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Analysis of a dynamic model of guard cell signaling reveals the stability of signal propagation XIAO GAN, RKA ALBERT, Pennsylvania State Univ — Analyzing the long-term behaviors (attractors) of dynamic models of biological systems can provide valuable insight into biological phenotypes and their stability. We identified the long-term behaviors of a multi-level, 70-node discrete dynamic model of the stomatal opening process in plants. We reduce the model's huge state space by reducing unregulated nodes and simple mediator nodes, and by simplifying the regulatory functions of selected nodes while keeping the model consistent with experimental observations. We perform attractor analysis on the resulting 32-node reduced model by two methods: 1. converting it into a Boolean model, then applying two attractor-finding algorithms; 2. theoretical analysis of the regulatory functions. We conclude that all nodes except two in the reduced model have a single attractor; and only two nodes can admit oscillations. The multistability or oscillations do not affect the stomatal opening level in any situation. This conclusion applies to the original model as well in all the biologically meaningful cases. We further demonstrate the robustness of signal propagation by showing that a large percentage of single-node knockouts does not affect the stomatal opening level. Thus, we conclude that the complex structure of this signal transduction network provides multiple information propagation pathways while not allowing extensive multistability or oscillations, resulting in robust signal propagation. Our innovative combination of methods offers a promising way to analyze multi-level models.

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