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Autonomous Boolean modeling of gene regulatory networks[1]

JOSHUA SOCOLAR, MENGYANG SUN, Physics Department and Center for Systems Biology, Duke University, XIANRUI CHENG, Department of Chemical and Systems Biology, Stanford University — In cases where the dynamical properties of gene regulatory networks are important, a faithful model must include three key features: a network topology; a functional response of each element to its inputs; and timing information about the transmission of signals across network links. Autonomous Boolean network (ABN) models are efficient representations of these elements and are amenable to analysis. We present an ABN model of the gene regulatory network governing cell fate specification in the early sea urchin embryo, which must generate three bands of distinct tissue types after several cell divisions, beginning from an initial condition with only two distinct cell types. Analysis of the spatial patterning problem and the dynamics of a network constructed from available experimental results reveals that a simple mechanism is at work in this case.

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