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Abstract

LiDAR is a promising tool for fast and accurate measurements of trees. There are several approaches to estimate aboveground woody biomass using LiDAR point clouds. One of the most widely used method consists in fitting geometric primitives (*e.g.* cylinders) to the point cloud, thereby reconstructing both the geometry and topology of the tree. However, current algorithms are not suited for accurate estimation of the biomass of finer branches, because of the unreliable point dispersions from the movements induced by wind, occlusion in the upper canopy, or the relatively large laser footprint compared to the structure diameter.

We propose a new method that couples point cloud-based reconstructions and structural models to estimate accurately the aboveground woody biomass of trees, including finer branches. The model was trained using branch samples from the trees, and accurately predicted the biomass with 1.6% nRMSE at the segment scale from a k-fold cross-validation. It also gave satisfactory results when up-scaled to the branch level with a significantly lower error (13% nRMSE) and bias (-5%) compared to fitting cylinders to the point cloud (nRMSE: 92%), or using the pipe model theory (nRMSE: 31%).

The model was then applied to the whole-tree scale, and showed that the sampled trees had more than 1.7km of structures in average, and that 96% of that length was coming from the twigs (*i.e.* <5 cm diameter). Our results showed that neglecting twigs lead to a significant underestimation of tree aboveground woody biomass (-21%) in our study case.

The structural model approach is promising for unbiased large-scale estimations, and could be used as a new way for accurate estimation of the standing biomass without the need for tree cutting.

Keywords: *tree; walnut; agroforestry; laser; architecture; allometry; topology; Multi-Scale Tree Graph*

1. Introduction

The three-dimensional reconstruction of plants with high accuracy is crucial for many fields (Calders et al., 2015). For example, it is used to precisely estimate the carbon stock of large populations of trees in forests and agroforestry systems, a key information to better understand the functioning of the terrestrial carbon cycle. It is also frequently used to estimate the aboveground woody biomass for logging, or to parameterize functional-structural plant models to simulate radiation interception, fluxes of carbon, water and nutrients, biomass allocation, or even assessing and optimizing innovative planting designs (Perez et al., 2018).

LiDAR is a promising tool for fast and precise acquisition of data at large scale (Dassot et al., 2011; Calders et al., 2020). There are several algorithms for the reconstruction of tree topology and geometry from LiDAR point clouds (Thies et al., 2004; Calders et al., 2020), and one of the most successful attempt to date is by generating Quantitative Structural Models (QSM) using *e.g.* TreeQSM (Raumonen et al., 2013) to adjust cylinders to the point cloud. However, this method tends to overestimate the volumes of the branches towards the top of the canopy (Wilkes et al., 2017) and the smaller branches (Demol et al., 2022). This is mainly due to occlusion, wind effect, co-registration errors and laser footprint that becomes large compared to the diameter of branches smaller than 2 cm (Abegg et al., 2021). Some attempts have been made to correct for the beam divergence issue (Wilkes et al., 2021), but correcting for wind effect, occlusion or under-sampling is more difficult.

New approaches are emerging to reduce such errors by coupling LiDAR data with structural models. For example Hu et al. (2021) report that TreeQSM made inaccurate individual branch extraction, and used four consecutive empirical models instead to estimate the positions of the whorl along the trunk, the number of branches in the whorls, the branch basal area and finally their biomass. Unfortunately, this approach needs a consequent database to parameterize each model, and with the assumption that the reconstruction of the branches is incorrect, the method

uses only a small portion of the rich LiDAR data (*i.e.* points of the main axes), neglecting valuable information such as actual number of axis, their lengths and the tree topology.

We agree that coupling LiDAR data, 3D reconstruction software and structural models is promising and can reduce the sensitivity to occlusion, co-registration errors and laser footprint. However, we argue that this method can be further improved by exploiting the full extent of the information from the LiDAR point clouds, by extracting more features from the tree such as lengths, topology and spatial arrangements of all the structures, including small branches.

In this study, we present a new approach for the estimation of the aboveground woody biomass with LiDAR. The approach uses 1/ the Plantscan3d software (see 2.3.1) to finely reconstruct the tree topology and geometry; 2/ a statistical model based on tree structural features (*i.e.* allometric relationships) to estimate the cross-sectional area of the structures; and 3/ the volumes of the structures and the wood density for the estimation of the aboveground woody biomass.

