

3D phenotyping of peach tree canopy architecture using terrestrial laser scanning

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ABSTRACT

Throughout history, pomologists have developed various trainings systems for temperate fruit trees to improve light interception, fruit yield, and fruit quality. To achieve this, these training systems enforce certain branch and canopy morphologies upon the tree. Quantifying architecture could aid the selection for trees that require less pruning or naturally excel in specific growing/training system conditions. Tree architecture is also directly associated with resource optimization, funneling what nutrients the plant absorbs into the most efficient, high-yielding configuration possible. In peaches [*Prunus persica* (L.) Batsch], branching indices (BIs) have been developed in attempts to quantify tree architecture. BIs can effectively focus on a particular area of tree architecture (e.g., an index focused on branching density, or BDi), producing quantitative measurements that can accurately represent a tree’s unique architecture. However, the required branching data to develop these indices is hard to collect. Historically, branching data has been collected manually. Often this process is tedious, time-consuming, and prone to human error. These barriers can be circumnavigated by utilizing 3D remote imaging technology, such as terrestrial LiDAR scanning (tLiDAR). To test this, young peach trees were scanned with 3D scanners and modeled using *TreeQSM*. This allowed us to collect branching data with which to calculate BDi values. Statistical analyses of BDi measurements from the 4 young trees will create a methodological pipeline with which mature and complex trees architectures may be simulated. These BDi values, either in young or adult trees, will be used to better phenotype trees’ architecture and to better select trees for further breeding and selection (i.e. future genomic studies - GWAS and novel QTL identification).

Keywords: Plant Breeding, Computational Biology, Phenomics, Phenotyping, Bioinformatics, 3D modelling, tLiDAR

1. INTRODUCTION

Nearly all fruit tree breeding programs focus on traditional complex traits, such as fruit yield, fruit quality, disease resistance, and freezing prevention/chilling requirements. However, tree architectural traits that could be used to optimize physiological processes and tree training are less understood [1]. Tree architecture is associated with resource optimization, which will be a critical factor in developing fruit trees that are resilient to the effects of climate change, especially in deciduous fruit trees such as peach [*Prunus persica* (L.) Batsch]. Setting up a successful training system is laborious and requires the trees to undergo regular pruning. Due to this, research that prioritizes better understanding tree morphology, branching patterns, and leads to reduced pruning costs is becoming a priority from an agronomic perspective [2]. Unfortunately, conducting research into tree morphology and architecture has classically been seen as immensely challenging due to the physical limits in collecting branching data [3]. However, new technologies may provide solutions for this area of research.

Algorithms to compute and quantify the necessary branching data to study trees have been constantly improved over the last decade [4][5]. Recording branching data (e.g., number of branching orders in a tree, number of branches per branching order, etc.) via manual methods are prone to human error and are exceedingly time-consuming. Due to this complication, development of a novel way to record branching data without the difficulties of manual collection would lead to potential breakthroughs in fruit tree physiology and breeding. Studies with access to reliable and readily available branching data could focus on quantifying specific traits associated with architecture and morphology [6]. As such, a main focus of this study is to evaluate the use of remote sensing technology, such as tLiDAR, to collect branching data in peaches [7]. This ‘*in-silico*’ data collection approach then will be compared to ‘*in-situ*’ field measurements of branching data. Utilizing tLiDAR technology will also allow for the generation of point cloud data from our scanned peach trees. This point cloud data can then be used in modelling softwares specifically to characterize unique aspects of tree architecture. For this purpose, *TreeQSM* v2.4.0 software was used to create novel 3D, quantitative structural models (QSMs) from our scans [8]. These QSMs then can be used to provide biometric information such as branching data. Such data is vital for utilizing BIs in order to accurately quantify aspects of canopy architecture; as with BDi values and branching density. As such, BDi values from in-silico and in-situ sources in juvenile trees will be calculated and compared. The main goal of this research is to construct QSMs of our young trees from point cloud data generated via tLiDAR remote scanners, ultimately allowing us to conceptualize and quantify the intrinsic aspects of tree architecture. This study will also provide tools for future breeding applications as well as agrobotics/phenotyping research [9].

