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Exploring symmetries in plant architectures

Romain Azais¹, Salaheddine Habibeche², Farah Ben-Naoum², Christophe Godin¹

¹ *Laboratoire Reproduction et Développement des Plantes, Univ Lyon, ENS de Lyon, UCB Lyon 1, CNRS, INRAE, Inria, F-69342, Lyon, France*

² *EEDIS Laboratory, University of Djillali Liabes of Sidi-Bel-Abbes, Algeria*

For correspondence: romain.azais@inria.fr and christophe.godin@inria.fr

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Symmetries and invariance

Symmetries are ubiquitous in living forms and often reflect repetition in the mechanisms of morphogenesis. They are closely related to the mathematical concept of invariance. An object x is said to be invariant under a certain operator T when it remains unchanged under the action of the operator, i.e. $Tx = x$. Observing symmetries means identifying operators under the action of which an object remains invariant. However, in living forms, because of intrinsic biological noise and environmental effects, symmetries are often imperfect and correspond to $Tx \approx x$. Here, we investigate how these concepts can be applied to identify symmetries in plant architectures.

Symmetries in plant architectures: the swap operator

A plant architecture can be modeled as a mathematical rooted tree (Godin and Caraglio, 1998), i.e. a connected graph with no cycle in which a node, called the root, has been selected. In addition, each node in the tree may carry some additional pieces of information such as the type and the geometry of the elementary component of the plant, or even its physiological state. A subtree is a subpart of a tree made of a node and all its descendants in the tree. Macroscopic parts that are susceptible to be similar in plant architectures are often subtrees (Arber, 1950; Ferraro et al., 2005; Godin and Ferraro, 2010). In order to identify the symmetries of plant architectures, we therefore introduce the swap operator that swaps two subtrees (see Fig. 1).

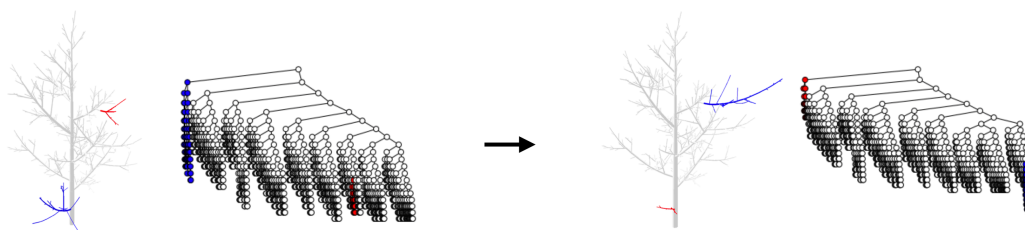


Figure 1: Illustration of the swap operator: red and blue subtrees in the original data (left) are swapped both in the mathematical tree and in the 3D plant architecture it models (right).

However, not every pair of subtrees can be swapped: if a subtree appears as a descendant of another, their swap does not make sense. A set of subtrees that can be swapped pairwise forms an antichain for the inclusion partial order: these subtrees are not related to each other by parent-child relationships. Now, we are going to see how antichains can be used to formalize the idea of symmetric (or close to symmetric) structures in trees.

Maximal symmetry antichain

A symmetry antichain is an antichain of subtrees such that their swap preserves the architecture of the plant, i.e. for any pair of subtrees t and s in the antichain, the tree T' obtained after their swap is equal (or at least very similar) to the original tree T . Such a symmetry antichain is said maximal when there is no other subtree within T that can be

swapped with one of the antichain while preserving the general architecture. Detecting the symmetries actually means identifying all the maximal symmetry antichains.

In a real plant architecture, one does not expect to observe exact symmetries. One must therefore be able to quantify the similarity between subtrees. For this, we use the tree edit distance developed in (Zhang, 1996) and already used for the comparison of plant architectures in (Godin and Ferraro, 2010). We have thus developed an algorithm to build all maximal symmetry antichains of the plant architecture that proceeds through a clustering of all its subtrees based on the above tree edit distance, instead of an exact match.

Visualization of symmetries

Within an antichain, the subtrees are not related, but from one maximal symmetry antichain to another, this may be the case. We can therefore consider the graph of maximal symmetry antichains: two maximal symmetry antichains are linked by an edge when subtrees of one appear as descendants of subtrees of the other, and the weight of the edge corresponds to the proportion of such links. Using this graph, we can therefore not only observe all the symmetries of a plant architecture but also their nesting, which represents a major difficulty when dealing with tree data (see Fig. 2). This symmetry graph actually represents the symmetry signature of the tree architecture.

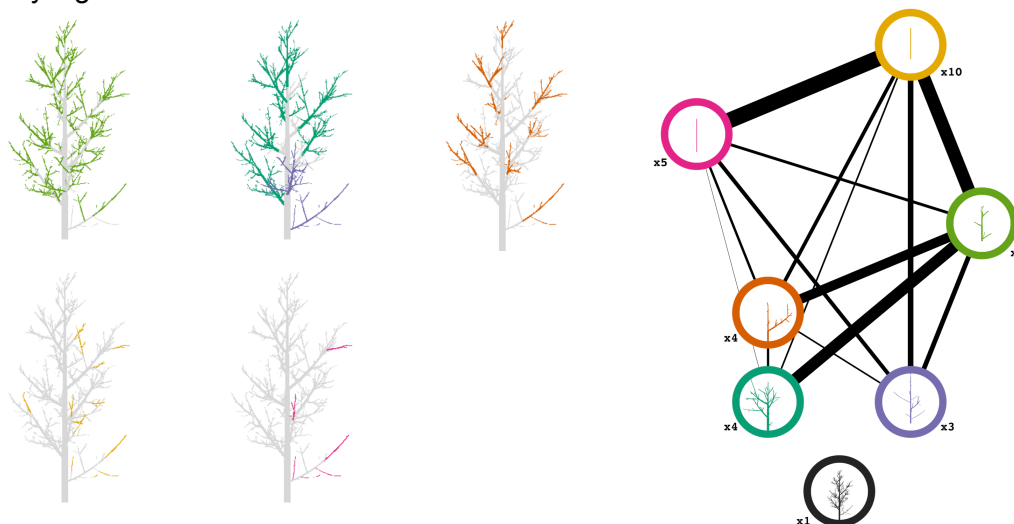


Figure 2: This 3D plant architecture presents 6 maximal symmetry antichains (identically colored subparts of the plant) which nesting links are given by the graph on the right. At the top of the graph, we find the smallest subtrees of the plant. At the bottom, we have the largest structures that contain all the others.

Towards reverse engineering?

By observing the symmetries of a plant, we can better characterize its structure but also study the production and growth mechanisms that generated it. The maximal symmetry antichains we have identified in this work were probably generated by identical biological, chemical and mechanical processes. This can be verified on simulated plants for which the construction rules are known. This also provides a new conceptual tool for the analysis of the functional origin (molecular, biophysical) of structure repetitions in plant architectures.

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