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*Modelling clonal structure of saltmarsh Spartina grasses*

For *Spartina* spp., clonal spread via extension of rhizomes represents a major means of colonization within saltmarsh restoration sites. Both dominant halotolerant grass species *Spartina alterniflora* and *Spartina patens* have remarkably different rhizomal structures, which affect both their rate of spread and their competitive ability. The rhizomal three-dimensional structure of both species is only superficially understood despite its apparent importance. The present work offers a detailed quantification of the rhizomal structure for both plant species and defines a set of growth rules from which this structure could arise. Quantification of rhizomal structure includes internode length, branching angles, short internode numbers and length, and node counts within functional rhizome sections, among other measurements. The rules include branching potential per node, apical bud activity variability between zones, and the sequence of functional sections. Rules hold regardless of the position within the plant while quantities change. To test whether these quantifications and rules are truly able to produce the observed structure, we implement them in a deterministic node-based three-dimensional model using Julia. As of now, the simulations capture the difference in forms characterizing each species quite well, although the details of these forms need further refinements. The results outline the need to understand both plant developmental processes and plant structures' geometric properties to obtain a set of rules that lead to a biologically realistic structure.