1. METHODS

2.1 Utilizing tLiDAR scanning equipment to create point cloud data from peach trees

This experiment was conducted at UGA Griffin Campus, Research and Extension Peach orchards at Dempsey Farm, University of Georgia, Griffin, GA. Both juvenile (one-year-old) and adult (six-year-old) peach trees were scanned in February 2021 when the peach trees were dormant (defoliated and before winter pruning). Approximately 50 adult trees, representing 25 different peach cultivars, were scanned (~2 trees per cultivar). In addition, approx. 46 one-year old trees were scanned. The young trees are of the same cultivar ‘Julyprince’; however, the young trees are budded onto two different rootstocks: ‘Guardian’ (GA) and ‘MP29’. The adult trees that were scanned all were grafted on GA rootstocks.

A FARO Focus3D X 330 laser scanner (Faro Technologies, Lake Mary, FL) was used to take scans of both the adult and young trees. An exposure time of 11 minutes and 29 seconds was kept constant throughout the scanning process, with 8 spherical targets being used when scanning both sets of trees. Of these 8 targets, 4 were moved between scans (advancing forward), while 4 remained stationary, and thus acted as references between each scan. The recorded raw scans were processed and registered using a FARO-based software, SCENE v2020.0.1 (Faro Technologies, Lake Mary, FL). In SCENE, adult and juvenile tree scans were separated into respective projects and processed. Adult trees were processed using options to remove stray-points and dark-points within the scans. Processing was similar in young trees, except for the dark-point processing, which was excluded. After finishing processing/registering the scans, point cloud data from individual trees (adult and young) were selected for reconstruction via *TreeQSM*. From this MATLAB-based software, QSMs from our point cloud selections were generated, alongside biometric and branching data (Fig. 1).

2.2 Optimization of 3D cylinder modelling pipeline *TreeQSM* for use in peaches

While *TreeQSM* had previously been shown to work in the modelling of apple trees, as of yet no work has been done to the same extent in peaches^[10]. To achieve this, *TreeQSM* first needs to be optimized for peach trees in order to provide accurate branching data and biometric data. In *TreeQSM*, there are several direct input parameters that are used to characterize the 3D cylinder reconstruction of a QSM. Of the five parameters that can be directly optimized, PatchDiam1, PatchDiam2Min and PatchDiam2Max are of the most importance. To quickly summarize, PatchDiam1 is responsible for the initial cover-set fitting of the 3D model. This initial fitting defines the trunk in addition to the rough outline of the tree’s branching structure. PatchDiam2Min and Max each can be optimized by adjusting values to correspond with biometric measurements (e.g., diameter at breast height [DBH]). The PatchDiam2 parameters are arguably the most important when it comes to model creation, as they essentially determine the second cover fit accuracy and heavily influence primary and higher branching order structure. All parameters have been adjusted for both young and adult trees, however only findings from the young trees have been analyzed and presented in this manuscript.

2.3 *In-situ* and *in-silico* data collection

Collection of *in-situ* branching data for the younger trees occurred several weeks following scanning. It is important to note that the *in-situ* data collection occurred after scanning, but before the young trees had been pruned going into the spring season. Thus, the branching structure for the young trees did not change between the time of scanning and the time of *in-situ* data collection. Four trees from the one-year-old trees were selected (trees 19, 20, 28, 29) for comparison of *in-situ* and *in-silico* data. *In-silico* data collection first required the previous optimization of parameters in *TreeQSM* in order to create reliable models that, within reason, are true to what would be observed in the field. Afterwards, 20 iterations of modelling process are run and branching data values are collected per tree. The standard deviations (SD) of these values were calculated until a batch of 20 iterations produced branching data that was within 1 SD of the mean calculated values. These accepted mean values were then used as representative values for the *in-silico* data.

