Automated Reconstruction of 3D Plant Architecture Applied to Grapevine Phenotyping

Volker Steinhage, Florian Schöler

Institute of Computer Science 4
University of Bonn
Friedrich-Ebert-Allee 144
53113 Bonn
steinhage@cs.uni-bonn.de

Abstract: We propose an approach to automated 3D reconstruction of plant architecture followed by a precise derivation of phenotypic traits. We applied and evaluated our approach within a grapevine phenotyping project. The reconstruction results and the derived phenotypic traits could be shown to be in line with given ground truth data. Furthermore, our approach that combines a generative modelling of plants with a probabilistic sampling of the space of reconstruction hypotheses seems to be a promising framework that could potentially improve automated plant reconstruction and automated phenotyping in a broader field of applications.

1 Introduction

For efficient plant breeding, both, efficient genotyping and phenotyping are needed. For phenotyping the challenge lies in achieving an efficient high-throughput procedure. This is not possible with current methods. In general, botanical ratings are done manually and in coarse categorizations, resulting in the so-called phenotyping bottleneck [FT11].

Within the interdisciplinary research network CROP.SENSe.net of *Bonn University* and the *Research Centre Jülich* several subprojects worked together on the non-destructive and quantitative screening of plant phenotype throughout plants' lifecycles. Different subprojects worked on different target plants. The target plant of subproject D2 was the grapevine and plant samples were provided by subproject partners of the *Julius-Kühn Institute for Grapevine Breeding*.

In grapevine breeding, low density of grape clusters (OIV descriptor 204) is an important breeding objective with respect to higher yields and higher resistance against the boletus destructor. To achieve this breeding aim efficiently, a fast and automated assessment of traits in lab and field was in demand to avoid time consuming and personnel-intensive screening of plant phenotype.

In this contribution, we report on the development of an automated sensor-based method for the 3D-reconstruction of grape cluster's architecture for the purpose of a detailed and precise phenotyping [SSB12], [SS12].

2 Sensor-based 3D reconstruction of grape clusters

Recently, RGB-D sensors, 3-D laser scanners and multi-view stereo approaches have made it possible to acquire 3-D sensor data in terms of 3-D point sets representing samplings plant's surfaces. Our reconstruction approach used 3-D point sets that were generated by laser rangefinder measurements showing a measurement accuracy of 0.024 mm. A typical 3-D point set of a grape cluster comprised ca. 250 000 points.

To meet the challenges of occlusions and self-occlusions in sensor data generation, we employed a model-based approach using the concept of *Relational Growth Grammars* (RGG) [Kn08] where graph structures represent growth stages of plants and rewriting rules model physical and functional processes and interactions of plant components.

Based on training data, we learned and constructed characteristic geometrical and relational descriptions of grape cluster's components (berries, pedicels, twigs, rachis, peduncle, etc.) and their structures of interconnectivity, i.e., their structural architecture. Furthermore, we learned in an automated approach the variations of the geometrical and structural parameters in terms of statistical distributions [BSS13], [SBS13]. This knowledge about grape clusters was encoded as graph structures and rewriting rules in an RGG model.

Our reconstruction approach is governed by a global coarse-to-fine strategy to improve the reconstruction results stepwise. The first step starts from the exterior plant components of a grape cluster (i.e., the peduncle and the outer berries) that are "visible" in a generated 3-D point set. The peduncle is reconstructed in terms of a sequence of frustums while the berries are reconstructed in terms of spheres or ellipsoids (depending on the given grapevine cultivar). In the second step an initial model-driven hypothesis of an interior standard structure of stem and branches is fitted into the set of reconstructed berries starting from the reconstructed peduncle. The third step iteratively optimizes this initial hypothesis with respect to the knowledge about the structures and geometries of grape cluster encoded in our RGG model on the one hand (defining the so-called model-induced constraints) and with respect to the measured data (defining the so-called data-induced constraints). Figure 1 illustrates the steps of this reconstruction approach.

In general, the space of hypotheses representing all possible 3D reconstructions of a given grape cluster is of infinite size due to the combinatorics given by all structural and geometrical parameters in the RGG model of grape clusters. Therefore, an exhaustive search for the best fitting reconstruction hypothesis is not possible. Instead, we defined a probability distribution over the elements of the hypotheses space and drew samples from this probability distribution in order to find the optimal reconstruction hypothesis. Since different reconstruction hypotheses can show different numbers of components (i.e., different numbers of twigs, berries, etc.), we employed a probabilistic sampling

approach that can deal with this so-called different dimensions of the overall hypotheses space. The method of choice is called *Reversible Jump Markov Chain Monte Carlo* (RJMCMC) [Gre95], [Gre03].

