A Model-Based Approach to High Performance Phenotyping

Volker Steinhage, Florian Schöler, Jenny Balfer¹

Abstract

Breeding pest resistant crops can reduce the application of plant protection products. This in turn will significantly reduce biotical stress of the plants, and damage to the environment. To enable greater efficiency in crop breeding and to optimize decision making in crop management, there is an increasing demand for non-biased and faster assessment of plant traits in lab and field. Within a subproject of CROP.SENSe.net, an interdisciplinary research network of Bonn University and the research centre Jülich, we are working on a non-destructive solution to analyze and screen plant phenotypes. We aim for complete and precise 3D reconstructions of plants based on sensor data. To meet the challenge of occlusions and self-occlusions in sensor-based measurements, we employ a model-based approach "to make hidden object parts visible." First results show that important breeding characteristics can be derived by combining the visible exterior plant components with the model-induced interior plant components.

1. Motivation

Crop breeding is not only of economical interest. For example, most crops demand for pest management. Thus, breeding pest resistant crops can reduce the application of plant protection products. This in turn will significantly reduce biotical stress of the plants on the one hand and damage to the environment on the other hand.

To enable greater efficiency in crop breeding and to optimize decision making in crop management, there is an increasing demand for non-biased and faster assessment of plant traits in lab and field. But the so-called 'phenotyping bottleneck' currently limits our ability to capitalize on plant functional genomics and modern breeding technologies. Thereby, phenotyping means to derive quantitative information on plant structure and functions as well as interactions with the environment.

To enable new phenotyping tools that are both efficient and automated, provide high throughput and high resolution, we are faced with the fact that plant structure is difficult to obtain with sensor-based automated procedures due to occlusions and self-occlusions.

2. Phenotyping using model-based 3D Reconstruction

Within a subproject of CROP.SENSe.net, an interdisciplinary research network of Bonn University and the research centre Jülich, we are working on a sensor-based and non-destructive solution to analyze and screen plant phenotypes. More precisely, we aim for complete and precise 3D reconstructions of plants based on sensor data. As an example plant we concentrate on grapevine. On this example plant we additionally aim for semantically labeled 3D reconstructions telling us which parts are berries, leaves, stems etc. In this contribution we focus on the interpretation of 3D laser range data.

To meet the challenge of occlusions and self-occlusions, we employ a model-based approach "to make hidden object parts visible" (Schöler/Steinhage 2011). This approach consists of three major components.

¹ Department of Computer Science III, University of Bonn, D-53117 Bonn, Germany
{steinhage, schoeler, balfer}@iai.uni-bonn.de
2.1 Geometrical, Semantic, and Topological Modeling

Geometric modeling employs the concept of a Relational Growth Grammar (RGG) (Kurth 2007, Kniemeyer 2008) which generalizes the Lindenmayer system approach (Lindenmayer 1968), most famously used to model morphology and growth processes of plants. In short, an RGG uses a graph-based representation of the geometry, structure, and functionality of plants. The grammar rules transform the graph-representations and thereby simulate processes of growing, nutrient flux, etc.

The relevant plant components are modeled by parameterized geometric primitives. For example, a berry’s geometry is represented by a sphere or an ellipsoid, stems are represented as frustums. Semantic modeling is done by labeling every geometric primitive as being an instance of a class of relevant plant components, i.e., leaf class, berry class, stem class, peduncle class, etc. Besides geometry and class labels of the plant’s components, the grammar model of a plant has to describe valid plant topologies, i.e., in what way the plant’s components are combined to form a complete and valid plant model. The grammar is used to specify rules for creating such complete and valid plant models. These rules can be thought of as modeling growing processes at different places and different stages of plant growth processes.

2.2 Preprocessing: Automated Derivation of Model Parameters

Most of the rules of the grammar model have morphological parameters. Some parameters specify sizes of plant components, e.g., radii of berries, lengths of stems, or lengths of internodes. Other parameters specify domain knowledge like mass density of berries and colors for visualization. Furthermore, the overall plant's topology and geometry is also determined by some parameters. For example, branching parameters specify the branching factors and angles between stems, distance parameters specify distances between nodes, etc. These morphological parameters are derived using statistic analysis of training data to obtain probabilities of the parameter settings in the interpretation rules of the grammar model.

In following sections, we will focus on stem skeletons to exemplify our approach. Stem skeletons are of particular interest since they form the "load bearing system of grape clusters" and therefore determine their overall structure and geometry. To enable a statistical analysis on laser range scans of stem skeletons, we first skeletonize the input. Skeletonization is a process to reduce a volumetric representation of a solid object to a skeletal remnant, the so-called curve skeleton that largely preserves the extent and connectivity of the original object.

Our skeletonization is based on a model-based approach (Livny et al. 2010) that aims to extract a smoothed and centered curve skeleton from point clouds of laser range data. But this approach relies on a rather general model that only employs constraints of smoothness, connectivity, and centeredness w.r.t. tree-like structured plant geometries.

