

Tradeoffs and limitations in determining tree characteristics using 3D pointclouds from terrestrial laser scanning: A comparison of reconstruction algorithms on European beech (*Fagus sylvatica* L.) trees

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Abstract Terrestrial laser scanning (TLS) has quickly gained momentum in forestry as a fast and nondestructive alternative to determine tree shape and volume. Determining tree shape and volume is fundamental for a wide range of forestry applications, including the estimation of carbon stock and development of volume and biomass allometric models. However, tree shape and volume are often determined from TLS data based on different available algorithms, with direct implications on the measured tree feature. In this study we compared several algorithms for tree reconstruction from TLS data, with respect to their capacity to accurately determine tree characteristics such as diameter at breast height (DBH), tree height (H), stem volume (V_{st}) and total aboveground tree volume (V_{tot}). The following algorithms were compared using Bland-Altman limits of agreement (LoA): (i) TreeQSM, (ii) 3D Forest, (iii) RANSAC and (iv) Poisson. The data used for the comparison was collected from 10 sample plots, totalizing 40 European beech (*Fagus sylvatica* L.) trees, covering a DBH range from 6.2 cm to 76.0 cm and H range from 9.5 m to 36.2 m. The results showed that the algorithm used to analyse the TLS data affected notably the tree characteristics. The LoA were up to 3.65 m³ for V_{tot}, up to 7.5 cm for DBH and up to 1.1 m for H, suggesting a rather weak agreement between algorithms. From our comparison, TreeQSM emerged as the most reliable algorithm for comprehensive trait reconstruction, while Poisson was well suited for stem volume estimation. Moreover, determining H seems to be less affected by the algorithm selection compared to DBH. Our findings raise awareness about algorithm selection in TLS data processing and highlight the importance of selecting an appropriate algorithm to meet the specific objective when using TLS to determine tree shape and volume.

Keywords: LiDAR, TLS, 3D tree shape, tree reconstruction methods.

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Introduction

Promoting sustainable forestry practices necessitates gathering precise measurements of key tree attributes, including diameter at breast height (DBH) and tree height. These measurements are crucial predictors for estimating tree volume or biomass (Ketterings et al. 2001, Dutcă et al. 2022). For instance,

improved biomass and volume estimates contribute to more accurate monitoring of forest carbon, benefiting climate modeling and conservation planning (Indirabai et al. 2019).

Traditionally, tree volume and biomass are estimated through allometric models or destructive sampling, but Terrestrial Laser Scanning (TLS) now provides a nondestructive,

efficient alternative by directly reconstructing tree structure from point cloud data. Unlike typical model-based estimations, TLS reconstruction utilises point clouds to develop geometric models that more accurately capture the unique architecture of each tree. This has allowed for faster and more detailed data collection, as demonstrated in ecological studies of tree architecture, which reveal complex branching structures that would otherwise be difficult to measure. Recent advancements in TLS technology have significantly improved the scanning and reconstruction of tree shape form (Malhi et al. 2018). That is a key step forward, offering a labor-efficient solution compared to destructive sampling methods.

Current forest management tools primarily use classic inventory methods combined with allometric equations, but TLS can be used to determine tree volume directly and avoid allometric model prediction error, producing more accurate volume estimates, beneficial for various applications, from estimating biomass and stock volume to improving accuracy in carbon estimations (Fischer et al. 2020).

TLS has also provided new insights into structural parameters of trees, which is crucial for understanding variations due to tree taper, diameter-height ratios, and growth patterns that affect volume estimation (McTague & Weiskittel 2021).

There is a need for volume measured at the tree level to develop models for estimating forest tree volume and biomass (Temesgen et al. 2015), especially in cases where allometric models and formulas are unavailable (Jan et al. 2021). Avoiding prediction errors due to regional variation of tree allometry (Jan et al. 2021) yields an improved the accuracy and precision of biomass and implicitly carbon estimates, which further improves the effectiveness of emission reduction initiatives (Petrokofsky et al. 2012).

Compared to traditional mapping methods, LiDAR offers more detailed information that can be used for many different applications

and mitigates errors associated with the tree architecture (Bornand et al. 2023). The emergence of LiDAR technology has changed the mapping paradigm (Niță 2021). Nowadays, it is increasingly used in practice as well as in scientific research regarding forestry, hydrology, geomorphology, urban management, and general survey assessments (Liang et al. 2018).

Reconstructing three-dimensional tree architecture and estimating tree parameters, using terrestrial LiDAR data, offers a nondestructive method that proves to be more cost-effective in the long term (Kankare et al. 2013). Terrestrial laser scanning can provide dense point clouds and tree point clouds with high accuracy and precision, which can be analysed to estimate layered forests and forest parameters that are more difficult to estimate from airborne laser scanning (Dassot et al. 2011, Friedli et al. 2016, Liang et al. 2016).

Occlusion was not addressed here because each tree was scanned from multiple angles using a tripod-mounted scanner, ensuring complete coverage and preventing any occlusion issues. However, employing these reconstruction methods presents two critical challenges to the research process. The initial bottleneck centers around the individual tree segmentation, a crucial step in the reconstruction process (Li et al. 2012, Hui et al. 2021). Segmentation involves the delineation or separation of individual trees from the point cloud data obtained through LiDAR scanning (Yang et al. 2023). Efficient segmentation methods play a pivotal role in distinguishing tree boundaries, ensuring that reconstructed models faithfully represent individual trees (Yang et al. 2023). The precision of biometrics is directly proportional to the accuracy of the segmentation process, underscoring that all approaches aimed at detailed 3D reconstruction are as good as the segmentation of point cloud data, and data acquisition (Bornand et al. 2023).

