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High-precision 3D detection and reconstruction of grapes from laser range data for efficient phenotyping based on supervised learning

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ABSTRACT

In this contribution, we present an automated approach to the phenotyping of grape bunches. To do so, our method analyses high-resolution sensor data taken from grape bunches and generates complete 3D reconstructions of the observed grape bunches. We extend a previous work from our group to earlier development stages with mostly visible stem structure, using an enhanced pre-classification of the sensor data into specific categories, i.e., berries and stems, yielding high precision and recall rates for the reconstruction of the berries of more than 98% and 94%, respectively. The same quality of results can be achieved by training a classification model on one grape bunch and applying it to the other grape bunches. Furthermore, we describe important observations concerning parameter initialization and optimization techniques resulting in a guideline for people working in the area.

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1. Introduction

1.1. Motivation

In this context, phenotypes refer to the set of observable traits of a plant resulting from its genetic properties and interaction with the environment. Measuring and evaluating these traits over time (phenotyping) is required for the improvement of selection efficiency in plant breeding and field management, predicting the yield potential of different genotypes and investigating their stress tolerance or disease resistance under different circumstances.

Manual phenotyping is widely recognized as a labour-intensive and costly task resulting in the so-called "phenotyping bottleneck" (Furbank and Tester, 2011). Therefore, several approaches to efficient phenotyping have been proposed, most of them employing automated analysis of image data (cf. Section 1.2). Recently, new approaches using 3D data for automated phenotyping were introduced (cf. Section 1.2). 3D data allows for automated reconstruction of complete 3D models of given plants or plant organs, providing the opportunity to derive arbitrary phenotype traits in a direct way in contrast to approximate estimations from 2D data that hamper from low contrasts, perspective distortions, and a larger amount of occlusions (including self-occlusions) compared to 3D data, as missing parts of the plant cannot be recovered by assuming a different viewpoint angle.

This article focuses on the automated phenotyping of grape bunches, showing three contributions:

1. We summarize the state of the art of automated 3D reconstruction and phenotyping of grape bunches using 3D sensor data.
2. We show a complete 3D reconstruction and phenotyping pipeline for grape bunches using methods of machine learning and object recognition.
3. We give practical advice on how to tune our automated reconstruction and phenotyping pipeline.

This approach can be seen as a showcase for developers and users for comprehensible parameter initialization and optimization of software systems. We optimize all parameters in an understandable way by explaining them in terms of expected sizes of plants and plant organs, whereas many software tools leave users in the dark with so-called magic numbers.

Schöler and Steinhage (2015) presented a fully automated approach to reconstruct grape bunch architecture in the development stage BBCH89 with berries fully ripe for harvest. The first step in their approach applies the Random Sample Consensus (RANSAC) to detect and estimate position and size parameters of the berries in the data set, followed by an optimization of a component model of the plant architecture with respect to the input data using the Reversible Jump Markov Chain Monte Carlo (RJMCMC) algorithm. Given the reconstructed complete architecture of the grape bunch, phenotype traits, e.g., from the OIV list

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(Organisation Internationale de la Vigne et du Vin, 2009), can be derived.

We start with the earlier development stage BBCH73 with groat-sized berries and mostly visible stem structure. Here, the diameter of the stem structure on the one hand and the berries on the other hand can be similar or even the same. While RANSAC has been shown to be both efficient and robust even in noisy data (Schnabel et al., 2007), under these circumstances we have to expect to find a sufficient number of points supporting a sphere placed inside the stem, leading to false detections of berries. Therefore, we employ a classification of the laser-range measurements included in a point cloud into surface points of berries or stems, before using RANSAC to identify berries.

1.2. Related work

In this contribution, we interpret point clouds generated with a 3D laser-range sensor (cf. Section 2.1). There are alternatives for the generation of 3D data, like, e.g., multi-view stereo vision as done by Klodt and Cremers (2014).

The Fast-Point-Feature Histograms (FPFHs) developed by Rusu et al. (2009) were used by Paulus et al. (2013) for the classification of laser range data to estimate quantitative plant traits, like volumes of plant organs. In this context, they also show their suitability to differentiate between basic shapes, like spheres and cylinders. Therefore, we apply FPFHs as descriptor for the classification of laser-range measurements using a Support Vector Machine (SVM, Vapnik, 1995) into surface points of berries (spherical regions) or stems (cylindrical regions). Other than Paulus et al. (2013), we aim at a precise 3D reconstruction of plant organs. Wahabzada et al. (2015) suggest to replace the supervised classification with an SVM with unsupervised clustering methods. This would be applicable to our approach as well. Examples for supervised alternatives to SVMs are Random Forests or Ferns (Bosch et al., 2007), but we choose SVMs for their robustness with respect to noise and very efficient openly available implementations. It would also be possible to refer to the 3D Hough Transform as used by Rabbani and Van Den Heuvel (2005) for the detection of cylinders in point clouds, but this is less efficient compared to RANSAC. Conditional Neural Networks could be used to reconstruct spheres from a point cloud in a single step, as done by Maturana and Scherer (2015) for planes, but are harder to interpret and require a large amount of training data.

