HAL open science

Reconstructing Plant Architecture from 3D Laser scanner data

Chakkrit Preuksakarn, Frédéric Boudon, Pascal Ferraro, Jean-Baptiste Durand, Ekko Nikinmaa, Christophe Godin

To cite this version:

Chakkrit Preuksakarn, Frédéric Boudon, Pascal Ferraro, Jean-Baptiste Durand, Ekko Nikinmaa, et al.. Reconstructing Plant Architecture from 3D Laser scanner data. 6th International Workshop on Functional-Structural Plant Models, Sep 2010, Davis, United States. pp.12–17. hal-00490064

HAL Id: hal-00490064

https://hal.science/hal-00490064v1

Submitted on 5 Oct 2010

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Reconstructing Plant Architecture from 3D Laser scanner data

C. Preuksakarn[1,2], F. Boudon[1], P. Ferraro[3], J.B. Durand[1], E. Nikinmaa[4] and C. Godin[1]

[1]CIRAD/INRIA, Virtual Plants INRIA Team, UMR DAP, TA A-96/02, 34398 Montpellier Cedex 5, France,
[2]Kasetsart University, Kamphaeng Saen Campus, Thailand
[3]PIMS – CNRS LABRI, University of Bordeaux, France
[4]University of Helsinki, Finland
Corresponding author: frederic.boudon@cirad.fr

Keywords: Architectural tree model, 3D Laser scanner, Reconstruction evaluation

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 [RHP96, SRG97, GCS99] 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 [GP04, PGW04]. These methods have been used to reconstruct small branching systems and were not adapted and tested on large trees. For such trees, a first successful method was proposed by Xu *et al.* [XGC07]. 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. To improve identification of branch segments, [YWM*09] extend point clouds segmentation with a k-means clustering and cylinder fitting. These methods produce realistic looking trees but are 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 [RLP07, PHL*09] were introduced to generate plausible artificial branching structures in a volume specified by 3D points called attractors. In a recent work, this algorithm was used by [CWFV09] to guess a plausible branching structure that could bear foliage observed with 3D scans. Here we suggest adapting SCA in a new way to reconstruct faithfully real leaf-free plant architectures observed with laser scans.

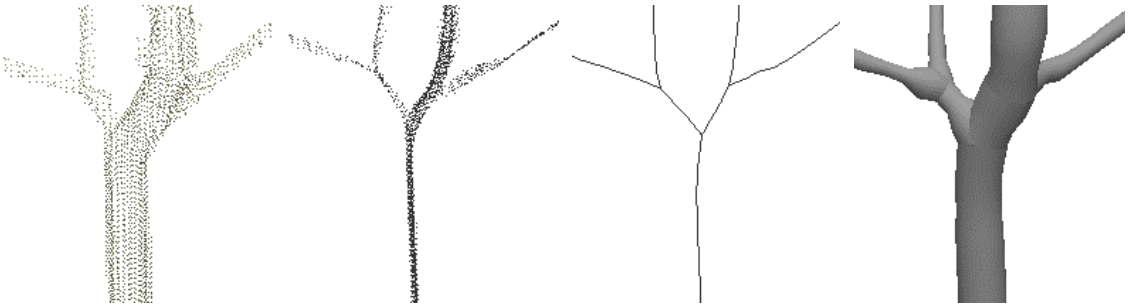
Material

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 [CSKG03]. 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 and are difficult to estimate on sparse data, we used a simple adaptive contraction scheme inspired from [GM99]. Let $P = \{p_i\}, i = 1,..., N$ 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. Let c_i^R be the centroïd of S_i^R. The original contraction operation is defined as the transform of each point p_i by the centroïd c_i^R of its neighborhood. 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 [PGK02]. λ_i is defined as k / r^2, where r is the 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.



Original data Contracted data Skeleton curves Surface

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) proposed by [RLP07, PHL*09] 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. An attractor has a local influence and attracts a skeleton node only if it is at a distance smaller than r_p. 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.

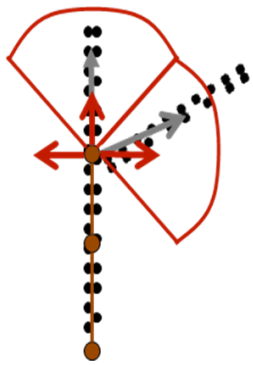


Figure 2: A step of SCA

Note that, at each node, directions of perception can be constrained to take into account some phyllotaxic patterns (in Fig. 2, cones of perception are initiated in decussate positions) or, in case of 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 [PGK02]. 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*: To produce the surface of the plant, all attractors are first assigned to the closest skeleton node. They are then projected onto the plane perpendicular to the growth direction of the node, and the average distance between the node and the projected attractors is computed. This distance is considered as the radius of the branch at this node. Then, from the sequence of skeleton nodes and associated radii, a generalized cylinder [Blo85] 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) [GC98]. Our evaluation procedure is based on the topological comparison method proposed in [FG00] 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 (see [OF09]). As a by-product, a mapping of nodes of both graphs is given by the evaluation and thus gives us 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 [God03] are used to create a more macroscopic representation of the tree structures. Vertices of the trees are gathered into groups that defines a common macroscopic scale of representation. The scale of comparison that we investigate 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.

