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Near-Perfect Adaptation in the *E. coli* Chemotaxis Signal Transduction Network YANG YANG, SIMA SETAYESHGAR, INDIANA UNIVERSITY TEAM — Biochemical reaction networks constitute the computing language of the cell, from converting external stimuli into appropriate intracellular signals to regulating gene expression. Precise adaptation is an important property of many signaling networks, allowing compensation for continued stimulation without saturation. Furthermore, a common feature of intracellular reaction networks is the ability to operate in a noisy environment where concentrations of key components, such as signaling molecules and enzymes controlling reaction rates are typically small and therefore fluctuations in their numbers are significant. In the context of the well-characterized *E. coli* chemotaxis signal transduction network, we present a new computational scheme that explores surfaces in the space of total protein concentrations and reaction rates on which (near-)perfect adaptation holds. The resulting dependencies between parameters provide conditions for (near-)perfect adaptation as well as ranges of numerical values for parameters not reliably known from experiments. We generalize the applicability of this scheme to other signaling networks.

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