Some studies derive the sizes of berries as one of the most important traits in grapevine breeding (Kicherer et al., 2015; Roscher et al., 2014) or estimate the fruit-to-leaf ratio using depth maps to segment RGB data into leafs, stems, berries and background (Klodt et al., 2015). Others perform yield estimation based on the detection of berries, as done by Nuske et al. (2014), Font et al. (2014) and Liu et al. (2013), or inflorescences (Diago et al., 2014) in images. Tello and Ibáñez (2014) developed an approach for the automated estimation of the density of grape bunches evaluating indexes and applying image analysis to field or lab imagery. Different ways to estimate the grape bunch density by sensor-based approaches have been proposed: Cubero et al. (2015) measure the proportion of pixels in a bunch corresponding to berries, rachis, and holes, while Ivorra et al. (2015) use the difference between the convex hull of the bunch itself and its berries. None of these studies aim at a complete reconstruction and only the approach of Cubero et al. (2015) detects the rachis of a grape bunch.

In contrast to these, we perform a complete reconstruction of grapevine berries and stem structure of grape bunches from 3D laser scanned point clouds in the context of high throughput plant phenotyping, making use of the Fast-Point-Feature Histograms to classify laser-range measurements with an SVM into points that are part of the surface of either a berry or the stem. We group the classified berry points into coherent regions (segments) using region growing as segmentation method. Then we apply RANSAC for berry detection to the resulting regions. Furthermore, we derive all parameters, like support radii or thresholds, based on known grapevine statistics and introduce initial results of a stem reconstruction approach using the newly derived berries. With the complete and detailed reconstruction it is possible to derive any known descriptor and investigate new traits for the characterization of grape bunches.

We use the *Point Cloud Library* (PCL, Rusu and Cousins, 2011) implementations of FPFHs, region growing and RANSAC and the PCL-Visualizer to provide screenshots. For the stem reconstruction approach, we employ the *Growth Grammar related Interactive Modelling Platform* (GroIMP, Hemmerling et al., 2008), a platform developed for the implementation of Relational Growth Grammars, and the GroImp-Visualizer to provide reconstruction screenshots.

2. Materials and methods

The overall workflow up to the step of berry reconstruction is shown in Fig. 1. It consists of the following steps:

(a) Compute a Fast-Point-Feature Histogram descriptor for each 3D measurement of the laser scanned grape bunch, representing the surface properties at this measurement.
(b) Based on the FPFHs, classify the laser-range measurements into surface points of a berry or a stem using an SVM model.
(c) Use a region growing approach to group the berry points into coherent patches of berry surfaces, so-called segments.
(d) Repeatedly apply RANSAC to each berry segment to generate berry hypotheses. Validate the berry hypotheses in a post-processing step.
(e) The resulting berries can be used as input for further reconstruction of the stem structure.

The next sections explain the steps in more detail.

Like most systems, our approach requires different parameters. While they are introduced and explained for every step of the workflow in the different parts of this section, Section 3.1 shows a collection of all parameters in Table 1 and explains how to derive and optimize their values, offering a blueprint for their practical employment.

2.1. Plant material and sensor

We use 3D point clouds generated with a Perceptron ScanWorks V5 (Perceptron Inc, 2016) attached to a Romer Infinite 2.0 articulated arm (Hexagon Metrology Inc, 2016). This sensor creates 7640 point measurements in lines at a frequency of 60 Hz with an accuracy of 0.024 mm. While the sensor is moved around the object, the sensor's software collects the line measurements into a single coordinate frame, resulting in a highly dense 3D point cloud. We apply a voxelgrid filter with a voxel side length of 0.2 mm in each axis direction to the point cloud, reducing the number of points from between 1.2 and 1.7 million to about 200 to 350 k and the overall running time from approximately 9000 s to about 200 s with Intel Core i7 CPU with 3.60 GHz and 8 GB RAM averaged over the different instances.

We use five scanned grape bunches (called 22B, 23A, 23B, 24A and 27B) of the cultivar Riesling (*Vitis vinifera* L.) in development stage BBCH73 according to the BBCH classification. The typical bunch size ranges between 7 and 13 cm, the berries are groat-sized and most of the stem system is visible. We determined the minimal and maximal berry radius of this development stage

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