Automated Parameter Estimation for a Plant Architecture Model

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Highlights: We present an automated procedure for the creation of architectural plant models. It uses an algorithm for the computation of skeletons from sensor data. The skeletons are annotated with semantic labels for the extraction of architectural parameters. The values of several samples are averaged and serve as the basis for the model, which is implemented as a Relational Growth Grammar.

Keywords: Architectural Modeling, Skeletonization, Relational Growth Grammar

INTRODUCTION

When creating a model for the architecture of a plant, questions arise, like what parameters describe the architecture, how they are captured, or how it is actually modeled. In one way or another many of those questions were already answered in previous works (Godin, 2000; Watanabe et al., 2005; Barthélémy and Caraglio, 2007; Dornbusch et al., 2007; Fourcaud et al., 2008). Almost always they contain a substantial amount of manual labor for determining parameter values, for example, for the length or the frequency of occurrence of a plant component. In this paper we show, using the example of berryless grape clusters of the grapevine plant (Vitis vinifera L.), how a large part of the process can be automated. To this end we make use of an algorithm that takes sensor data of the plant as input and computes a skeleton, which is a set of connected line segments that represents the structure of the original object. That skeleton is annotated with semantic labels like rachis or pedicel. Then, parameter values like lengths or frequency of occurrence of components are extracted from that skeleton. The values of several samples are averaged and serve as the basis for the actual model. We construct our architectural model as a Relational Growth Grammar (RGG) (Kurth et al. 2005). Figure 1 gives an overview of the process. In general, this procedure is also applicable to other plants or plant parts. To our best knowledge this is the first attempt of an automated parameter value extraction for the architectural plant modeling. Of course, the presented procedure still relies on a careful selection of plant samples and architectural parameters, but the process of extracting and averaging their values is greatly simplified.
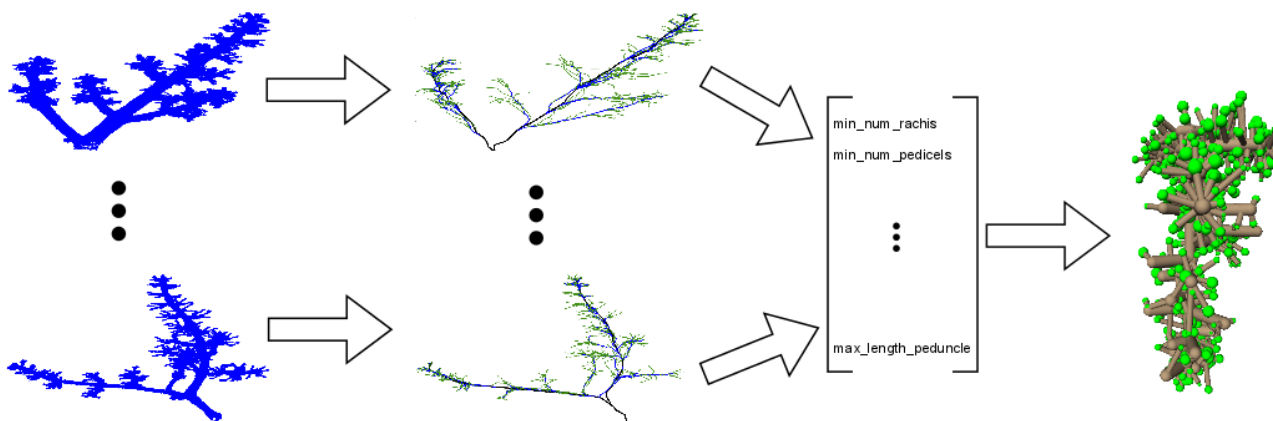

Figure 1: Overview of the procedure. From left to right: From every point cloud a skeleton is computed. The colors in the skeleton refer to the different semantic annotations (black: rachis, blue: lateral branch, green: pedicel). Based on the skeleton, values of architectural parameters are extracted and averaged. This is the basis for the RGG-model. See section MODEL CONSTRUCTION for an example of how the parameters are integrated into the model.

DATA AND PARAMETERS

For computing the skeletons we use the algorithm presented in (Balfer, 2012; Balfer et al., 2013). This algorithm not only computes the bare architecture but also adds semantic labels to the different parts: rachis,

lateral branch, and pedicel.

We have gathered 20 exemplars of grape clusters of the cultivar Riesling, an example of a very popular cultivar that usually produces very compact grape clusters. The clusters were cut off the trunks of ten grapevine plants and we always took the lowest two clusters. The plants were grown in the field, not in lab-conditions. According to the extended BBCH-scale from Lorenz et al. (1994) the clusters were taken at stage BBCH 65 "full flowering: 50% of flowerhoods fallen." (BBCH is short for *Biological Institute of Agriculture and Forestry, Federal Office for Plant Varieties and Chemical Industry* – in German: *Biologische Bundesanstalt für Land- und Forstwirtschaft, Bundessortenamt und Chemische Industrie*). For each of the clusters we cut off the flowers (but not the pedicels), counted the flowers and scanned the clusters with a Perceptron ScanWorks V5 laser rangefinder, resulting in 20 dense point clouds with a minimum point-to-point resolution of 12 µm. These point clouds and their "starting points" were used as input to the skeletonization algorithm. The starting point is where the cluster was formerly connected to the plant.

