Numerical Analysis of Steady State Patterns in Cell-Based Auxin Transport Models

 $\underline{\text{Delphine Draelants}}, \text{Przemyslaw Klosiewicz}, \text{Jan Broeckhove}, \text{Gerrit T.S.}$

Beemster, Wim Vanroose Universiteit Antwerpen Delphine.Draelants@ua.ac.be, Przemyslaw.Klosiewicz@ua.ac.be, Jan.Broeckhove@ua.ac.be, Gerrit.Beemster@ua.ac.be, Wim.Vanroose@ua.ac.be

Keywords: bifurcation analysis, pattern formation, parameter dependence. Cell-based models that describe the pattern formation and the flow of chem-

icals in plant organs are important building blocks in a multiscale simulation of a whole plant. An example of an important mechanism is the transport of the hormone auxin throughout the plant's organs because it is closely related to the growth characteristics of roots, shoots and leaves. Based on experimental evidence, a number of cell-based auxin transport models were developed. Due to the intercellular transport of chemicals, these models are complex dynamical systems with a large set of endogenous and exogenous parameters. The models share underlying mathematical principles w.r.t. steady state pattern formation which plays a central role in the growth and development of plant organs. This calls for a uniform computational approach. In our research we focus on computer simulations of general cellbased transport models and more specifically we use numerical bifurcation analysis to study the steady state patterns. It indicates how the stability of patterns is lost or gained as the system parameters change. Bifurcation analysis of ODEs is widespread in biology and various numerical tools produce bifurcation diagrams. However, these automatic tools do not work for large scale problems, such as biological patterning. Indeed, realistic simulations of large tissues that take multiple interacting chemicals into account give rise to very large and sparse systems of coupled ODEs. We analyze recent large scale transport models with new mathematical and computational tools that enable quantitative prediction of the bifurcations that appear at the macroscopic level in these models. This allows us to predict the patterns and self-similar solutions that appear during organ growth and to see how their stability changes as endogenous parameters are modified or as externally applied changes are enforced. We use these methods to compare the model output with observed data such as the auxin distribution and venation patterns in leaves in order to get a better understanding of the processes that regulate organ development in plants.