

Reconstructing Plant Architecture from 3D Laser scanner data

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Introduction

Automatic acquisition of plant phenotypes constitutes a major bottleneck in the construction of quantitative models of plant development. This issue needs to be addressed to build accurate models of plant, useful for instance in agronomic and forestry applications. In this work, we present a method for reconstructing plant architecture from laser scanner data. A dedicated evaluation procedure based on a detailed comparison between expert and automatic reconstruction was developed to quantify accurately the quality of the reconstruction method.

Previous work

In the last decade, digitizing techniques were developed to acquire plant architectures using sonic or electromagnetic devices. However, these manual techniques are time consuming and difficult to carry out in the field. Recently, first works used laser scanner data to identify the structure of trees. A first successful method was proposed by Xu *et al.* (2007). Points were first connected with their neighbors to form a graph. This graph was segmented into clusters of points according to the distance to the root. Centers of the clusters were used to produce the skeleton of the tree. This method produces realistic looking trees but is sensitive to occlusion and sparse point density. Here we use a space colonization algorithm (SCA) to improve the robustness of the reconstruction algorithms to occlusion and perturbed data. SCA (Runions *et al.*, 2007) were introduced to generate plausible artificial branching structures in a volume specified by 3D points called attractors. Here we suggest adapting SCA in a new way to reconstruct faithfully real leaf-free plant architectures observed with laser scans.

Material

We use two types of material: laser scanned plants and virtually scanned models. For the first type, we use city trees (*Tilia x vulgaris*) growing at street alley from Helsinki, Finland scanned with *Leica Geosystems HDS 2500 laser scanner* and *Basis Software Surphaser 25HSX*. The second type of data is generated from 3D plant models of trees acquired manually by experts with a magnetic technique. In this study, we used an apple tree. Such models are mainly interesting for validation purpose. Point sets are generated by virtually scanning the 3D models using Z-Buffer capabilities of graphic cards. Point sets usually contain different point patterns. On the trunk and the biggest branches, points are usually dense and typically distributed on a 3D surface rather than volumes. By contrast, points belonging to small branches or twigs are sparser. Furthermore, some data are missing due to occlusion.

Method

Reconstruction from laser scanner data - Our method is based on the following steps:

1. *Point contraction*: Points are shifted from the border of the shape towards its medial axis. Since normals are not available from scans, we used a simple adaptive contraction scheme inspired from Giannitrapani *et al.* (1999). Let $P = \{p_i, i \in [1, N]\}$ be the points set. Let S_i^R be the neighborhood of p_i defined as the set of points p_j at a distance less than R from p_i . The original contraction operation is defined as transforming each point p_i by the centroid c_i^R of its neighborhood S_i^R . However, this scheme has some validity only in dense regions. Thus, we

adapted it according to the local density λ_i of the point set. λ_i is defined as k / r^2 , with r radius of the enclosing sphere of the k nearest neighbors of p_i . The radius of contraction of p_i is thus redefined as a linear interpolation between predefined minimum and maximum radii of contraction, R_{\min} and R_{\max} , according to the rank of the density λ_i in the range of densities $[\lambda_{\min}, \lambda_{\max}]$ of the point set.

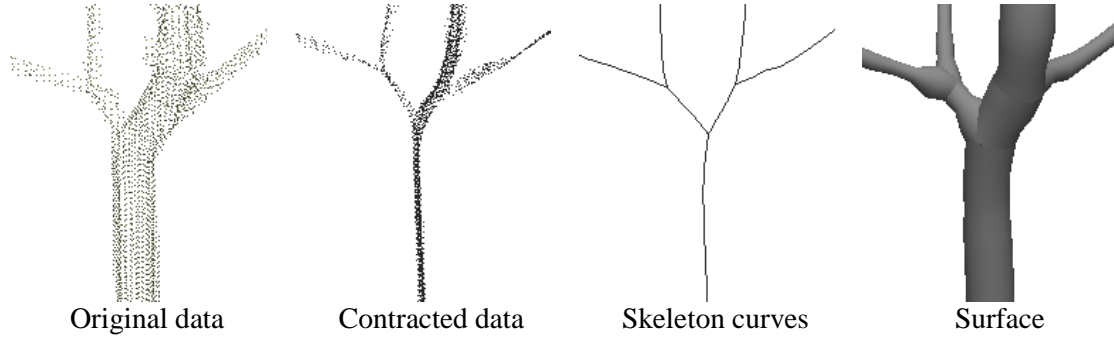


Figure 1: The software pipeline for reconstruction 3D Plant Models

2. *Skeleton reconstruction:* We then used the contracted form of points set to extract the skeleton of the tree. Our work is inspired from the space colonization algorithm (SCA) for generating artificial branching structures. We start from an initial node at the basis of the trunk. The procedure iteratively creates a *skeleton* as an arborescence of nodes by adding new nodes from existing ones in the direction of the attractors. In this work, contracted points are used as attractors. Each existing node has some *perception volumes* that allow it to sense the surrounding space and check if some attractors are around. In the positive case, a new node is created. A conical volume of perception, defined by a given angle θ and a distance r_p , is used. From a skeleton node, new nodes can grow in several directions according to the different perception volumes (see Fig. 2). The growth direction of a new node is estimated as the sum of normalized direction vectors toward all influencing attractors. Attractors closed to a skeleton node are then deleted. This algorithm is repeated until the attractor set is empty.