To address challenges in individual tree segmentation, such as noise in the point cloud (Xie et al. 2018), missing trees (Windrim &

Bryson 2020), and the complexities of dense forests where trees can be mixed (i.e., branches from a tree or small under trees are attributed to another tree), manual segmentation is considered a superior approach, as it benefits from human expertise (Weiser et al. 2022).

The second bottleneck pertains to tree reconstruction itself. The literature presents various techniques for reconstructing 3D tree models using point clouds. These techniques can be grouped into three main categories, each of which facilitates extraction of tree characteristics. The first approach involves creating a skeletal model of the tree. This model, which is a wireframe with zero thickness, is embedded within and aligns with the shape outlined by the point cloud. Its primary benefit is maintaining the connectivity and topological relationships between branches (Cornea et al. 2005). The second approach involves fitting geometric shapes such as cylinders, cones, and spheres to the point cloud data of the tree. Among these shapes, cylinders are often preferred because of their ability to yield realistic tree models and extract geometric features (Rahman et al. 2015, Shen et al. 2022). The third approach involves the use of meshing solutions to create detailed tree models. Commonly employed methods include quantitative structure models (QSMs) for skeletal representations, Random Sample Consensus (RANSAC) for geometric fitting, and the Poisson algorithm for mesh reconstruction.

Studies on the implementation of TreeQSM have revealed certain limitations, particularly in accurately reconstructing thinner branches with a lower point cloud density (Raumonen et al. 2013b). This method tends to underestimate the length of smaller branches and shows a systematic underestimation of tree volume, especially for thinner branches. A conceptual difference in determining the termination point of the main stem compared with manual measurements has also been identified (Lau et al. 2018a). While the RANSAC method proves effective in estimating stem volume, it exhibits

limitations, notably the tendency to overestimate stem attributes when applied to diverse forest structures (Panagiotidis & Abdollahnejad 2021). Regarding mesh reconstruction in exploring the efficacy of Poisson surface reconstruction, it is essential to consider both its accuracy influencing factors, such as point cloud density and shape complexity, which contribute to its accuracy, as well as its limitations, including sensitivity to abrupt changes, potential computational delays, and specific applicability ranges (Morel et al. 2018). These insights underscore the importance of tackling both the segmentation challenge and the limitations associated with tree reconstruction methods, such as RANSAC, POISSON, and QSM. Emphasizing the need for reliable methods are required to precisely delineate individual trees and overcome reconstruction challenges from LiDAR point cloud data.

The aim of this study is to compare four algorithms for tree reconstruction from TLS data (i.e., TreeQSM, 3D Forest, RANSAC and Poisson), with respect to their capacity to accurately determine tree characteristics such as DBH, tree height (H), stem volume (V_{st}) and total aboveground tree volume (V_{tot}).

Materials and Methods

Collection of TLS data

A Faro Focus S70 terrestrial laser scanner (TLS) was employed to scan the trees, providing a maximum range of 70 m and an accuracy of 2 mm at a 10-meter distance. We scanned 40 trees from 10 different locations across seven counties in Romania: Brasov, Bihor, Covasna, Prahova, Timis, Hunedoara, and Harghita (Figure 1). Each plot contained three to six trees. To ensure comprehensive data collection, we conducted 8 to 10 scanning stations for each sample plot, capturing a sufficient number of laser returns to accurately represent the tree branches. The scans were performed under favorable weather conditions, specifically on sunny days with low wind

speeds. The diameter at breast height (DBH) of the sampled trees ranged from 6.2 to 76 cm, with a mean DBH of 30.4 cm and a standard deviation of 16.6 cm. Tree heights (H) ranged from 9.5 to 36.2 m, with a mean height of 25.4 m and a standard deviation of 7.9 m.

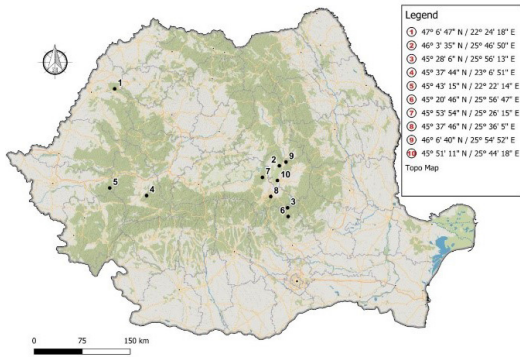


Figure 1 Location of the sample plots.

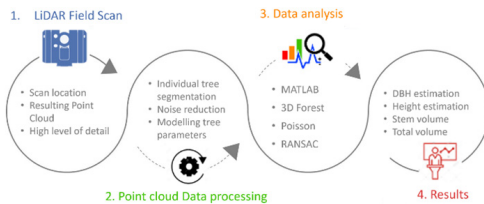


Figure 2 Process workflow.

The workflow starts with field terrestrial LiDAR scanning to acquire a high-resolution three-dimensional point cloud of the forest plots. The subsequent data processing stage involves the segmentation of individual trees, noise reduction, and the modelling of tree parameters. Advanced analytical techniques, including MATLAB-based algorithms, specialized forest modeling tools (e.g., 3D Forest), Poisson surface reconstruction, and RANSAC fitting - were used to extract key forest inventory metrics, such as diameter at breast height, tree height, and stem volume and total volume. The results provide a comprehensive basis for further quantitative assessments. The following sections provide a detailed, step-by-step explanation of each component within this workflow, offering

insights into the specific methodologies, algorithms, and parameters utilised.

