Quantitative assessment of automatic reconstructions of branching systems

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Highlights: In this work, we propose a method to evaluate and compare different reconstruction methods from laser data using expert reconstruction and a new structural distance.

Keywords: Structural comparison, plant architecture, laser data

INTRODUCTION

In the context of biology and agronomy, acquisition of accurate models of real plants is still a tedious task and a major bottleneck for the construction of quantitative models of plant development. Recently, 3D laser scanners have made it possible to acquire 3D images representing a sampling of the surfaces of objects. To process such new type of data, dedicated reconstruction methods were developed. Although successful in most applications such as urban geometry, these methods fail on plants structures as they usually contain a complex set of irregular and branching surfaces distributed in space with varying orientations. A number of specific methods have been proposed to reconstruct plausible branching structures from laser data.

The first noticeable method was proposed by Xu *et al.* (2007) that extends the approach of Verroust and Lazarus (2000) to reconstruct branching structures. In their approach, points from the scans are first connected to their *k* closest neighbours to form a graph. The distance between any points can then be defined as the length of the shortest path between these points on the graph. The graph is then segmented into clusters of points according to the distance to a root point. The centres of clusters are then used to generate the skeleton of the tree. Alternatively, Livny *et al.* (2010) proposed to use a series of global optimisations to reconstruct major skeletal branches. Starting from the graph of shortest paths, long paths are favoured and used to align and prune the points. Remaining paths form the skeleton of the tree. Finally, the concept of space colonisation was introduced by Runions *et al.* (2007) and consists of guiding a simulated growing tree process with a set of points that represent the volume of the plant. It was first exploited by Coté *et al.* (2009) to generate realistic foliage of a tree from laser scans. Preuksakarn *et al.* (2010) extend this idea to follow precisely the point patterns of the scans to reconstruct the skeleton of trees.

While these methods produce realistic structures as shown by Fig. 1, no method to compare them quantitatively or evaluate their respective accuracy has been proposed so far. Such evaluation is of major importance for further exploitation of reconstructed models in biological applications. In this work, we address the problem of evaluating the accuracy of reconstructed structures from laser scanner data. For this, we first present a software tool that allows experts to define reconstruction from the point cloud. Using these expert-defined structures that will be considered as reference, we then propose different indices and algorithmic methods to quantify the similarities and differences between automatically reconstructed and reference structures. Such indices make it possible to compare the reconstructions made with the different methods proposed in the literature.

Fig. 1. Example of a lime tree reconstruction with the method of Preuksakarn et al. (2010). Left: an original picture of the tree. Right: the reconstructed virtual model inserted into same background.

MATERIALS

In this study, we use laser scans from city trees growing in the streets of Helsinki, Finland, which were scanned with a Leica Geosystems HDS 2500 laser scanner. We also use a scan of a Cherry tree near Clermont-Ferrand, France, which was scanned with a Leica Geosystems HDS 6200 laser scanner. Trees were scanned

from 3 to 4 positions to reduce occlusion. The scanner specification gives a range of accuracy of 4 mm for the position of a point in space. To assess more precisely the effect of the resolution and the quality of the scans on the accuracy of the reconstruction, we also use a virtual model of a Walnut tree (Sinoquet *et al*. 97), whose structure was first manually digitized from a real tree. This mock-up was virtually scanned and different levels of noise are introduced by removing a number of points.

On these data, reconstructions are performed using our implementation of methods of Xu *et al*. (2007), Preuksakan *et al*. (2010) and Livny *et al*. (2010). These procedures are now part of the PlantGL open source library (Pradal *et al*. 2009) of the OpenAlea platform.

For scanned trees, reference 3D models were built by editing the skeleton resulting from an automatic tree reconstruction. For this, we designed a visual tool and asked experts to correct the automatically reconstructed structure. Experts can edit the skeletal structure of each tree by adding, deleting, repositioning or reorganizing segments in the structure. Different visualisation tools of the software make it possible to focus display of the laser points on a specific location making it possible to identify clearly the local branching configuration. The results are tree-like structures, whose nodes are associated with branch segments, and that represent the skeleton of the tree branching structure. A database of such expert-defined structures has been established.
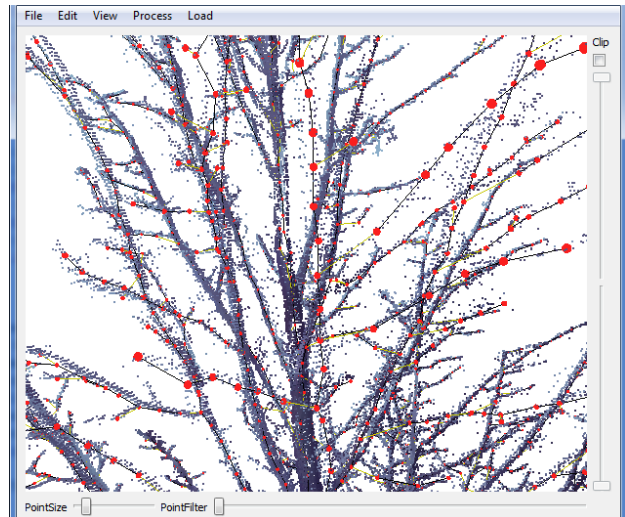

Fig. 2. The software tool used to create expert-defined structures from laser data. Red spheres represent nodes of the structure. Sliders make it possible to control the location and size of the laser points displayed. The user can edit the plant structure by adding, deleting, moving or changing properties of nodes.