The structural model is then applied to the whole trees to compute general features and visually assess its performance when upscaling.

2. Material and methods

2.1.Experimental site

The experimental site is located in Roumassouze in the South of France (44°03'29.6 "N 4°06'43.5 "E). It is an agroforestry system based on hybrid walnut trees (*Juglans regia* × *J. nigra*) associated with a diversified and organic vegetable production. This experiment was conducted on a plot of three hectares planted in 1996 with a tree spacing of 10 m x 10 m (*i.e.* 100 trees ha^{-1}). The trees were thinned at 90 trees ha^{-1} in 2011, and lightly pruned in 2015 by removing the lower branches (*c.a.* 1.9 kg dry mass $tree^{-1}$). The trees were free growing since then.

2.2.Measurements

2.2.1. LiDAR acquisition

Measurements were conducted on three walnut trees from the experimental site. Two branches per tree were identified, one close to the ground and the other upper in the tree canopy. Reflective tape was placed at the branch basis for identification in the point cloud and for further measurements.

The three trees were scanned prior to destructive sampling and without leaves on March 2021 with a Riegl VZ-400 LiDAR scanner (RIEGL Laser Measurement Systems GmbH). Twenty positions were scanned both in upright and tilted positions. The scans were then co-registered with RiScan Pro 2.11.3 using the reflective targets positioned in the field.

2.2.2. Destructive method

The six branches identified by reflective tape were cut at their basis. Measurements of topology, wood density, woody biomass and dimensions were performed. The branches were 5.5 m long in average, with a total of *c.a.* 390 m of segments measured by hand.

The topology was encoded for each branch using the Multi-scale Tree Graph (MTG) format (Godin and Caraglio, 1998), and described using three complementary scales: the branch, the axis and the segments. The axis (A) were defined as the succession of segments produced by the apical meristem, and the segments (S) as the wood portion between two ramifications (Figure 1).

The branching order of each axis were determined considering the first (*i.e.* principal) axis as an axis of order one by convention. Then the branching order recursively increased for each branching point. A total of 5287 topological data point were collected in the six branches.

The fresh and dry density of the branches were estimated from the average value of ten sections evenly sampled along the principal axis (A1) for each branch. Fresh biomass was measured for the whole branch and for each second order axis (A2) including the structures of lower order.

The biomass of the first order axis (A1) was then calculated as the total branch biomass minus the cumulated biomass of the second order axis, unless there are missing measurements for A2, in which case it was not used for comparison (*i.e.* branches 13-h and 13-l).

Radius was measured at the mid-point of each segment with two perpendicular orientations using digital calipers. Segment length was also recorded with a measuring tape. The volume of each segment was then computed using the radius and length considering segments as cylinders. The biomass of each segment was estimated using the volume and average wood density. This method was found sufficient when comparing the computed biomass of the axis with the actual measurement with a scale (see Figure A 1).

All measurements were encoded into the MTG as attributes.