Tree segmentation

To maximize point-cloud density and accuracy in tree segmentation, manual segmentation was performed to prevent cross-attribution of points between trees. This process utilised the CloudCompare software’s “2D polyline cut” function, which allowed precise delineation of individual trees within the point cloud. The 2D polyline cut function defines boundaries based on user-drawn polylines, ensuring segmentation accuracy by excluding extraneous points from surrounding vegetation.

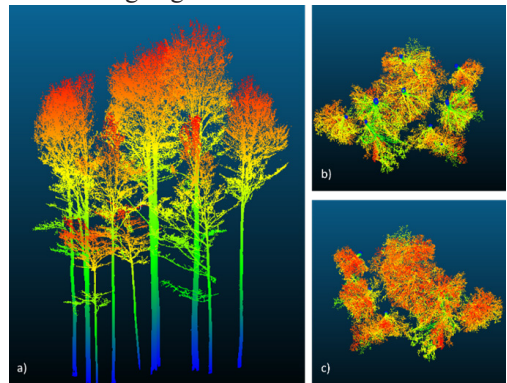


Figure 3 Individual trees view from CloudCompare (a-profile, b-bottom, c-top).

Tree parameters

We used four algorithms to extract DBH, H, stem volume or total tree volume (Table 1).

Table 1 The identification of tree attributes estimated by compared methods.

Method	Tree attribute			
	DBH	H	Stem volume	Aboveground tree volume
<i>CloudCompare reconstruction methods</i>				
Poisson	no	no	yes	no
RANSAC	no	no	yes	no
<i>QSM algorithms</i>				
TreeQSM				
MATLAB	yes	yes	yes	yes
3D Forest	yes	yes	no	yes

CloudCompare reconstruction methods

To approximate the tree surface, we used triangulation techniques. These methods ensure consistent orientation of normals across the point cloud, which improves the model’s

surface accuracy. The minimum spanning tree function further stabilizes the model, aligning points within each tree to reduce spatial inconsistencies. Users need to define the maximum number of neighbors at each node, balancing accuracy with computational resources. In this study, we employed the maximum value for computing the normals to ensure a comprehensive analysis.

We applied the Poisson surface reconstruction algorithm plugin from CloudCompare to generate a triangle mesh and estimate tree volume by solving a Poisson system, considering all points simultaneously, and minimising the impact of noise for the complete tree pointcloud. However, because of the complex branching system, this algorithm produced high deviation for total volume, leading us to eliminate branches and calculate only trunk volume. To address the fitting errors and volume distortion caused by gaps in the trunk, we iteratively cut the trunk until accurate estimations were achieved. In addition, in CloudCompare, we employed the random sample consensus (RANSAC) algorithm to fit the tree shape into a cone, simulating classical tree measurements (a caliper like approach) and allometric relationships. Although RANSAC provides a single-cone trunk and may not estimate well, it aligns with traditional methods and compensates for positive values with negative values in a neoid form.

QSM algorithms

a. TreeQSM in MATLAB

TreeQSM utilises point clouds to reconstruct quantitative structure models (QSMs) of trees, employing cylinders to estimate the topological, geometrical, and volumetric aspects of the woody structure. Utilising the "cover sets" function, the algorithm divides the point cloud into small sets representing the trunk and each branch, where identified branches serve as starting points for segmentation, identifying trunk and initial branches, pinpointing potential bifurcations, and iteratively segmenting up to the last branching order, aligning with the tree's

natural growth pattern. This precision allows for volume reconstruction and quantification of parameters, such as total volume, height, length, basal area, and DBH.

b. 3D Forest

3D Forest is an open-source software designed for the segmentation, analysis, measurement, and export of data derived from terrestrial laser scanning. It extracts by extracting key parameters related to forest structure, such as stem positions (X, Y, Z), tree height, and diameter at breast height (DBH). Within the Tree menu, the 'Position RHT' (Randomized Hough Transform) function was used to identify a circular structure within the tree points at a specified height. The tree position, representing the center of the tree base, is established, and the software adds a dot to the lowest point on the tree point cloud to demonstrate the fitting of a circle. Two methods, DBH RHT and Least Square Regression (DBH LSR), compute tree diameters at breast height, and the DBH cloud is a subset using a horizontal slice above the lowest point of the tree cloud.

This study employs DBH RHT for circle detection, comparing its results with caliper measurements and evaluating sensitivity and computational time. The Tree Height parameter was calculated as the difference between the lowest and highest points of the point cloud, with the green circle line representing the breast height and the number indicating the resultant diameter. Trochta et al. (2017) conducted several precision tests with 3D Forest to compare its accuracy with that of other classic forest measurement tools. The Haglöf caliper provided 1 cm precision in DBHs, and the TruPulse laser rangefinder provided 0.1 m precision for tree heights compared to the 3d Forest software, for a sample of 181 trees.

The quantitative structure models (QSM) tree reconstruction function provides information about branches and stems by employing known tree positions and heights. After dividing the tree into voxels, stem reconstruction involves searching for neighbors, categorizing

connected neighbors as segments and non-connected groups as branches of different orders. Parametric tree reconstruction yields connected cylinders for each branch, with an attribute table containing information regarding volume, length, and order.

Compared parameters

We compared the performance of the algorithms based on Bland and Altman's limits of agreement (LoA), evaluating differences across parameters such as DBH, H, and Volume. This approach assesses the algorithms' consistency and highlights which algorithms are best suited for specific tree traits such as diameter at breast height, tree height, stem volume and total tree volume.

Diameter at breast height (DBH)

A total of five DBH versions were compared, two derived from TreeQSM algorithm in MATLAB, and three from 3DForest.