2.4 Utilization of branching indices (BIs) to characterize aspects of peach tree architecture

As discussed previously, branching data can be further adapted via the use of BIs, which will help quantify specific aspects of tree architecture (such as branching density). One such BI mentioned earlier (BDi) will be used to quantify branching density in our young trees. This BDI was developed at the University of Florida (UF) [2], with its formula listed here as:

$$BDi = \prod_{i=1}^k 2^{(x_i + \frac{n_i}{100})}.$$

Carrillo et al. (2010) described the formula as follows “..where x = absence (x = 0) or presence (x = 1) of first-, second-, third-, or subsequent order branches; n = number of branches within a branching order; and k = the maximum order of branching”. BDi measurements from the 4 selected young peach trees will be calculated and analyzed for differences in values between in-situ and in-silico data collection methods. Differences in BDi in the young peach trees possessing different rootstocks will be examined as well for reference.

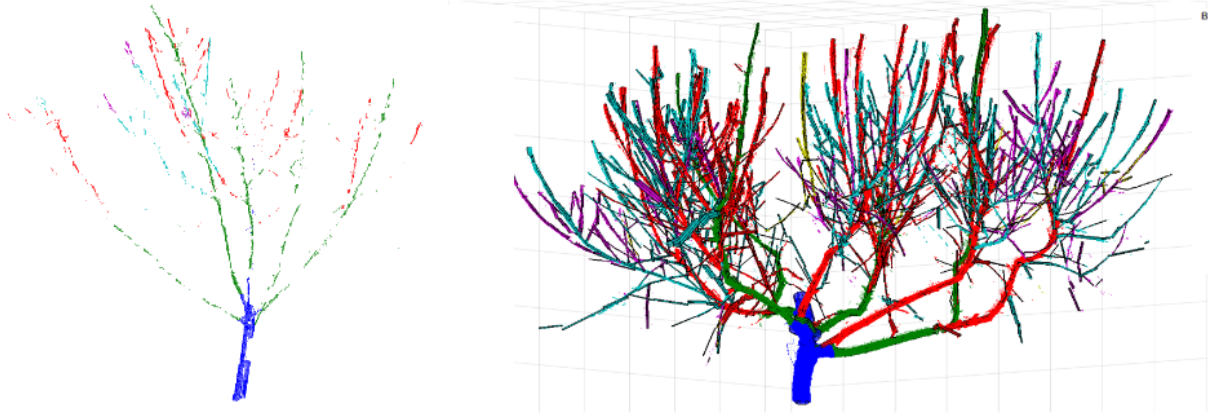
1. RESULTS & DISCUSSION

3.1 Initial 3D reconstruction and QSM modelling

Following the optimization of parameters in *TreeQSM* for adult and young peach trees, varying levels of success were achieved in creating the 3D models during the first several iterations. Ultimately, younger trees models were chosen be our first analyzed models. This is due to their lack of complexity when compared to adult trees, allowing us to run multiple iterations of modelling necessary to generate quality QSMs. *In-situ* branching data also proved much easier to collect from younger trees when compared to adult peach trees, which allowed us to have more individual tree’s entire architecture and branching structure measured by hand. However, models from the adult peach trees, even with the

inherently larger amounts of complexity within the point clouds, objectively had less fluctuations during the 3D cylinder reconstruction process when compared to the younger trees.

