

Semantic Skeletonization for Structural Plant Analysis

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Highlights: Computational plant modeling from 3D sensor data is crucial for the early assessment of plant traits. Semantic modeling enables the incorporation of knowledge about the plant species, leading to an improvement of purely geometrical skeletonization approaches. Structural plant features can thereby robustly be extracted from the sensor data.

Keywords: Plant modeling, Structural plant analysis, 3D skeletonization, Feature extraction

INTRODUCTION

Structural plant analysis can help plant breeders to detect, e.g., a susceptibility of a new breed to a certain disease. Currently, the phenotyping bottleneck limits the throughput of automated plant trait assessment. In this work, we are interested in the automated extraction of structural features of plants, in particular grapevine, from 3D laser range data. We employ a skeletonization algorithm, which reduces the structure of an object represented by a point cloud to a vectorized representation in the form of a set of connected line segments, whilst preserving its topology and geometry. But for our purpose, structural preservation alone is not sufficient. We also need to know what part of the curve skeleton refers to what part of the original plant.

Therefore we propose to add a further layer to the skeletonization, namely semantics. Our goal is to automatically identify curve skeleton components as plant components. In order to achieve this we include a biological model into the skeletonization algorithm. This model enables a semantic annotation of the plant components, which in general allows us to extract the structural features.

RELATED WORK

Owing to an extensive survey by Cornea et al., it is widely accepted that curve skeletons should fulfill certain properties such as homotopy, thinness, centeredness, reliability, component-wise differentiation, smoothness, and hierarchy (Cornea et al., 2005; Cornea et al., 2007). Some of these properties may contradict each other, and especially for point cloud data with irregular sampling, some properties can be hard to achieve and evaluate. This is why many methods for the skeletonization of plants from 3D point clouds additionally incorporate model knowledge. One common prerequisite is to have the root point of the plant structure identified (Livny et al., 2010; Preuksakarn et al., 2010; Verroust and Lazarus, 2000; Xu et al., 2007). Other approaches try to fit cylindrical structures (Pfeifer et al., 2004; Runions et al., 2007) into the point cloud, thus implicitly simulating the geometric properties of branches.

Our work is based on a skeletonization method that follows a global optimization approach (Livny et al., 2010). This approach is specifically designed for the skeletonization and reconstruction of tree structures.

SEMANTIC MODELING, ANNOTATION, AND GEOMETRY CORRECTION

We exemplify our method on the berryless grape cluster, in the following termed grapevine stem system. This choice is motivated by two main reasons: First, stem systems determine the overall structure and geometry of the grape cluster. Second, they show typical characteristics that are generally challenging in plant analysis, namely self-occlusion, self-touching, and very fine structures.

The knowledge incorporated into the algorithm arises from a number of observations about the biological structure of the plant to model. To formalize these inherently informal observations, we utilize the implicit graph structure of the curve skeletons. We define the structural depth d of a vertex v in a curve skeleton as shown in equation 1, where p denotes the parent of vertex v , J denotes the set of junctions, i.e., vertices with more than one child, and $l(v)$ the Euclidean length of the longest edge chain in v 's subgraph. The proposed semantic annotation algorithm utilizes this definition of depth to annotate each vertex according to the structural plant part it belongs to. Figure 3 visualizes this semantic annotation with different colors, where each edge is assumed to have the label of its end vertex.

$$d(v) := \begin{cases} 0 & \text{if } p = \emptyset \\ d(p) & \text{if } p \notin J \vee l(v) = l(p) - \|v - p\| \\ d(p) + 1 & \text{otherwise} \end{cases} \quad (1)$$

The curve skeletons obtained by the method of Livny et al. (Livny et al., 2010) contain a number of erroneous edges for our data. Therefore, the approach presented herein aims at the automated identification and removal of these unnecessary edges. The semantic annotation described before is employed to assign each edge one of the labels "rachis", "lateral branch", "pedicel", or "vascular remains of berries". Edges that contradict biological constraints, e.g. by representing decreasingly long lateral branches in basipetal direction, are removed. Furthermore, all edge segments classified as vascular remains of berries are contracted. Figure 3 shows one remaining curve skeleton, which constitutes our final result.

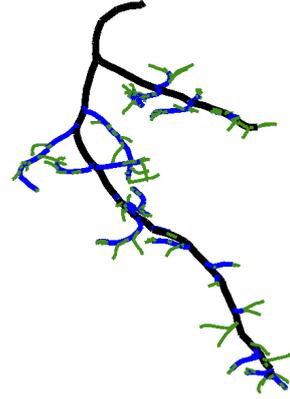
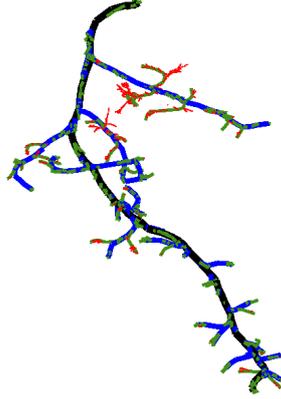
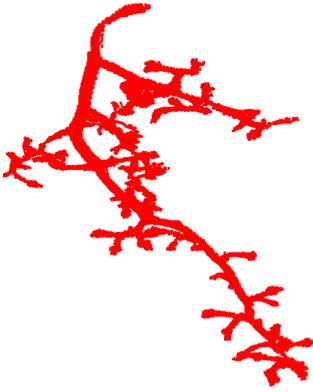


Fig. 1: Point cloud of a stem system.