- DBH1 – is the DBH resulted from 3DForest, derived using the *Randomized Hough Transformation (RHT)*, fitting a circle to the tree's DBH subset by searching for the most frequent circle center in the projected horizontal plane at a height between 1.25 m and 1.35 m above the tree base (“3d-forest-classic/3DF_wiki_guide.pdf at master · VUKOZ-OEL/3d-forest-classic · GitHub,” n.d.).
- DBH2 - is the DBH resulted from 3DForest, calculated through *Least Squares Regression (LSR)* by fitting a circle to the DBH subset, minimising the mean square distance between the fitted circle and data points, sensitive to outliers, at a height between 1.25 m and 1.35 m above the tree base (“3d-forest-classic/3DF_wiki_guide.pdf at master · VUKOZ-OEL/3d-forest-classic · GitHub,” n.d.).
- DBH3 – is the DBH resulted from 3DForest determined from a specific subset of points within the tree cloud, referred to as the DBH cloud, derived at a height between 1.25 m and 1.35 m above the tree base (“3d-forest-

classic/3DF_wiki_guide.pdf at master · VUKOZ-OEL/3d-forest-classic · GitHub,” n.d.).

- DBH4 – is the DBH resulted from TreeQSM algorithm, that was calculated as a mean of stem diameters between 1.1 and 1.5 m from the ground (“TreeQSM/Manual/TreeQSM_documentation.pdf at master · InverseTampere/TreeQSM · GitHub,” n.d.).
- DBH5 – is the DBH resulted from TreeQSM algorithm in MATLAB that corresponds to the diameter of the section of the stem at 1.3 m, using fitted cylinders, from the ground (“TreeQSM/Manual/TreeQSM_documentation.pdf at master · InverseTampere/TreeQSM · GitHub,” n.d.).

Tree height

- H1 – is the tree height as resulted from 3DForest, calculated by measuring the vertical distance between the tree base position and the highest point of the tree. This process involves identifying the tree base and then finding the maximum Z coordinate value within the tree cloud (“3d-forest-classic/3DF_wiki_guide.pdf at master · VUKOZ-OEL/3d-forest-classic · GitHub,” n.d.).
- H2 – is the tree height as resulted from TreeQSM algorithm in MATLAB, calculated as the difference between from the base of the tree to the highest point of the tree represented in the QSM (“TreeQSM/Manual/TreeQSM_documentation.pdf at master · InverseTampere/TreeQSM · GitHub,” n.d.).

Stem volume

For stem volume we compared three algorithms:

- Vst1 – is the stem volume in TreeQSM, calculated by fitting cylinders to the point cloud data of the tree. The total stem volume is then obtained by summing the volumes of these individual cylinders (“TreeQSM/Manual/TreeQSM_documentation.pdf at master · InverseTampere/TreeQSM · GitHub,” n.d.).
- Vst2 – is the stem volume calculated with

RANSAC in CloudCompare, which calculates stem volume by detecting and fitting cylindrical segments in the point cloud through random sampling. Cylinders are generated, scored by inlier points, and the best fit is iteratively selected. Volumes of detected cylinders are calculated and summed for total stem volume, handling noise and outliers efficiently (Schnabel et al. 1981).

- Vst3 – is the stem volume calculation in CloudCompare using Poisson reconstruction, which involves defining a gradient field from surface normals, handling non-uniform sampling and using an adaptive octree for efficient, detailed 3D surface reconstruction and volume calculation (Kazhdan et al. 2006).

Total tree volume

Two algorithms were used to derive the total aboveground tree volume:

- Vtot1 - is the tree total volume calculated using 3DForest, which involves reconstructing the tree into segments using voxel segmentation and fitting cylinders to these segments. Each segment's volume is calculated based on its geometric properties, and the total volume is obtained by summing the volumes of all the segments (“3d-forest-classic/3DF_wiki_guide.pdf at master · VUKOZ-OEL/3d-forest-classic · GitHub,” n.d.).

- Vtot2 - is the tree total volume calculated using TreeQSM, where the algorithm fits cylinders to the entire point cloud. Each cylinder's volume is calculated, and the tree total volume is then determined by summing the volumes of all the cylinders in the QSM, which includes both the trunk and branches (“TreeQSM/Manual/TreeQSM_documentation.pdf at master · InverseTampere/TreeQSM · GitHub,” n.d.).

- Error (Point-model distance structure) - represents the point-model distance structure in TreeQSM, which evaluates the accuracy (expressed in millimeters) of the model by comparing the 3D point cloud data with the reconstructed Quantitative Structure Model (QSM).

Table 2 The identification of abbreviations with their respective algorithms and traits.

Abbrev.	Algorithm	Trait Assessed
DBH1	3D Forest	Diameter at Breast Height
DBH2	3D Forest	Diameter at Breast Height
DBH3	3D Forest	Diameter at Breast Height
DBH4	TreeQSM	Diameter at Breast Height
DBH5	TreeQSM	Diameter at Breast Height
H1	3D Forest	Tree Height
H2	TreeQSM	Tree Height
Vst1	TreeQSM	Stem Volume
Vst2	CloudCompare RANSAC	Stem Volume
Vst3	CloudCompare Poisson	Stem Volume
Vtot1	3D Forest	Total Tree Volume
Vtot2	TreeQSM	Total Tree Volume