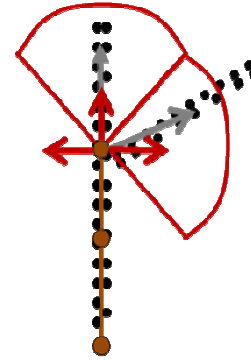


Figure 2: A step of SCA

Directions of perception can be constrained to some phyllotaxic patterns (in Fig. 2, they are initiated in decussate positions) or, in dense region, estimated from statistical analysis of the local point set around the node. For this, a principal direction is estimated for each attractor from a principal component analysis (PCA) of its neighborhood. Clustering of these principal directions using Gaussian mixture models gives us local main directions of the clouds and thus possible branch directions.

3. *Surface reconstruction:* An average radial distance between the node and the attractors is computed. Then, a set of generalized cylinders is computed to define the surface of the branches.

Evaluating the reconstructed model

Quantitative validation of the reconstructed architecture makes it possible to assess relevance and accuracy of models in their biological context. To address this problem, we quantified the differences between the structure produced by the reconstruction method and the actual structure of the tree. Digitized trees manually acquired by expert are used as reference and virtual scans as input of the reconstruction procedure. Formally, the structures are represented as multi-scale tree graphs (MTGs) (Godin *et al.*, 1998). Our evaluation procedure is based on the topological comparison method proposed in Ferraro *et al.* (2000) that we parameterize with geometrical information. Evaluation of the distance between two tree graphs consists in determining a sequence of edit operations, namely insertion, deletion and substitution of vertices, of minimum cost needed to convert one tree-graph into the other. As a by-product, a mapping of nodes of both graphs is given by the evaluation and thus gives reconstructed and missed parts.

Two problems need to be addressed to setup such a procedure. First, the expert plant has been decomposed and measured at specific scales (internodes, shoots and axes). The reconstructed plant is a set of segments of fixed length. To compare both plants we need to define a common scale of decomposition. For this purpose, the MTG are used to create a more macroscopic representation of the tree structures. The scale of comparison that we investigated considers segments between branching points. It leads to a fast evaluation but may overestimate differences in the case of missing branching points in the reconstruction.

In a second step, the cost of the different edit operations needs to be defined. We use geometrical criteria. For substitutions, differences between two compared nodes have to be evaluated. A geometrical comparison is made, defined as the Hausdorff's distance between skeleton curves of the compared nodes. It comes down to compute the maximum distance between the points defining skeleton curve of the nodes. For insertions and deletions, the cost is proportional to the size of the skeleton curve of the node.

Results

The proposed pipeline has been tested on various tree datasets. The results of the 3D reconstructed models are presented in Fig. 3. Visually, the general appearance and density of branches is respected.

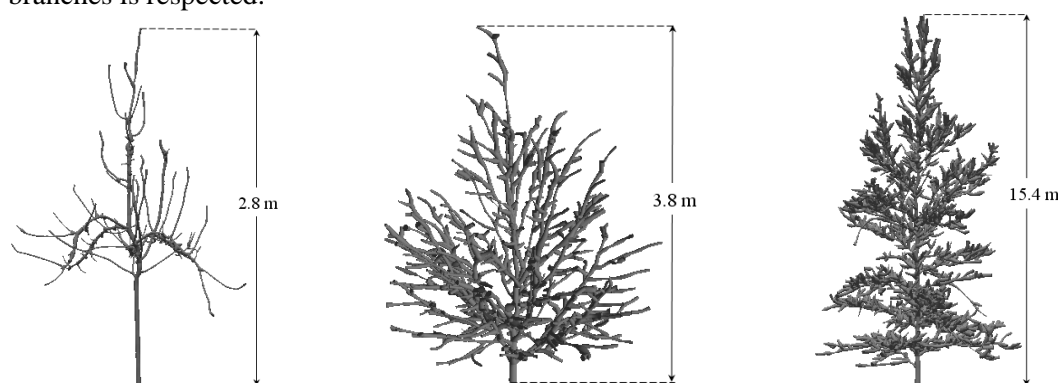


Figure 3: 3D reconstructed models. From left to right, a virtual scans of an apple tree, and two laser scanned city trees (*Tilia x vulgaris*).

We have evaluated our algorithm with the above described method on the apple tree presented Fig. 2 left, and for which an expert acquisition is available. Distance between the reference and reconstructed structures show that 90% of the geometry of the tree has been correctly reconstructed. Generally, most of the non reconstructed components are small segments or nearby branches reconstructed as one. Reconstructions from space colonization algorithm are indeed sensitive to the size of the skeleton node which is used.

Conclusion

Well parameterized, SCA seems adequate to reconstruct faithfully complex tree architecture. Moreover, to enhance its accuracy, this local reconstruction process can certainly be extended with botanical knowledge to adapt to particular architecture. In a phenotyping pipeline, such method can help characterizing answer of plant to variation of environment and genotype.

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