METHODS

Two classes of quantitative evaluation tests can be made. The first one consists of summarizing an individual tree by a small number of global variables such as wood content, crown volume, amount of intercepted light from several directions, etc. The similarity of the models is then measured by the distance between these synthetic variables. As a first approach, the different reconstructions are compared to the reference trees with such global indices. We also compare the reconstructions with the original point sets by estimating the mean distance of the point set to the reconstructed models. While this gives a general assessment of the reconstruction quality, these indices give no information on the quality of the topology.

A second class of tests consists of comparing in more detail the three-dimensional structure of the models. For this, more structural comparison tools are required. As a first test, we experimented with the edit distance proposed by Ferraro and Godin (2000). The computation of this distance consists in determining a sequence of edit operations of minimum cost which transform an initial tree T_1 into a target tree T_2. Three edit operations are usually considered: substituting a vertex i of T_1 with a vertex j of T_1, deleting a vertex i in T_1 and inserting a vertex j in T_2. Each operation is associated with a cost that we parameterized according to geometrical similarities between nodes. As a side-product, the set of substitutions gives a mapping between elements of T_1 and T_2. However, only mappings that preserve the ancestor relationship between elements of the two trees are considered by the method. As a result, a simple inversion in the branching position of elements can create important differences with this comparison method.

To overcome the previous limitation, we designed a more flexible comparison pipeline that makes it possible to detect similarities between structures even in the case when connections mismatch. For this a number of algorithmic steps are performed to finally estimate two indices that reflect geometrical and structural similarities. Three main steps compose our pipeline: first, a homogenization of the scales of the tree T_1 and T_2 is made; second, a mapping of their nodes is determined, and finally a mapping of their edges. From these mappings, two indices are estimated. A more precise description of these different steps follows.

Before comparing a test reconstruction against the reference (expert) reconstruction, a homogenization procedure has to be carried out. Indeed, the two compared tree-like skeletal structures are in general composed of different types of segments with different sizes. To address this issue, we homogenized both skeletal

structures by re-segmenting both trees in terms of inter-ramification branch segments, *i.e.* one-piece segments connecting two branching points.

Based on the homogenized structures, the comparison of the test and reference structures could then be carried out. In 3D space, these two structures correspond to two sets of segments that may overlap partially making it difficult to find exact correspondence from the test reconstruction to the reference one. This association is often ambiguous and for each segment of the test (resp. reference) structure, one can associate a list of candidate segments in the reference (resp. test) structure. We formalize this matching as an optimization problem. Let us call T_1 and T_2 the reference and test tree skeletons respectively. For any two segments that can possibly be associated in T_1 and T_2, we quantify the distance between these two segments as the Hausdorff distance between their skeleton curves that intuitively represents the maximal deviation between the curves. During the mapping between the two structures, some element in the reference skeleton may have no counterpart in the test skeleton, and reciprocally. In this case, we say that we have respectively a deletion or an insertion with respect to the reference structure. A mapping has a cost that is defined as the sum of the costs of each individual mapping and of the deletions and insertions of nodes. The comparison of our two skeletal structures thus comes down to finding the mapping M that minimizes the cost of the mapping. To solve this assignment problem, we use an optimal flow formulation which is solved using Tarjan's (1983) extension of Edmonds and Karp's algorithm.

In the resulting optimal mapping M^*, some elements may be deleted or inserted. However, some of these insertions/deletions may simply result from the fact that several segments in one tree altogether cover a single segment in the other tree. To take this into account, a post processing step refines the mapping produced from the previous step by testing and adding mapping configurations that include multiple segments. As a result of this mapping procedure, a geometrical correspondence between elements is defined and can be quantified with the index $D_G = |M^*| / (|T_1| + |T_2|)$.

Finally, to evaluate the difference of topology between the two structures, we then inspect whether elements are connected in a similar way in their respective structures. We quantify the topological matching between the two structures with the index $D_T = 2* |M^T| / (|E_1| + |E_2|)$, where M^T is the set of preserved relationships between T_1 and T_2, and E_1 and E_2 is the set of relationships of T_1 and T_2, respectively.

RESULTS AND DISCUSSION

A comparative evaluation of tree reconstruction using different methods from the literature was performed. An illustration of such an evaluation is given in Fig. 3. A more detailed comparison will be given in the presentation, such as the performance of each method with different levels of noise in the scan. Application of our method to the evaluation of automatic reconstruction of root architecture from images will also be presented.

Method	Mean Point Distance (mm)	Volume (Ref: 13.17m²)	D_G	D_T
Xu *et al.* (2007)	12.55	12.76	0.81	0.87
Livny *et al.* (2010)	6.49	12.7	0.69	0.65
Preuksakarn *et al.* (2010)	7.26	13.3	0.90	0.72

Fig. 3. Results of our comparison for lime tree reconstructions with different methods from the literature. Global indices and geometrical and structural accuracy indices are used.

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