Comparison of reconstruction methods

We used Bland-Altman plots and the limits of agreement (Bland & Altman 1983) to compare each set of two reconstruction methods. For each tree we calculated the mean and the relative difference of the two compared methods:

$$SLC = \frac{H}{DBH} \tag{1}$$

$$Dif_i = \frac{X1_i - X2_i}{M_i} \cdot 100 \tag{2}$$

where $X1_i$ is the measurement of i^{th} tree using reconstruction method 1; $X2_i$ is the measurement of i^{th} tree using method 2. The mean difference (\overline{Dif}) between estimates of each set of two methods was calculated as:

$$\overline{Dif} = \frac{1}{n} \sum_{i=1}^n Dif_i \tag{3}$$

where n is the total number of trees; we further calculated the limits of agreement (LoA) as:

$$LoA = \overline{Dif} \pm 1.96 \sqrt{\frac{1}{n-1} \sum_{i=1}^n (Dif_i - \overline{Dif})^2} \tag{4}$$

Results

DBH reconstruction algorithms

The Bland-Altman plots comparing the algorithms for DBH reconstruction are presented in Figure 4. The largest mean differences between two algorithms used for

DBH reconstruction were observed for DBH3 vs. DBH4 (+8.4%), DBH3 vs. DBH5 (+7.8%), DBH1 vs. DBH3 (-7.6%) and DBH2 vs. DBH3 (-7.5%), whereas the smallest mean differences were recorded for DBH1 vs. DBH2 (-0.1%),

DBH1 vs. DBH5 (+0.2%) and DBH2 vs. DBH5 (+0.3%).

The LoA roughly followed the results observed for the mean difference. The widest LoA were observed for DBH3 vs DBH4 (-12.2% to 29.1%), DBH3 vs DBH5 (-13.5% to +29.1%), DBH1 vs DBH3 (-29.5% to 14.3%) and DBH2 vs DBH3 (-28.6% to 13.7%). What all these pairs have in common is the algorithm DBH3. Therefore, it seems that algorithm used for DBH3 was in strong disagreement with all the other compared algorithms. The smallest LoA, and, therefore, the greatest agreement between any two compared algorithms was observed for DBH1 vs. DBH2 (-4.2% to +3.9%).

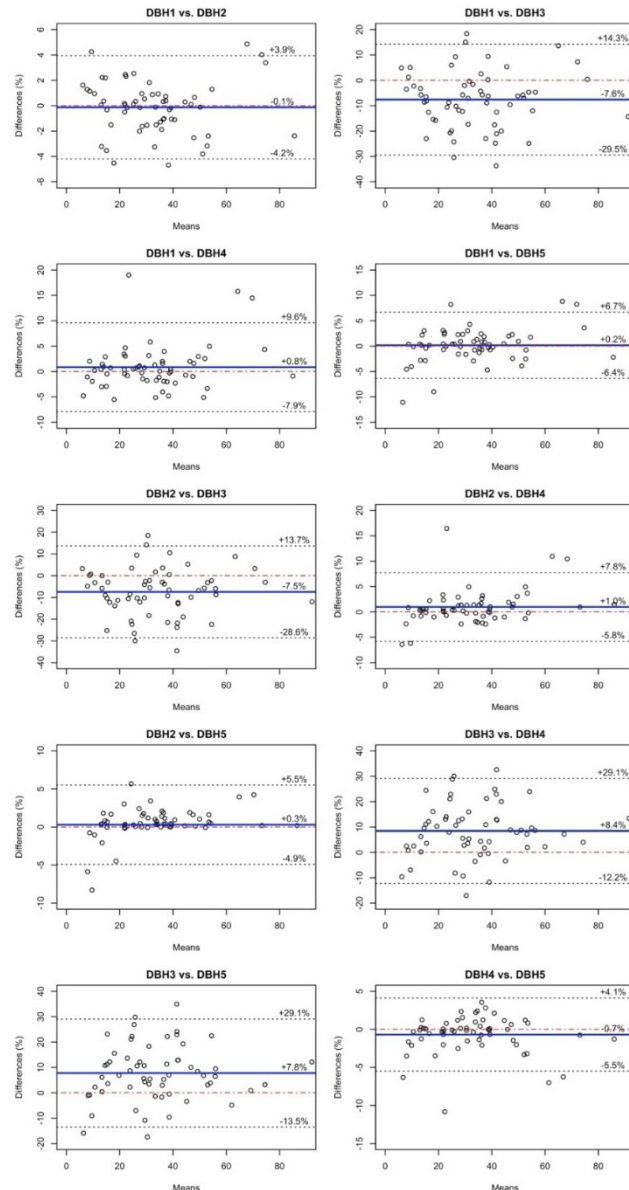


Figure 4 The Bland Altman plots for the compared methods of retrieving DBH. The blue line represents the mean difference (\bar{Dif} , Eq. 3), the dotted lines represent the limits of agreement (LoA, Eq. 4) and the dash dot red line is through origin ($Dif = 0$).

Height reconstruction algorithms

The compared H reconstruction algorithms, 3DForest (H1) and TreeQSM (H2), were in good agreement, with LoA within ± 1.11 m, which relative to the mean was between -1.2% and +2.0% (Figure 5). However, the H estimated by 3D Forest was, on average, 0.31 m larger compared to H estimated by TreeQSM. The relative differences showed a decreasing trend, suggesting that for smaller trees the H1 algorithm produced higher heights compared to H2, and for taller trees, the opposite.

