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Tuning stochastic transition rates in a bistable genetic network. VIJAY CHICKARMANE, California Institute of Technology, CARSTEN PETERSON, Lund University, Sweden — We investigate the stochastic dynamics of a simple genetic network, a toggle switch, in which the system makes transitions between the two alternative states. Our interest is in exploring whether such stochastic transitions, which occur due to the intrinsic noise such as transcriptional and degradation events, can be slowed down/speeded up, without changing the mean expression levels of the two genes, which comprise the toggle network. Such tuning is achieved by linking a signaling network to the toggle switch. The signaling network comprises of a protein, which can exist either in an active (phosphorylated) or inactive (dephosphorylated) form, and where its state is determined by one of the genetic network components. The active form of the protein in turn feeds back on the dynamics of the genetic network. We find that the rate of stochastic transitions from one state to the other, is determined essentially by the speed of phosphorylation, and hence the rate can be modulated by varying the phosphatase levels. We hypothesize that such a network architecture can be implemented as a general mechanism for controlling transition rates and discuss applications in population studies of two differentiated cell lineages, ex: the myeloid/erythroid lineage in hematopoiesis.

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