The resulting semantic skeletons each produced one vector of parameter values. We then had to combine the single vectors into one vector representing the twenty clusters. For parameters with continuous values like the length of the rachis we could just compute the average and the standard deviation assuming a normal distribution. For other, non-continuous, parameters we had to do different calculations. For example, for the number of pedicels that branch from the same node we computed a relative histogram of the gathered values. In total we extracted 89 different parameters and, for now, assumed them to be independent. Some of the parameters are taken from the descriptor list of International Plant Genetic Resources Institute (IPGRI 1997), and the second edition of the descriptor list of the International Organization for Vine and Wine (OIV 2009). For example, for the number of rachises we found occurrences of 1, 2, 3, 4, 5 and corresponding occurrence probabilities of 0.05, 0.85, 0.05, 0.0, 0.05 respectively. This means that in 17 of the 20 cases we found exactly two rachises; one main rachis and one secondary rachis.

MODEL CONSTRUCTION

The thus gathered and averaged parameter values are the basis for the model construction. We demonstrate this by means of an example. We have several values concerning the main rachis of the grape cluster: Their lengths, number of lateral branches per node, number of secondary rachises, internode lengths, number of nodes, etc. These pieces of information are concentrated in a new module in our RGG, called *MainRachis*. For the main rachis module also a specific grammar rule exists. This rule demands that the first branching point on the main rachis can lead to a lateral branch or a secondary rachis. After that point only lateral branches or pedicels may emerge from nodes. In addition we know, for example, how long the rachis can be and how many nodes in what distances can be expected. Thereby we create only such rachises that are topologically and geometrically realistic, according to our model, which itself is based on real grape clusters. Likewise we create RGG-modules for secondary rachises, lateral branches and pedicels. Furthermore, this parameterized model allows setting the parameters to a different, consistent set of values to produce grape clusters of other cultivars or in other development stages.

DISCUSSION AND CONCLUSION

See Figure 2 for an overview of six example runs of the grape cluster model. As can be seen, lateral branches get shorter from base to tip, internode lengths vary, and sometimes there is a secondary rachis. As was shown in Steinhage et al. (2012) such a model can be used not only for virtualization or visualization purposes. Utilized for a reconstruction algorithm it helps vastly decreasing the space of possible reconstruction hypotheses. In this respect the term 'possible' is described in terms of the model since only such hypotheses are allowed that can be constructed by the model.

In conclusion we have shown (a) how the extraction of architectural parameter values of plants can be automated by use of a skeletonization algorithm, (b) how those values can be combined to gain averages for a specific cultivar, and (c) how such a model can be used for the purpose of reconstruction from sensor data. There are several possible paths to follow from here. One could make the skeletonization algorithm more adaptable to other plants, gather more parameter values and investigate possible dependencies, and optimize the algorithm for shorter runtimes.
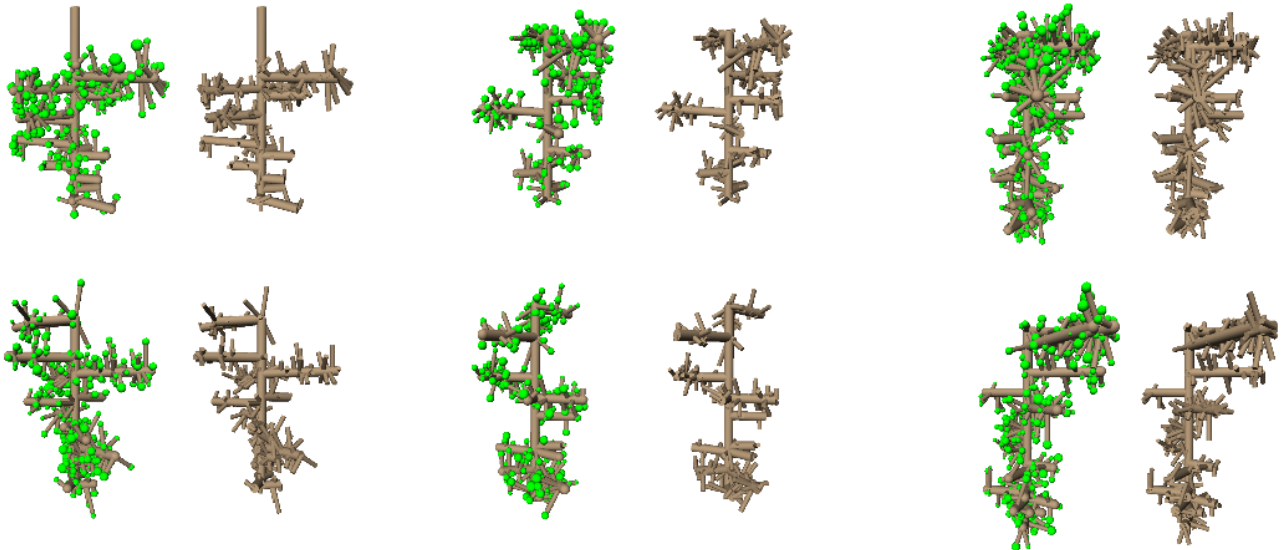
Figure 2: Six example runs of the RGG-model. For each run we show the generated grape cluster with and without flowers. One can see typical properties of grapevine grape clusters. For example, the lateral branches get shorter from base to tip, there can be secondary rachises, and from lateral branches pedicels emerge.

ACKNOWLEDGEMENTS

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