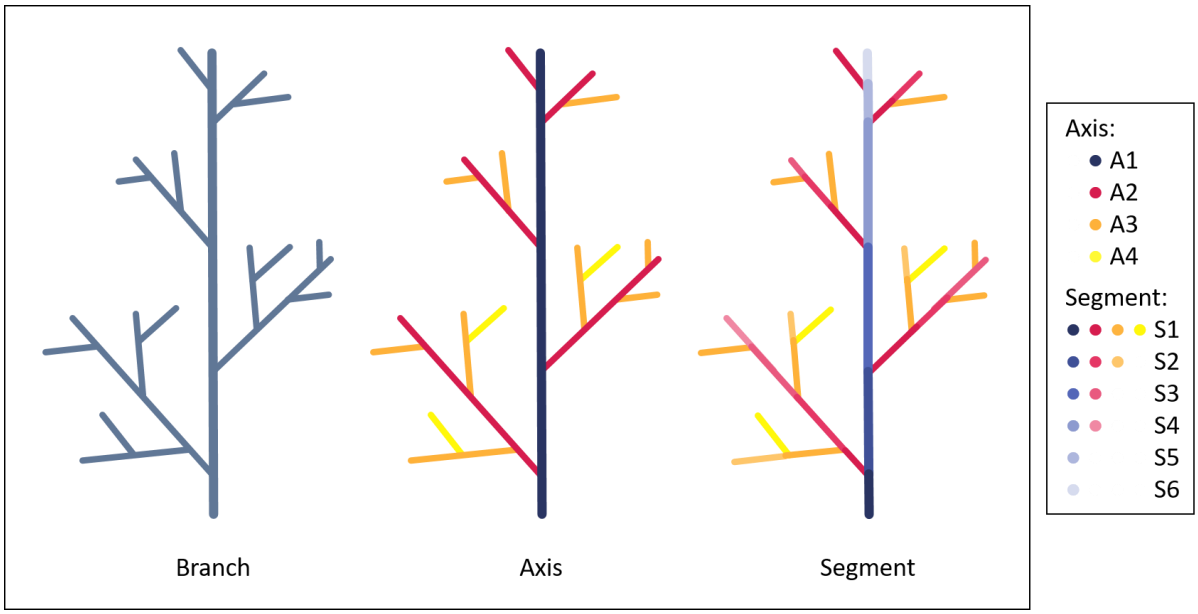

Figure 1: Schematic representation of the topological encoding of a branch at three scales: the branch, the axis, and the segment. The axes are defined as the succession of segments produced by the apical meristem, and the segments as the wood portion between two ramifications, including the portion of the ramification at the apex. Axes are numbered by branching order, segments by acropetal index on the axis.

2.3.Reconstruction

2.3.1. Plantscan3D

The plantscan3D software (https://github.com/openalea/plantscan3d) was used for the reconstruction of the topology, length and diameter of the branches and the whole-trees from

the LiDAR point clouds (Figure 2). The topology was reconstructed using the skeletonization algorithm from Xu et al. (2007). This algorithm first builds a Riemannian graph by connecting the k closest neighbors points. The graph is then segmented into clusters of points using the distance from a root point, and the center of each cluster is finally used as nodes for the tree skeleton (Boudon et al., 2014). Light manual corrections were performed to ease the comparison with the destructive method, for example by correcting the branching type between nodes (*i.e.* branch or follow), or the position of the base of a branch when two ramifications are branching close to each other. The radius of each segment was estimated using the average point distance algorithm that fits a cylinder to the neighbor points.

The resulting topology was exported as an MTG file, and further processed with the MultiScaleTreeGraph.jl package (Vezy, 2022).