Fig. 2: Semantic annotation

Fig. 3: Corrected curve skeleton.

FEATURE EXTRACTION

The semantic model and its implementation are designed to remove all edges from the curve skeleton that do not reflect branches in the grape cluster. This removal is crucial for the derivation of phenotypic characteristics for grapevine breeding. We will show how the semantically labeled and corrected curve skeletons can be used for the extraction of a formal grapevine descriptor from sensor data.

To identify possible features of grapevine, existing descriptor lists can be consulted. (IPGRI, 1997; OIV, 2009). The list of phenotypic features we compute include, amongst others, the existence of secondary bunches, the size of branching angles, or the length and thickness of branches and internodes.

Several of these features refer to the growth direction of the stem system or the number of internodes in one branch. In order to encode the growth direction and identify the number of vertices (and thus internodes) in one structural component, a unique numbering scheme for vertices is introduced. As a consequence, the formal features can be easily derived and used in a statistical analysis. The resulting statistical model can be used to infer knowledge about hidden object parts in the grape cluster including berries, and can furthermore serve as parameters for plant reconstruction (Schöler et al., 2013).

EXPERIMENTAL RESULTS

To quantitatively evaluate the obtained curve skeletons, we compare them to manually created reference skeletons. To operationalize the comparison of two curve skeletons, we formulate the given task as an assignment problem (Munkres, 1957) and match the number of skeletal junctions in both skeletons to each other. Then we compute precision and recall as performance measure for the number of skeletal junctions that are part of the assignment A (cf. Equation 2). Here, the precision P is given as the fraction of junctions J_S in the obtained curve skeleton that are part of the assignment, and therefore measures correctness of junctions. The recall R is the fraction of junctions in the reference skeleton J_R that are part of the assignment, and measures completeness of the obtained curve skeleton.

Our evaluations show that we are able to significantly improve the skeletons' precision by semantic geometry correction. Furthermore, we were able to keep high recall due to the deletion of erroneous edge segments, thus enabling a robust feature extraction. Figures 5 and 6 report the precision and recall values for a curve skeleton before and after semantic-driven geometry correction.

$$P := \frac{|J_R \cap A|}{|J_S|}, \quad R := \frac{|J_R \cap A|}{|J_R|} \quad (2)$$

For the evaluation of structural plant features, we compare the automatically computed values to those given by the manually created reference skeletons. We found that the errors of these feature values in the semantically corrected curve skeletons are significantly smaller than in the uncorrected ones. One example is the length of the peduncle, i.e., the “distance from insertion point on the shoot to the 1st ramification of primary bunch” (OIV, 2009). Due to erroneous edges in the curve skeletons before the semantic geometry correction, the first ramification of the primary bunch is detected too early, resulting in a very short peduncle. After semantic geometry correction, its length can be robustly measured (cf. figures 5 and 6).

CONCLUSION

In conclusion, we have shown how the skeletonization of 3D point clouds of grapevine stem systems can be enhanced by the introduction of a biological model. By means of this model, we can add semantic annotations to curve skeleton components. These annotations are used to correct the computed curve skeletons and to improve on the extraction of structural features. We performed an extensive evaluation of our approach and were able to show that both skeletonization and feature extraction could be significantly improved. Moreover, first investigations on whether the structural features can be used to distinguish different cultivars have shown to be beneficial for plant reconstruction results (Steinhage et al., 2012).

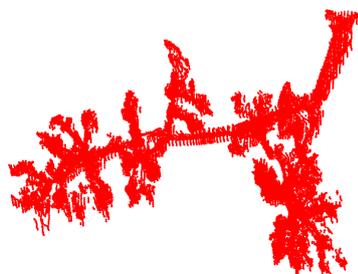


Fig. 4: Point cloud of a stem system (29,922 points).



Fig. 5: Curve skeleton before geometry correction ($P = 0.29$, $R = 1.0$).

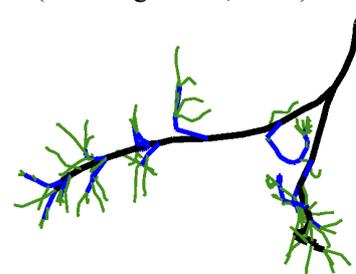


Fig. 6: Curve skeleton after geometry correction ($P = 0.55$, $R = 1.0$).

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