

Abstract Submitted
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Topologies for perfect adaptation in gene transcription WENJIA SHI, CHAO TANG, Center for Quantitative Biology, Peking University — Adaptation is commonly used in sensory systems and signaling networks to allow the detection of further stimuli. Despite enzymatic network topologies for adaptation have been investigated systematically, the topology of transcriptional network that could perform adaptation still remains unclear, due to the complexity of transcriptional regulation. Here, we systematically investigated all three-node transcriptional networks, and found the topologies of transcriptional networks for adaptation are different from that of enzymatic ones. While both negative feedback loop (NFBL) and incoherent feed forward loop (IFFL) are capable of performing adaptation analytically, a positive self-regulation on buffer node is necessary for NFBL topology and more flexible structures emerge for IFFL than that of enzymatic networks. Most of the simulation results agree with analytical predictions. This study may explain the mechanism of adapted gene regulation behavior and supply a design table for gene regulatory adaptation.

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