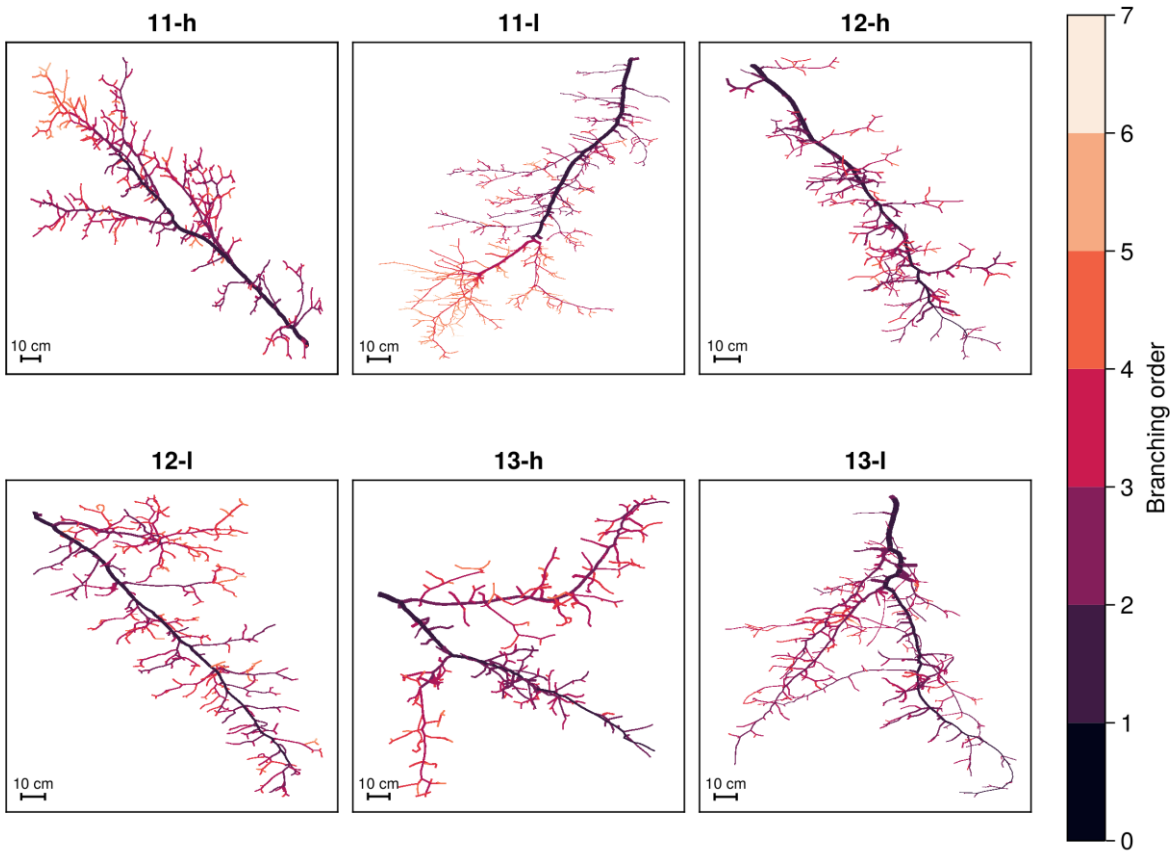

Figure 2. Fully automated reconstruction of the topology and geometry of the six branches using Plantscan3d. The branch is named after the tree index and the position in the tree: high (h) or low (l).

2.3.2. Pipe model theory (PMT)

The pipe model derives from a simple and intuitive theory that states that each leaf in a plant is connected to the stem base via a pipe with a constant cross-sectional area (Shinozaki et al., 1964; Valentine, 1985). One of the property of the theory is that "*the conductive surface area of a stem at a given height is equal to the cumulative basal area of its daughter axes above that height*" (Lehnebach et al., 2018). In this paper, we used a simplified formulation earlier defined by Leonardo da Vinci that replaces the conductive cross-sectional area by the total cross-sectional area (CSA). This theory is over-simplified but simpler to use with LiDAR data where only the CSA is available. In practice, we used this method to compute the diameters of all segments in a branch or tree starting from the basal segment, and iteratively partitioning the CSA to its children segments, weighted by the total number of terminal segments in the child subtree. This model was applied on the MTG of the branches to estimate the diameters of all segments using the radius of the first segment estimated by plantscan3D as a starting point.

2.3.3. Structural model

The new method presented in this paper uses Plantscan3d to reconstruct the skeleton of a branch or tree, and a model based on structural traits to compute the CSA of the structures. To do so, a statistical linear model is defined and fitted using manual measurements at segment and axis scale only using features we can also derive from LiDAR point clouds such as:

- CSA estimated using the PMT
- Total length of the subtree
- Branching order
- Relative acropetal position of the segment (*i.e.* from the tip) on its axis
- Number of segments in the subtree
- Number of terminal segments

- Number of segments on the axis
- Length of the axis

The first step for building such model is to identify which candidate variable explains the variability in the cross-sectional area of the segments. The p-value of each variable selected for the model was controlled for its significance, and all variables with a p-value lower than 0.05 was discarded from the model.

The second step consisted in the evaluation of the robustness of the model using a k-fold cross-validation (k = 10). The model is trained and evaluated k-times on sub-samples of the data, which helps computing the out-of-sample nRMSE.

In the third step, we trained the model using the whole dataset to compute its parameters for use in the reconstructions, and evaluate its accuracy with the in-sample nRMSE.

Finally, the last step was to apply the model on the MTG obtained from the Plantscan3d reconstruction to predict the cross-sectional area of any segment in the tree or branch.

2.4.Merging manual and LiDAR-based reconstructions

Matching the results of the manual measurements and the model reconstructions is not trivial because a little difference in *e.g.* the definition of the main axis or in the position of the base of a branch can lead to very different MTG outputs. Furthermore, the manual measurements were performed months after the LiDAR acquisition, which eventually lead to missing broken structures in the manual measurements.

To alleviate these issues, the MTG of both methods were compared manually, and all axes that could be recognized in both were identified with a unique identifier. In this paper, all comparisons between manual and LiDAR-derived measurements are done using these axes.

2.5.Data and code availability

The code developed in this study for analysis, modelling, 3D reconstruction, statistics and figures is available on a GitHub repository (https://github.com/VEZY/Biomass_evaluation_LiDAR) and fully archived on Zenodo (Vezy et al., 2022).

