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Optimal Information Processing in Biochemical Networks

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A variety of experimental results over the past decades provide examples of near-optimal information processing in biological networks, including in biochemical and transcriptional regulatory networks. Computing information-theoretic quantities requires first choosing or computing the joint probability distribution describing multiple nodes in such a network — for example, representing the probability distribution of finding an integer copy number of each of two interacting reactants or gene products while respecting the 'intrinsic' small copy number noise constraining information transmission at the scale of the cell. I'll given an overview of some recent analytic and numerical work facilitating calculation of such joint distributions and the associated information, which in turn makes possible numerical optimization of information flow in models of noisy regulatory and biochemical networks. Illustrating cases include quantification of form-function relations, ideal design of regulatory cascades, and response to oscillatory driving.