The increased amount of perturbation found when modelling the younger trees could be the result of a number of different factors. The main factors however that resulted in these difficulties are the conditions under which the young tree scans were taken, as well as the nature of how the *TreeQSM* modelling process works. While scanning the young trees, low-light conditions were largely present. During the initial processing/registration of the young tree scans, the inclusion of dark-point filtering led to the SCENE software having difficulties accurately identifying the targets in the respective scans. This caused issues with registration, and lower overall quality of point clouds that were generated as a result. This ultimately led to the decision to not include the dark-point processing filter, which improved overall point cloud configuration. However, this also led to more noise within the models than if the filter was used, resulting in a wider breadth of configurations during modelling.



was further compounded by the specifics of how modelling is done in *TreeQSM*. The resulting issues were difficulties assigning the correct branching order to the appropriate cylinder segments during the segmentation process. This initial step occurs after a general cover set is used to roughly define the structure and general branching order of the model. However, since *TreeQSM* was initially designed with arboreal settings and trees as the intended model subjects, adaptations have been made to co-opt this modelling software for use in peaches. Specifically, the peach trees used in this study (adult and young) have been grown using an open-base training system. This system is used to create 3-5 (mostly 4) primary branches, or ‘scaffolds’ per tree, instead of a single strong, apical meristem. This produced some trouble when modelling the younger trees in *TreeQSM*, as the software wants to assign an apical meristem to the tree, and thus has difficulties assigning the smaller, less robust scaffolds to the primary branching order, instead seeing them as continuations of the

trunk. Workarounds however were implemented to fix this issue. The resulting models for the four young trees (19, 20, 28, 29) were found to have averaged SD of branches equal to 0.77, 1.05, 0.92, and 1.05 respectively. These branch SD scores were averaged from the SD values from each branching order from each respective tree. The aggregate branching SD from amongst all the young trees was 0.95. As a result, point cloud data from both adult and young trees have proved successful in generating 3D models that also could be used to provide branching and biometric data by utilizing remote sensing methods such as tLiDAR technology as seen in Fig. 1.

Figure 1. 3D reconstruction models of an adult (right) and young (left) peach tree from our orchards via *TreeQSM*. The key on the right provides correspondence of branching order to color of limbs. Notice the difference in complexity between the two, one of the reasons the younger trees were selected first selected to analyze our modelling process.

3.2 Comparing *in-situ* branching data/BDi values to *in-silico* *TreeQSM* data

After successfully generating models for the young trees and optimizing parameters, results from the preliminary *in-silico* data collection could be compared to *in-situ* data. A two-way ANOVA test was done to compare branching data collected for the different branching orders (1-4) amongst in-situ and in-silico sources. Results from this test showed the interrelationship of the two variables (branching data and data source) were not different in a statistically significant factor (F-value = 0.200, p-value = 0.895).

1. CONCLUSION

Our study has assessed the feasibility of creating 3D reconstructed models of young peach trees, as well as the validity of the quantitative data collected from these QSM 3D models. Findings from these QSM models were deemed *in-silico* data, and compared alongside previously collected *in-situ* data from the field. Statistical analyses show that there was no significant difference (p-value < 0.05) between the two sets of data between branching orders. In addition, when the respective sets of data were used to create BDi indices for the young trees, the results of which were likewise found to have no significant difference in value.

As such, results from comparing the branching data in younger trees' *in-situ* and *in-silico* have been statistically analyzed and were found to have no statistically significant difference between the two sets of data. This provides supportive cause to move forwards with focus now shifting to modelling of adult trees, as analyses from the young tree 3D models give interesting insight to the applicability and fidelity of utilizing *TreeQSM* in modelling peach trees, especially with regards to adult and more developed juvenile trees. Successful model creation, in addition to comparison to *in-situ* branching data, proved significant in advancing our efforts to use these remote sensing techniques for the upcoming defoliate season. This would provide not only important branching data, but

3D QSM models as well. Branching data could be useful in designing future branching indices, as well as calculating BDi values. These values can then be used in selection trials, or in phenomic/genomic studies as a trait of interest. Furthermore, the QSM models being generated have strong implications for use in agrobotics and AI learning algorithms, advancing areas of research such as automated pruning and fruit harvesting.

DATA AVAILABILITY STATEMENT

https://github.com/Computational-Plant-Science/young_peach_treeqsm

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