3. Results

3.1.Axis length

The axes lengths estimated by Plantscan3d using the LiDAR point clouds were compared to the destructive measurements. The comparison is performed using the total length of all segments forming an axis. As expected, the lengths estimated by Plantscan3d were close to the manual measurements, with only 1% nRMSE and a bias close to zero (0.2%), which indicates that the error is not cumulative (Figure 3).

The estimation is correct for all the range of axis lengths whatever the number of segments, and the error is conservative between trees, which shows the genericity of the method.

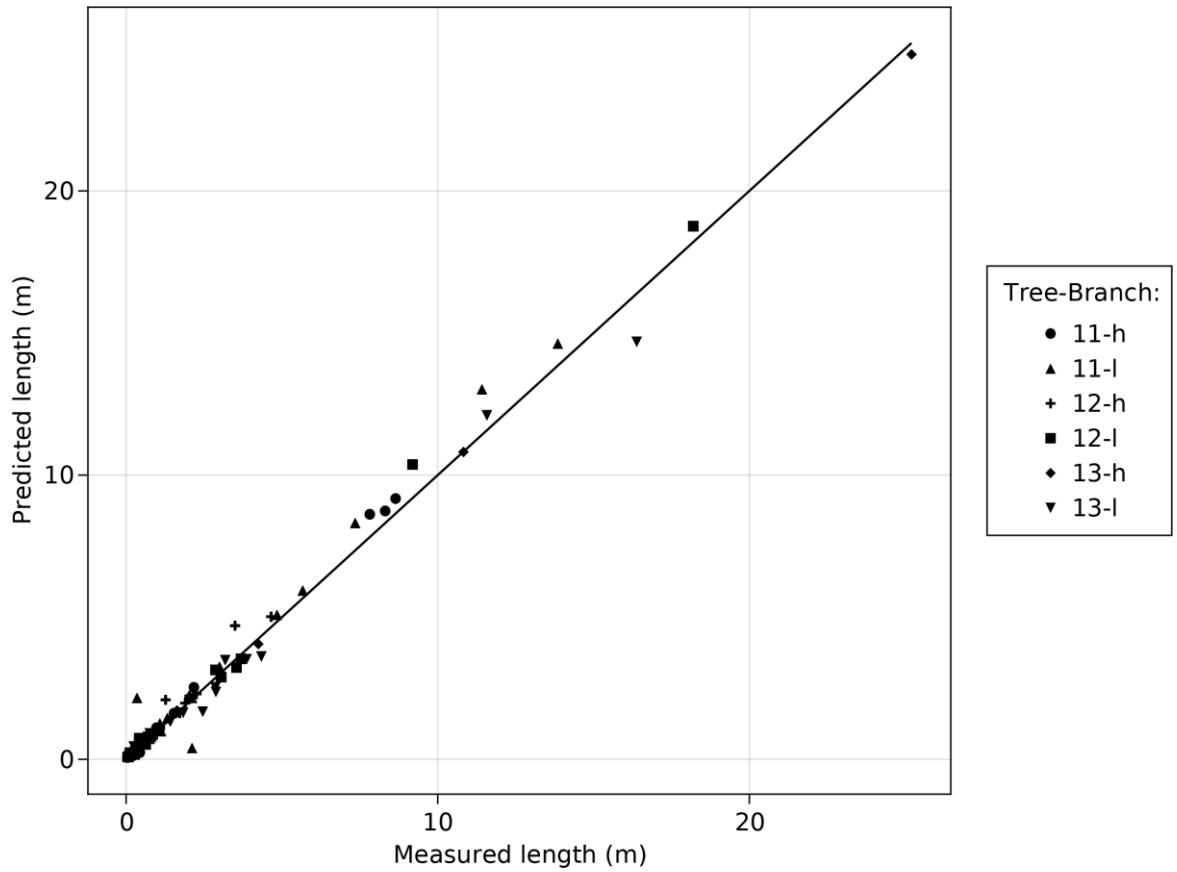

Figure 3. Measured (x-axis) and predicted (y-axis) length at axis scale. Normalized Root Mean Squared Error (nRMSE): 1%; Modelling Efficiency (EF): 0.99; Normalized Bias: 0.2%. The branch is named after the tree index and the position in the tree: high (h) or low (l).

3.2.Model training and evaluation

The final model had six variables, and obtained an nRMSE of 1.58% ±0.4 on the cross-validation evaluation, and 1.4% when trained on the full dataset. Two variables did not explain significantly the variability in the cross-sectional area and were excluded from the model: the number of segments on the axis and the length of the axis.