We enhance this approach by adding a semantic model that incorporates explicit morphological constraints on the stem skeletons of grapevine. These constraints are used within a new annotation algorithm that exploits the notion of branching depth given in the semantic model of stem skeletons. The algorithm starts at the root vertex and proceeds in acropetal direction of the stem skeleton, i.e., towards the tips. It results in a complete semantic annotation that classifies all edges of a curve skeleton as being parts of the rachis, lateral branches, pedicels, or vasculature (cf. fig. 1). Only this semantic annotation enables the detection and resolution of inconsistencies in the curve skeletons that are likely to be caused by sensor noise and cannot be detected by solely using the more general approach of Livny et al. In consequence, we are able to derive more reliable morphological parameters.
Our semantically annotated curve skeletons are represented as graph structures in 3D Euclidean space. Hence, the automated extraction of morphological parameters can be done by measuring lengths, distances, and angles of and between vectors followed by statistical analysis. Some of the morphological features automatically derived that way correspond to well-known OIV descriptors. The acronym OIV refers to the International Organization of Vine and Wine, which is concerned with the compilation of global statistics within its field. To give some examples, we are able to robustly detect the number of rachises and thus the existence of wings and secondary bunches, the length of the primary bunch's peduncle (according to the OIV descriptor 206), width and length of the primary bunch, volume of the berryless stem skeleton (analog to the OIV descriptors 202 and 203), branching angle between different branch segments, lengths and diameters of branches and internodes, number of branching points on rachises and lateral branches, overall curvature, and elongation.

### 2.3 Grammar-Based Reconstruction Framework

The morphological parameters derived by our preprocessing (cf. section 2.2) are used for the reconstruction of grapevine structures employing a *Relational Growth Grammar* (RGG). The key idea of the automated reconstruction is to achieve an optimal balance between fitting the input data on the one hand (data-driven part of optimization) and fulfilling all the topological, geometrical, and statistical constraints given by our grammar-based grapevine model (model-driven part of optimization).

To achieve this balance, we employ a probabilistic sampling of the hypothesis space (i.e., the space of all possible reconstruction hypotheses fitting in some way the data- and model-driven optimization criteria). Generally, sensor data of plants can be explained by models consisting of different numbers of stems, leaves, berries etc. Because of this, the space of hypotheses will consist of models with different parameter sets. Therefore, we have to employ a flexible sampling approach that can jump between parameter subspaces of differing dimensionality. This is done using the *Reversible jump Markov chain Monte Carlo* (RJCMC) formalism (Green 1995). Additionally, Simulated Annealing is used to avoid local optima and to ensure convergence (White 1984).

Summing up so far, our reconstruction framework shows three components: the Relational Growth Grammar to provide the knowledge about the plant structures, the probabilistic RJCMC to sample the space of reconstruction hypotheses, and Simulated Annealing to ensure convergence to the global optimum.
As mentioned, the point clouds derived by laser scanning suffer from occlusions and self-occlusions. For example, when scanning a grape cluster with berries, most of the points relate to surfaces of the berries and only few points relate to the stem skeleton. In regions of the point clouds, where no interior structure is visible, the RJMCMC sampling in combination with the RGG rules is used to generate and evaluate complete hypotheses. But in those regions, where the interior structure is clearly visible, the reconstruction can be significantly accelerated. In this case, we generate a partial start hypothesis, consisting of only one frustum, and use the rules of our RGG to let this local start hypothesis grow in its literal sense step-by-step and part-by-part into the point cloud. The growing process is implemented using a look-ahead cone at the tip of each current growing state. The look-ahead cone checks for spatial input data and sets the tip of the growing state (i.e., the frustum) according to those data. After reaching a certain length the frustum is cut into two, which enables the hypothesis to follow curvatures (cf. fig. 2).

Figure 2
First steps of the model-based step-by-step fitting of a stem skeleton reconstruction into a point cloud.

Figure 2 stresses an important aspect in the 3rd and 4th snapshot. The point cloud shows some swelling before the stem is bending into its curve. Thus, our modeler might propose to insert a branching to fit these input data. This more data-driven variant of our fitting algorithm is depicted in the 3rd snapshot. But using the statistical model constraints derived in the preprocessing (cf. section 2.1) the grammar-based model knows about mean distances and variances between branching locations and can therefore avoid wrong branching hypotheses as depicted in the 4th snapshot. Figure 3 shows snapshots of the stepwise fitting of a grammar-based interpretation model into a point cloud of a stem skeleton.
For the reconstruction of interior plant components that are largely hidden by exterior plant components, we still have to rely partially on the sampling of more complete reconstruction hypotheses. For example, the stem skeleton of a bunch of grapes is largely hidden by all the berries of the bunch of grapes (cf. fig. 4). Thus, the visible top part of the stem skeleton can be reconstructed using the efficient stepwise growing process. This yields a partial reconstruction of the stem skeleton that must be completed by sampling the space of all complete hypotheses of stem skeletons that (1) fit the data, (2) contain the partial reconstruction of the visible top part of the stem skeleton, and (3) follow the constraints encoded in the relational growth grammar.