Stem volume reconstruction algorithms

The Bland-Altman plot comparing V_{st1} and V_{st2} shows a mean difference of -2.6%, with limits of agreement ranging from +60.4% to -65.5%. This indicates a slight negative bias, where V_{st2}

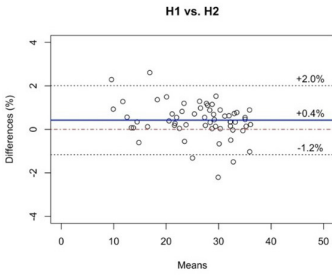


Figure 5 The Bland-Altman plot of height estimation using two QSM methods: 3D Forest and TreeQSM.

measurements tend to be slightly higher than those of Vst1.

In the plot comparing Vst1 and Vst3, the mean difference is -6.6%, with limits of agreement ranging from +30.7% to -43.8%. This reveals a noticeable negative bias, indicating that Vst3 measurements are generally lower than those of Vst1 by an average of 6.6%. The limits of agreement, while not as wide as the previous comparison, still indicate a moderate level of variability between these two sets of measurements.

The comparison between Vst2 and Vst3 displays a mean difference of -4.1%, with limits of agreement ranging from +58.2% to -66.4%. This reveals a slight negative bias, where Vst3 measurements tend to be lower than Vst2.

Overall, all three Bland-Altman plots indicate some level of bias and variability among the stem volume measurements. Vst1, Vst2, and Vst3 each show differing degrees of agreement with each other, with Vst3 consistently measuring lower than the other two.

The Poisson-based method produced larger stem volume estimates compared to TreeQSM, and these differences increased with tree size. However, the RANSAC method was in better agreement with TreeQSM (LA = 0.561 m³), showing a smaller mean difference of only 0.067 m³, with RANSAC producing larger stem volume estimates. When the RANSAC and Poisson-based methods were compared, the agreement was highest (LA = 0.537 m³). There was also a linear trend in the differences between these two methods, showing that

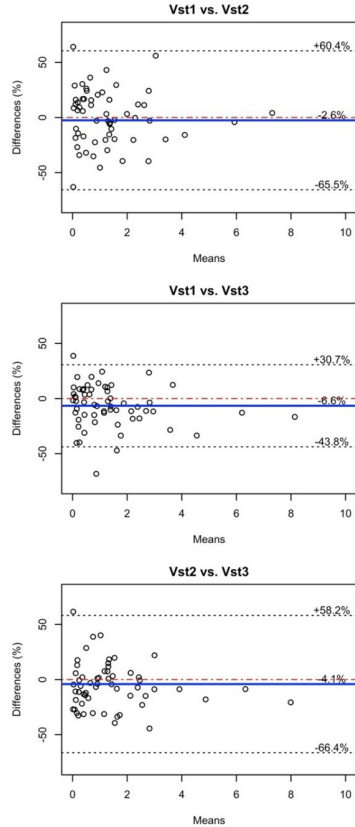


Figure 6 The Bland-Altman plots for comparing the methods of stem volume reconstruction.

Poisson tended to produce larger stem volume estimates for large trees compared to RANSAC.

The positive correlation between stem volume and measurement error ($r = 0.85, p < 0.05$) indicates the accuracy of stem volume measurements decreases as the stem size increases (Figure 7). This could be due to several factors such as increased complexity in the stem's structure, higher occlusion rates in taller stems, or because taller trees are more prone to crown and branches movements caused by air movements (i.e., light wind). The presence of outliers suggests that there might be specific conditions or anomalies that cause exceptionally high errors in some large stems. Identifying and addressing these conditions could enhance reconstruction accuracy for larger trees.

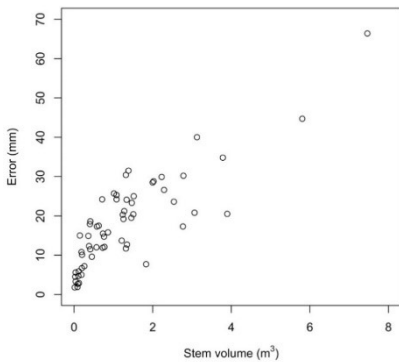


Figure 7 The stem reconstruction error vs. stem volume.

The relationship between branch volume and reconstruction error (Figure 8) indicates a weaker correlation ($r = 0.38$) although still significant ($p < 0.05$). Larger reconstruction errors are more likely for larger trees, although the

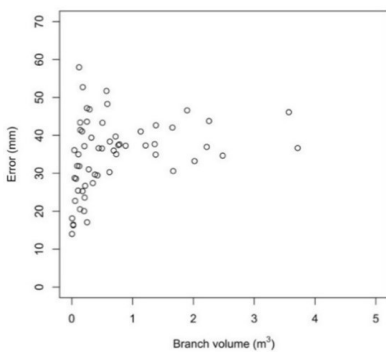


Figure 8 The Bland-Altman plots for Measurement Error vs. Branch Volume.

greatest reconstruction error was recorded for a small tree (Figure 8). Nevertheless, the branch and stem reconstruction error were strongly correlated with the tree height (Figure 9). The correlation between branch reconstruction error and tree height was $r = 0.76$ ($p < 0.05$) and the correlation between stem reconstruction error and tree height was $r = 0.66$ ($p < 0.05$). This result suggests that taller trees are more prone to larger reconstruction errors. These errors may be caused by the increased likelihood of taller trees to move in the light wind or by their increased crown architecture complexity.

Total aboveground tree volume reconstruction algorithms

The two methods compared, Vtot1 (3DForest) and Vtot2 (TreeQSM), produced highly variable estimates of total tree volume.

