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Stochastic models in quantitative biology: how they fail and why we need them (I)

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Many biological processes in cells are complex yet sparsely characterized. Constructing physical models of such systems then often requires making many assumptions based on guesswork. Instead of ignoring or guessing unknown details in complex processes we have derived universal balance relations to rigorously characterize stochastic fluctuations in incompletely specified systems. Specifying some features of a system while leaving everything else unspecified then allows us to establish physical performance bounds for classes of intracellular processes. Additionally, we can turn general network invariants into experimental data analysis tools. For example, exploiting naturally occurring cell-to-cell variability allowed us to test specific hypotheses about gene expression, showing that observed fluctuations in *E. coli* contradict the majority of published models of stochastic gene expression.

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