3. Results

First results are encouraging: Interior and therefore hidden plant components can be interpolated in a model-based way. In consequence, important breeding characteristics can be derived by combining the visible exterior plant components with the model-induced interior plant components.

Such results can then be used to improve semantic segmentations of point clouds of bunches of grapes. For example, figure 4 shows two perspectives on a model-based interpretation of laser range data of a bunch of grapes. They both show a pre-segmentation of an observed bunch of grapes. Results of the pre-segmentation are visualized by colors: surface patches of stems are colored in green, surface patches of berries are colored in magenta. Pre-segmentation is based on local curvature analysis and therefore erroneous: too many interpolated surface patches of the berries are misclassified as stems and therefore colored in green. The model-induced interior stem skeleton is visualized in metallic blue. The stem skeleton provides information about the interior structure and plant components. In combination with the berry size, the stem skeleton tells the breeder important vine breeding characteristics about the plant structure and the plant components like the density of packaging, i.e., densely-packed or loosely-packed can be derived.
Figure 4
Two perspectives on a model-based interpretation of laser range data of a bunch of grapes.

Figure 5 compares the erroneous pre-segmented surface model of an observed bunch of grapes (left) to the result after model-induced fitting of the stem skeleton (right). Classifications of the surface patches can be corrected according to the model-induced evidence, i.e., where stems and berries have their places.

Figure 5
Erroneous pre-segmented surface model (left) and corrected segmentation due to the fitting of the stem skeleton that was derived by grammar-based reconstruction (right).
4. Related Work

Many approaches have been proposed for modeling plants. Rule-based methods use sets of rules or grammars for creating models of plants and trees. Many approaches base on the idea of the generative Lindenmayer system (Lindenmayer 1968). Some new approaches take also into account various kinds of plant interaction with the environment (e.g., Prusinkiewicz et al. 2001, Noser et al. 2001, Van Haevre et al. 2004). But most of these approaches aim at synthesizing impressive looking plants, trees, and forests for visualization, for simulations in large scales, or for the movie industry. Sensor-based methods directly model the plant using sensor samples, i.e., mostly image samples. Some approaches start with ad hoc prior models and a rather limited modeling scope (Han/Zhu 2003, Binney 2009). Other approaches approximate shapes with limited realism, i.e., without recovering explicit geometries of the branches and leaves (e.g., Shlyakhter et al. 2001, Reche-Martinez et al. 2004). For example, visual hulls of trees obtained from silhouettes are employed to derive rough shapes of the trees (Shlyakhter et al. 2001). The rough tree volumes are used to create a tree branching structure for synthesizing leaves. Some new approaches are in fact dealing with explicit reconstruction but employ interactive steps or aim for approximate reconstructions (e.g., Quan et al. 2006, Kang/Quan 2009).

Approaches concerned with the skeletonization of plants from laser range data commonly apply implicit domain knowledge, e.g., by fitting cylindrical structures (Pfeifer et al. 2004) or so-called arterial snakes (Li et al. 2010) into the point cloud to reconstruct stems and branches. Others do not restrict the curve skeletons topologically (Bucksch 2011, Cao 2010), hence being able to compute curve skeletons from arbitrary objects, but possibly contradicting the topological characteristics of plants.

5. Conclusion

We have presented an approach to 3D plant reconstruction that combines model-driven and data-driven procedures. For modeling we employ a grammar-based framework, namely that of Relational Growth Grammars (RGG). The RGG encodes the knowledge of plant structures and their components. Thus, the RGG models all relevant aspects of a plant's geometry, topology, and semantics. Sensor measurements of plants provide information about the specific structure and geometry of an observed plant. Matching generic plant knowledge with specific plant measurements means to interpret the sensor data using the rules of the RGG. To obtain an optimal - or at least approximate optimal - interpretation, we employ a probabilistic sampling approach, namely Reversible jump Markov chain Monte Carlo. First results are encouraging: Interior and therefore hidden plant components can be interpolated in a model-based way to obtain important breeding characteristics. To our knowledge, we are the first to aim for detailed plant reconstructions in a fully automated way by employing a grammar-driven interpretation of sensor measurements of plants. Therefore, our grammar models plants in terms of geometry, topology, and semantics of their overall structure and their components.

Acknowledgements

This work partially was done within subproject D2 "Interpretative 3D plant architecture" of the interdisciplinary research project CROP.SENSE.net. The project is funded by the Federal Ministry of Research and Education (BMBF) and the European Union by the European Regional Development Fund (ERDF).

Thanks go to our partners in subproject D2 for providing us with domain knowledge (R. Töpfer, K. Herzog at the Julius-Kühn Institute for Grapevine Breeding, Siebeldingen, Germany) and with pre-segmented laser range measurements (W. Förstner, H. Kuhlmann, R. Roscher, S. Paulus at the Institute of Geodesy and Geoinformation, Bonn Univ., Germany).
Bibliography