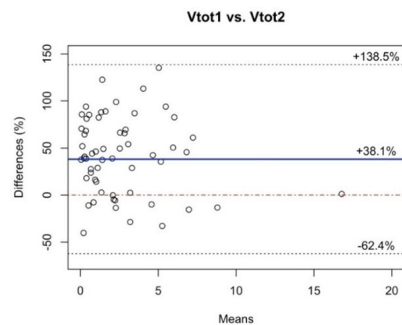


Figure 10 The Bland-Altman plots for comparing the methods of stem volume reconstruction.

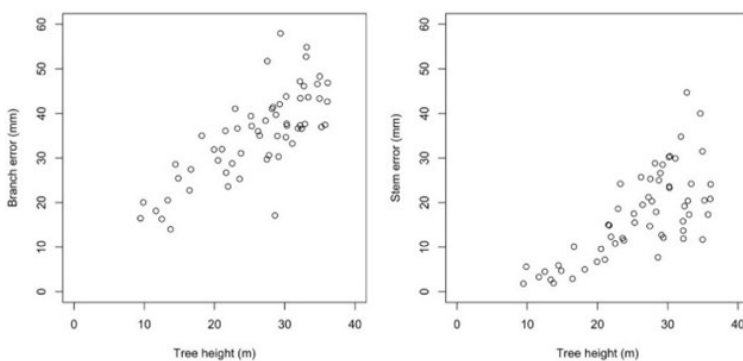


Figure 9 The Bland-Altman plots for branch (left) and stem measurement (right) errors vs. tree height.

In Figure 10, the estimates of tree total volume obtained from TreeQSM are compared against that obtained from 3DForest algorithms. For the smallest trees, the differences in absolute values were minimal. However, for large trees, these differences increased substantially.

The largest absolute difference was 6.9 m³ (~138%); it was observed for a tree for which the volume retrieved from TreeQSM was 1.55 m³ while for the same tree the 3D Forest algorithm estimated a total of 8.44 m³ (Figure 10). As a result, the limits of agreement for the total volume were large (LoA were between -62.4% and +138.5%). The average difference between the two methods was 1.25 m³, showing that 3DForest systematically produced larger volume estimates (by +38.1%).

Discussion

DBH reconstruction

Minor differences were observed in diameter at breast height (DBH) measurements between DBH1 and DBH2, with errors increasing for larger diameters. Five DBH reconstruction methods were compared: i) DBH1 and DBH2, using 3DForest with Randomized Hough Transformation and Least Squares Regression; ii) DBH3, using 3DForest with the DBH cloud method; and iii) DBH4 and DBH5, using TreeQSM algorithms with mean stem diameters and fitted cylinders at 1.3 m, respectively.

The results highlight that DBH measurements derived from 3DForest using the DBH cloud method (DBH3) tend to be less reliable than those obtained through other methods. Cylinder fitting methods (DBH4 and DBH5) provided more precise and consistent measurements, underlining the importance of method selection based on the tree size and point cloud quality.

The DBH was reconstructed using two primary approaches: one based on fitting a cylinder and the other on triangulation. In the 3D Forest method, DBH is derived from fitting a circle to the tree's base; however, this method can fail if the point cloud data at the base is unclear. In contrast, methods that utilise cylinder fitting tend to produce more precise measurements due to their ability to generate surfaces from the point cloud data. Despite the higher error propensity of the circle-fitting

method, both approaches are highly dependent on the accuracy of the underlying modeling process. Any failure in modeling can lead to significant measurement inaccuracies.

Our comparison of DBH reconstruction methods highlights notable variations, especially for large-diameter trees. The differences between DBH1, DBH2 (3DForest), and DBH4, DBH5 (TreeQSM) align with findings from (Raumonen et al., 2013a), who observed that TreeQSM excels in estimating DBH due to its precise cylinder-fitting technique. However, the underperformance of DBH3 (DBH cloud) corroborates similar challenges reported in other studies where circle-based fitting methods struggled with irregular cross-sections and noise (Friedli et al. 2016, Lau et al. 2018b).

The increasing discrepancies for larger DBH values suggest that trees with pronounced taper or irregularity in trunk shape deviate from circular assumptions. This finding echoes results from (Liang et al. 2016b) who noted the importance of shape irregularities when reconstructing tree metrics. These results underscore the need to prioritize algorithms such as TreeQSM for larger trees and use caution with simpler methods like RHT-based circle fitting when point cloud quality is insufficient.

Height reconstruction

The height estimation using the two methods, 3DForest (H1) and TreeQSM (H2), demonstrated relatively consistent results, with limits of agreement within 1.11 m. However, the heights estimated by 3DForest were, on average, 0.31 m larger compared to those estimated by TreeQSM. The discrepancies in height estimation were not uniform across the height range but tended to increase with the height, indicating heteroscedasticity. For trees shorter than 20 m, the agreement between the two methods was excellent. In contrast, for trees taller than 20 m, the height estimation became more challenging, resulting in larger

differences between the two methods. These findings suggest that the method of calculating normals in 3DForest and TreeQSM plays a significant role in the observed estimation errors.

The height estimates from TreeQSM and 3DForest showed good agreement for smaller trees but diverged for trees taller than 20 meters. This increasing discrepancy with tree height reflects findings from other studies (Dassot et al. 2011, Liang et al. 2016b, Niță 2021b), where occlusion and point cloud density limit reconstruction accuracy for tall or structurally complex trees.

The trend of overestimation by 3DForest suggests its reliance on maximum Z-values within the point cloud, which can be skewed by canopy noise or data outliers. In contrast, TreeQSM's hierarchical segmentation reduces such errors, in line with results by (Lau et al., 2018b). These findings highlight the importance of integrating occlusion correction techniques for tall trees.