For sampling the space of hypotheses, the RJMCMC method employs so-called jumps. Every jump defines a transformation from one reconstruction hypothesis to another one. Via acceptance probabilities, the RJMCMC method supports the acceptance of those hypotheses that fit the model-induced and data-induced constraints well. To enforce convergence the RJMCMC sampling toward an optimum of the underlying distribution,, we combined RJMCMC with Simulated Annealing [KGV83] . The challenge in using the RJMCMC method is the design of the set of jumps. This set must be one the one hand complete for exploring the complete hypotheses space in general. Therefore, the set of jumps must allow modifying all plant components and their parameters. On the other hand, the size of the set of jumps should be small for the sake of efficiently sampling the space of hypotheses.

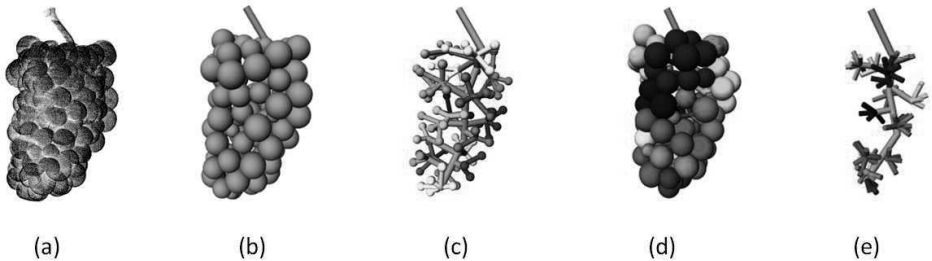| (a) | (b) | (c) | (d) | (e) |

Figure 1: (a) Measured point set, (b) step 1: reconstructed berries and peduncle, (c) step 2: initial hypothesis of interior architecture, (d) complete reconstruction result after optimization in step 3, (e) final interior architecture after optimization in step 3.

3 Results, conclusion and outlook

For a quantitative evaluation of the approach, we applied our approach on fully ripe Riesling grape clusters that show a significant amount of self-occlusions. Within a comprehensive and detailed evaluation we had shown that the reconstruction results and the derived phenotypic traits were in line with given ground truth data [Sch14].

Additionally, derived phenotypic traits are now stated precisely in the form of quantified measures instead of informal descriptions, thereby forming the groundwork for the development of new traits and correlations between traits.

In our experiments, we applied our model-based 3D reconstruction of plant architecture followed by the derivation of phenotypic traits to grape clusters. But, we believe that this approach is worth to be investigated with respect to applications to other plants. Of course, the extraction of plant components from sensor data will be different for other plants and must be designed carefully with respect to occlusions etc. But the combination of an RRG-modelling approach with the probabilistic RJMCMC sampling seems to

be an appropriate framework that could potentially improve the automated plant recon-struction and the automated derivation of phenotypic traits in a broader field of applications.

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References

[BSS13] Balfer, J.; Schöler, F.; Steinhage, V.: *Semantic Skeletonization for Structural Plant Analysis*. Intern. Conf. on Functional-Structural Plant Model , 2013, pp. 42-44.

[FT11] Furbank, R. T.; Tester, M. (2011). Phenomics – technologies to relieve the phenotyping bottleneck. Trends in Plant Science , 16 (2), 635–644.

[Gre95] Green, P. J.: *Reversible jump Markov chain Monte Carlo computation and Bayesian model determination*. Biometrika. 1995, Vol. 82, 4, pp. 711-732.

[Gre03] Green, P. J.: *Trans-dimensional Markov chain Monte Carlo*. In Green, P. J., Hjort, N. L., Richardson, S. (Eds.): *Highly Structured Stochastic Systems*. Oxford University Press, 2003, pp. 179-198.

[KGV83] Kirkpatrick, S., Gelatt, C. D., Vecchi, M. P.: *Optimization by Simulated Annealing*. Science. 1983, Vol. 220(4598), pp. 671–680.

[Kn08] Kniemeyer, O.; Barczik, G.; Hemmerling, R.; Kurth, W.: *Relational Growth Grammars - A Parallel Graph Transformation Approach with Applications in Biology and Architecture*. In Gasteratos, A.; Vincze, M.; Tsotsos, J. K. (Eds.): Computer Vision Systems, LNCS, vol. 5008 pp. 152–167, 2008, Springer.

[SBS13] Schöler, F.; Balfer, J.; Steinhage, V.: *Automated Parameter Estimation for a Plant Architecture Model*. Int. Conf. on Functional-Structural Plant Models, 2013, pp. 22-24.

[Sch14] Schöler, F.: *3D Reconstruction of Plant Architecture by Grammar-based Modeling and Markov Chain Sampling*. Ph.D. thesis, University of Bonn, Department of Computer Science, 2014.

[SSB12] Steinhage, V.; Schöler, F.; Balfer, J: *A Model-Based Approach to High Performance Phenotyping*. Intern. Conf. on Informatics for Environmental Protection (EnviroInfo), 2012, pp. 303-310.

[SS12] Schöler, F.; Steinhage, V.: *Towards an Automated 3D Reconstruction of Plant Architecture*. Schürr, A., Varró, D., Varró, G. (eds.): AGTIVE 2011. LNCS, vol. 7233, pp. 51-64, Springer, 2012.