Table 1. Linear model fitting summary (*i.e.* structural model). Coef.: estimate of the coefficients; Std. Error: standard error; t: t-value; Pr(>|t|): p-value; Lower/Upper 95 %: lower and upper values of the confidence interval; CSA: cross-sectional area; PMT: pipe model theory.

Variable	Coef.	Std. Error	t	Pr(>|t|)	Lower 95%	Upper 95%
CSA from the PMT	0.52	0.015	34.34	<1e-99	0.49	0.55
Path length of the subtree	0.015	0.0007	21.35	<1e-94	0.0139	0.0167
Branching order	6.38	1.28	5.00	<1e-06	3.88	8.89
Segment index on axis	10.94	0.41	26.65	<1e-99	10.13	11.74
N of terminal segments	-10.14	2.13	-4.77	<1e-05	-14.31	-5.97
N segments on the subtree	4.47	1.05	4.2	<1e-04	2.40	6.54

As expected, the CSA computed using the PMT was the variable with the highest importance (t-value= 34, Table 1), followed by the index of the segment on the axis (t-value= 27), and the total length of the subtree (t-value= 21). Although significant, the three other variables had a lower importance (|t-value| ≤ 5) in the model.

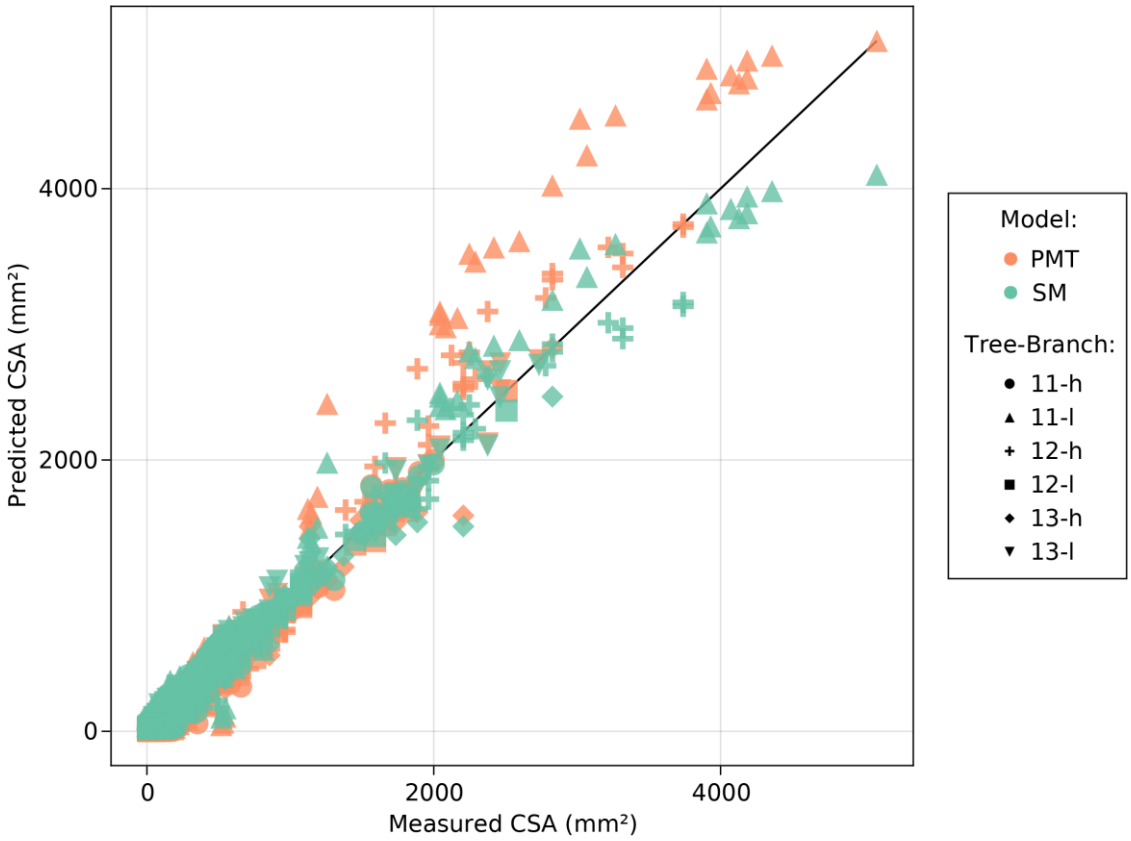

Figure 4. Measured (x-axis) and predicted (y-axis) cross-sectional area (CSA) at segment scale by the structural model (SM, this study), or the pipe model theory (PMT). The branch is named after the tree index and the position in the tree: high (h) or low (l).