Stem volume reconstruction

In this study, stem volume was estimated using three methods: TreeQSM (Vst1), RANSAC in CloudCompare (Vst2), and Poisson reconstruction in CloudCompare (Vst3). The Bland-Altman plot comparing Vst1 and Vst2 shows a mean difference of -2.6%, with limits of agreement ranging from +60.4% to -65.5%, indicating a slight negative bias where Vst2 measurements are slightly higher than Vst1. The comparison between Vst1 and Vst3 reveals a mean difference of -6.6%, with limits of agreement from +30.7% to -43.8%, showing a noticeable negative bias where Vst3 measurements are generally lower than Vst1 by an average of 6.6%. Comparing Vst2 and Vst3, the mean difference is -4.1%, with limits of agreement from +58.2% to -66.4%, indicating a slight negative bias where Vst3 measurements tend to be lower than Vst2.

The Poisson-based method (Vst3) consistently produced larger stem volume

estimates compared to TreeQSM (Vst1), particularly as tree size increased. However, the RANSAC method (Vst2) showed better agreement with TreeQSM (Vst1), with a smaller mean difference of only 0.067 m³ and limits of agreement of 0.561 m³, suggesting it is more reliable. Despite this, the Poisson method displayed gaps in the trunk and incomplete volumes due to its sensitivity to the point cloud density and shape complexity, leading to less accurate estimations for larger trees.

Stem volume reconstruction demonstrated significant variability, particularly for larger trees. TreeQSM and RANSAC exhibited better agreement, whereas Poisson-based reconstruction overestimated volumes, consistent with (Capalb et al. 2024), who reported Poisson's sensitivity to point cloud gaps and shape irregularities. The higher errors in Poisson and RANSAC algorithms for large stems align with findings by (Maas et al. 2008, Raunonen et al. 2013a) emphasizing challenges in dense forest environments. These errors may arise from noise, occlusions, or incomplete scanning angles. Our results suggest that TreeQSM's stepwise segmentation delivers the most reliable volume estimates, as also reported by (Pascu et al. 2019).

Total aboveground tree volume reconstruction

Total tree volume estimation was compared using 3DForest (Vtot1) and TreeQSM (Vtot2), revealing considerable variability between the two methods. For smaller trees, the absolute differences in volume estimates were minimal, but as tree size increased, these differences became more pronounced. The largest discrepancy observed was 6.9 m³, where TreeQSM estimated the volume at 1.55 m³ while 3DForest estimated it at 8.44 m³. Consequently, the limits of agreement were broad (LA = 3.65 m³), indicating substantial variability. The average difference between the methods was 1.25 m³, with 3DForest consistently producing larger volume estimates.

These findings underscore the systematic

overestimation by 3DForest compared to TreeQSM. The discrepancies highlight the challenges of accurately estimating total volume for larger trees, where the complexity of tree architecture and potential occlusions play significant roles. Accurate total volume estimation is crucial for applications in forestry, emphasizing the importance for selecting appropriate algorithms based on tree size and structural complexity to ensure reliable measurements.

In the volume estimation process, the whole point cloud is divided into horizontal slices, and each of these slices is further divided into clusters based on user-defined parameters. Cluster size and distance between two points are defined by users, meaning each cluster is regarded as a potential tree. The closest clusters from other slices are merged vertically with the nearest clusters. However, this method of reconstruction is prone to errors when dealing with complex trees (Calders et al. 2020).

TreeQSM, by using cover sets, segments the point cloud into the stem first and then the individual branches. The segmentation starts at the base of the trunk and proceeds step-by-step along the stem and later along the branches. As the algorithm segments the tree from bottom to top, potential bifurcations are identified, and if there is a branch, its base is preserved for later segmentation. After the stem is segmented, the process is repeated from the base of the first found branch, determining the first-order branches, then the second-order branches, and so forth. This method of reconstruction is more accurate, which is why TreeQSM results are more accurate and in better correlation with other methods.

Results from the 3DForest QSM model did not agree well with others due to the fact that it does not account for tree architecture as effectively as the one in TreeQSM, resulting in the upper branches being reconstructed larger than in reality and causing data overestimation. The difference between the methods lies in the way TreeQSM's (MATLAB) segmentation

algorithm works, which is based on the natural growth patterns of trees. TreeQSM begins with the reconstruction of the stem and then proceeds to branches in the first order, second order, and so on, not allowing the reconstruction of branches that cannot be supported gravitationally. In contrast, 3D Forest overestimates the upper branches.

Conclusions

The conclusions of this study can be summarized as:

(i) Considerable differences were observed between tree measurements derived from different algorithms, emphasizing the need for careful algorithm selection based on specific measurement requirements.

(ii) The differences between compared algorithms were primarily driven by anomalies in the reconstruction of branches and crowns, highlighting the importance of visual inspection of 3D models to detect and correct reconstruction errors.

(iii) The highest agreement between algorithms, indicated by the lowest Limits of Agreement (LoA), was observed for tree height (H).

(iv) Higher relative differences among reconstruction algorithms were noted for diameter at breast height (DBH) and stem volume, particularly for larger trees.

(v) Among the evaluated algorithms, TreeQSM produced the fewest abnormalities in the crown reconstruction, this is why it is our recommendation as the most reliable algorithm.

(vi) Overall, this study highlights the importance of selecting appropriate tree reconstruction algorithms to ensure accurate and reliable tree characteristics. Future research should focus on improving the precision of algorithms and the quality of the point-cloud, particularly for complex tree structures, to enhance the accuracy of non-destructive tree measurement methods.

Compliance with ethical standards

Conflict of interest

The authors declare that they have no conflict of interest.

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