

Computational modelling approach to understanding shoot architecture including plant branching and flowering

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Abstract

While the network topologies of developmental regulatory networks (DRNs) governing plant architectural traits have been elucidated in the literature, little is known regarding how these networks translate into the expression of a plant in 3D space. Our laboratory has developed an R package (PSoup) which parses visual representations of plant DRNs and computes their steady-state values. PSoup has successfully recapitulated phenotypes of branching mutants and mutant-wild-type rootstock-scion combinations in garden pea. However, PSoup cannot readily account for the influence of dynamical changes in ontogenetic processes such as basal branches affecting growth of aerial branches or agricultural practices like pruning.

To enhance our ability to model phenotypic plasticity, we present L-Soup, an integration of PSoup with functional-structural plant models (FSPMs). FSPMs allow for phenomena such as hormonal fluxes, carbon allocation and light propagation to be modelled in 3D space. Our approach leverages PSoup as a 'decision-maker' at each developmental step of the FSPM. Through this, ontogenetic responses arise as emergent properties of the FSPM, rather than by being hardcoded into the model. Such flexibility empowers plant developmental biologists to better understand how DRNs interplay with the determinants of shoot architecture in a spatially- and temporally-aware fashion.