on motifs that can be viewed as the building blocks of genetic switches: a non-regulated gene, a self-inhibiting gene, and a self-promoting gene. The role of the extrinsic noise properties (magnitude, correlation time, and distribution) on the statistics of interest are systematically investigated, and the effect of fluctuations in different reaction rates is compared. Due to its analytical nature, our formalism can be used to quantify the effect of extrinsic noise on the dynamics of biochemical networks and can also be used to improve the interpretation of data from single-cell gene expression experiments.