The structural model presented the lowest error for the prediction of the segments' CSA compared to the standard PMT, especially for the lower branch of tree 11 (11-l) that was systematically overestimated by the PMT (Figure 4). The structural model predicted the segments' CSA with higher accuracy than the PMT for all computed statistics; with an nRMSE half as high and a bias five times lower (Table 2).

Table 2. Prediction accuracy of the models related to Figure 4 (n = 3461 each). RMSE: Root Mean Squared Error, nRMSE: normalized RMSE, EF: Modelling Efficiency, nBias: normalized bias. Best statistics are highlighted in bold. PMT: Pipe Model Theory, SM: Structural Model (this study).

Model	RMSE	nRMSE	EF	Bias	nBias
PMT	103.3	0.02	0.95	17.92	0.0035
SM	57.7	0.01	0.98	2.89	0.0007

3.3.Model evaluation with destructive measurements

The model was evaluated using destructive measurements of the branches' woody biomass with a scale. The average point distance algorithm from Plantscan3d lead to a poor estimation of branch biomass with a systematic overestimation, an nRMSE of 92% (+3.38 kg) and an nBias of 82% (2.99 kg, Table 3). The PMT improved the estimation with only 31% nRMSE but systematically underestimated the biomass by 27%, which represented *c.a.* -1 kg in average.

