THE COMPUTABLE PLANT: A MATHEMATICAL FRAMEWORK FOR DEVELOPMENTAL MODELING IN PLANTS

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We utilize symbolic processing to automatically generate both chemical and differential equations describing biochemical regulatory networks. Even modest networks have >10,000 reactions, with the number of ODEs increasing combinatorically with the number of chemical species involved. This technique has been verified in simulations of mitogen activated protein kinases (MAPK), proteins that play a central role in a wide variety of processes including cell cycle regulation, growth, stress, memory development, wound healing, and cancer pathology.