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Generation of nonlinear-differential-equations system from a model of Boolean relationships in Arabidopsis salt stress network

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Generation of nonlinear-differential-equations system from a model of Boolean relationships in Arabidopsis salt stress network.

Boolean modeling of complex biological systems is straightforward, and allows for analysis on a discrete time scale. However, parameters associated with these models may be difficult to interpret. These models also may have difficulty in recovering the transient dynamics of some components. We implemented a standard composition modeling strategy to computationally generate a set of nonlinear differential equations based on a matrix of Boolean relationships. The algorithm produces code that can be directly pasted into a Matlab file for immediate simulation. As proof-of-concept, we converted a Boolean model of the salt stress network in Arabidopsis that is made of 60 network Boolean components (Albert et al., 2017) to a system of nonlinear differential equations. The resulting system of equations improve the recovery of the transient dynamics of key components in the signaling cascade, such as phosphatidic acid (PA), phospholipase D (PLD α), and SNRK2 protein kinase activity. Furthermore, the resulting set of equations allow us to conduct frequency response analysis (FRA) on the plants against abscisic acid (ABA). In this presentation, we show extreme responses of the plants against oscillated application of ABA, which is predicted by the newly constructed system of nonlinear differential equations.