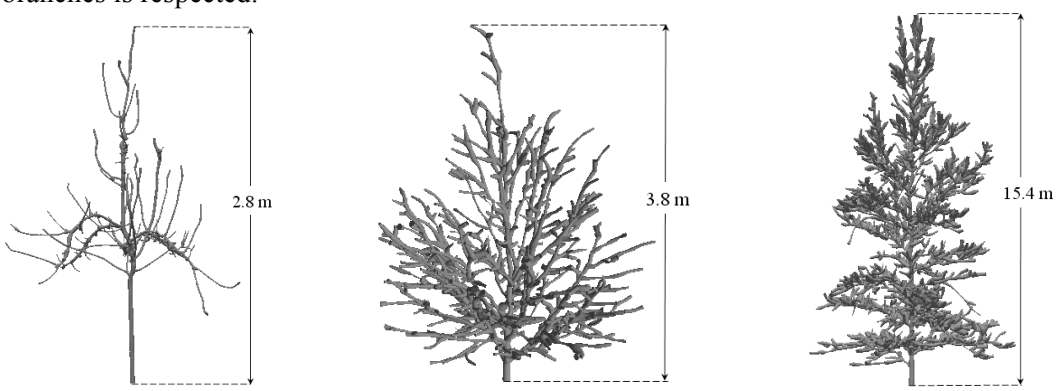


Figure 3: 3D reconstructed models. From left to right, a virtual scans of an apple tree [CSKG03], and two laser scanned city trees (*Tilia x vulgaris*).

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. However, 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.

References

[Blo85] BLOOMENTHAL, J.: Modeling the mighty maple. *SIGGRAPH Computer Graphics* 19,3 (1985), 305–311.

[CSKG03] COSTES E., SINOQUET H., KELNER J., GODIN C.: Exploring within-tree architectural development of two apple tree cultivars over 6 years. *Annals of Botany 91* (2003), pp. 91–104.

[CWFV09] CÔTÉ J.-F., WIDLOWSKI J.-L., FOURNIER R. A., VERSTRAETE M. M.: The structural and radiative consistency of three-dimensional tree reconstructions from terrestrial LIDAR. *Remote Sensing of Environment 113*, 5 (2009), pp. 1067 – 1081.

[FG00] FERRARO P., GODIN C.: A distance measure between plant architectures. *Annals of Forest Science 57*, 5/6 (2000), pp. 445–461.

[God03] GODIN C.: Introduction aux structures multi-échelles. Application à la représentation des plantes. *Habilitation thesis* (2003).

[GC98] GODIN C., CARAGLIO Y.: A multiscale model of plant topological structures. *Journal of Theoretical Biology 191* (1998), pp. 1–46.

[GCS99] GODIN C., COSTES E., SINOQUET H.: A method for describing plant architecture which integrates topology and geometry. *Annals of Botany 84* (1999), 343–357.

[GM99] GIANNITRAPANI R., MURINO V.: Three-dimensional skeleton extraction by point set contraction. In *ICIP (1)* (1999), pp. 565–569.

[GP04] GORTE B., PFEIFER N.: Structuring laser-scanned trees using 3D mathematical morphology. In *Proceedings of 20th ISPRS Congress* (2004), pp. 929–933.

[OF09] OUANGRAOUA A., FERRARO P.: A constrained edit distance algorithm between semi-ordered trees. *Theoretical Computer Science 410*, 8-10 (2009), pp. 837–846.

[PGK02] PAULY M., GROSS M. H., KOBBELT L.: Efficient simplification of point-sampled surfaces. In *Proceedings of the Conference IEEE Visualization '02* (2002), pp. 163-170.

[PGW04] PFEIFER N., GORTE B., WINTERHALDER D.: Automatic reconstruction of single trees from terrestrial laser scanner data. In *Proceedings of 20th ISPRS Congress* (2004), pp. 114–119.

[PHL*09] PALUBICKI W., HOREL K., LONGAY S., RUNIONS A., LANE B., MECH R., PRUSINKIEWICZ P.: Self-organizing tree models for image synthesis. In *SIGGRAPH'09: ACM SIGGRAPH 2009 papers* (New York, NY, USA, 2009), ACM, pp. 1–10.

[RHP96] P. ROOM, J. HANAN, and P. PRUSINKIEWICZ. Virtual plants: new perspectives for ecologists, pathologists and agricultural scientists. *Trends in Plant Science Update*, 1(1):33–38, 1996.

[RLP07] RUNIONS A., LANE B., PRUSINKIEWICZ P.: Modeling Trees with a Space Colonization Algorithm. Ebert D., Merillou S., (Eds.), Eurographics Association, (2007) pp. 63–70.

[SRG97] SINOQUET H., RIVET P., GODIN C.: Assessment of the three-dimensional architecture of walnut trees using digitising. *Silva Fennica 31*, 3 (1997), pp. 265–273.

[XGC07] XU H., GOSSETT N., CHEN B.: Knowledge and heuristic-based modeling of laser-scanned trees. *ACM Transaction On Graphic 26*, 4 (2007), 19.

[YWM*09] YAN D.-M., WINTZ J., MOURRAIN B., WANG W., BOUDON F., GODIN C.: Efficient and robust reconstruction of botanical branching structure from laser scanned points. In *11th IEEE International conference on Computer-Aided Design and Computer Graphics (CAD/Graphics 2009)* (2009). pp. 572-575.