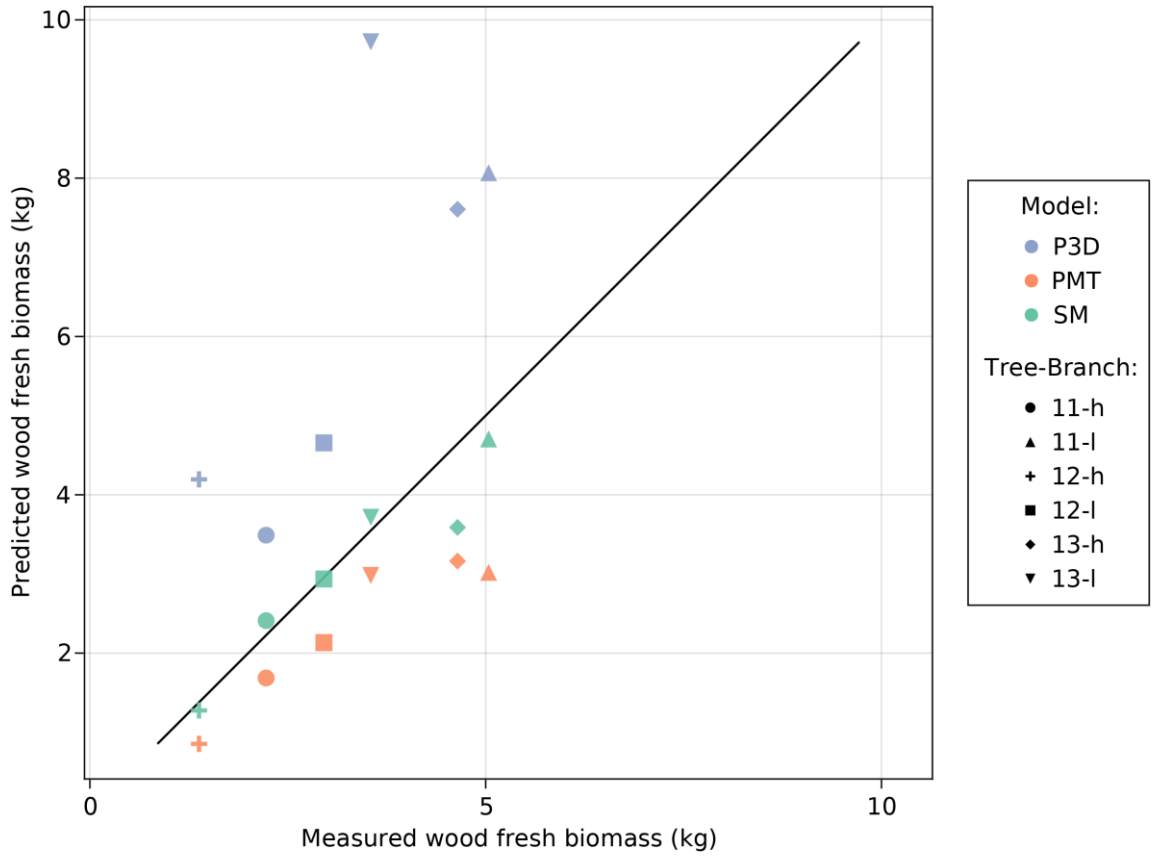

Figure 5. Measured (x-axis) and predicted (y-axis) fresh wood biomass at branch scale. Branch scale is defined as the sum of the biomass of all manually identified axes to control for the error induced by missing structures between LiDAR scans and destructive measurements. P3D: Plantscan3d reconstruction using the average point distance algorithm; PMT: Pipe Model Theory; SM: Structural Model (this study). The branch is named after the tree index and the position in the tree: high (h) or low (l).

The structural model however was the only model to present a modelling efficiency (EF) close to one, with a value of 0.87. It also presented a lower nRMSE of 13% and a bias closer to zero (-5%). The slight bias towards underestimation came from one branch in particular (-23%), the

highest branch from tree 13 (13-h), that presented a high number of broken axes (35). The error was relatively higher for the finer structures though, with an error of 20% for structures below 10 cm diameter.

Table 3. Statistics about the model prediction of the fresh biomass at branch scale (n = 6, see Figure 5). RMSE: Root Mean Squared Error, nRMSE: normalized RMSE, EF: Modelling Efficiency, nBias: normalized bias. Best statistics are highlighted in bold. P3D: Plantscan3d; PMT: Pipe Model Theory; SM: Structural Model (this study).

Model	RMSE	nRMSE	EF	Bias	nBias
P3D	3.38	0.92	-5.95	2.99	0.82
PMT	1.14	0.31	0.21	-0.99	-0.27
SM	0.47	0.13	0.87	-0.19	-0.05

3.4.Model application

The structural model was applied at the whole tree level over the three walnut trees. The distribution of the aboveground woody biomass was similar between trees according to the three supervised classes of segment diameter. The trunk represented in average 50% of the biomass, the main branches 29%, and the twigs 21% (Figure 6). The total length of the structures in the tree represented in average 1735 m, with 96% of that length coming from the twigs.

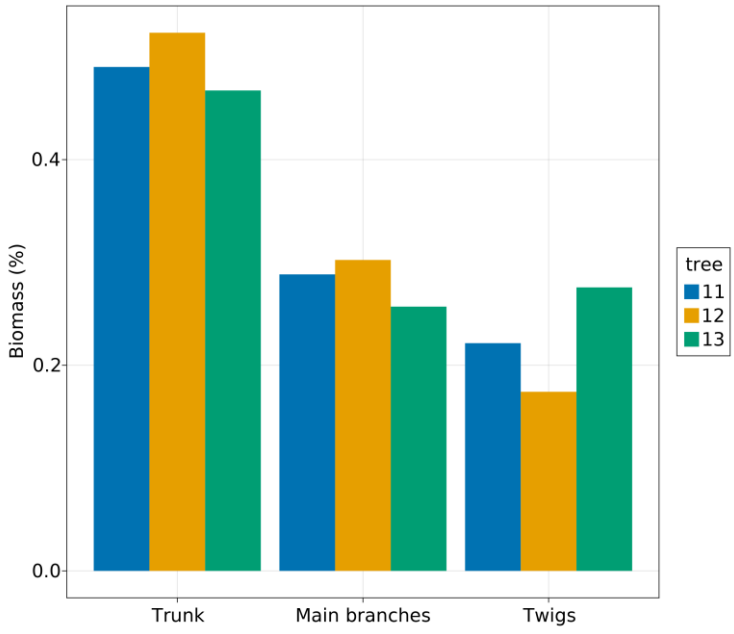

Figure 6. Relative distribution of the aboveground woody biomass estimated by the structural model for each segment diameter class in the three walnut trees. Twigs: [0, 5); Main branches: [5, 15); Trunk: [15, 50) cm.

Overall, the coupling of LiDAR point clouds, Plantscan3d skeletonization and the structural model lead to precise 3D reconstructions of the targeted branches and the whole trees (Figure 7). At the branch level, even the smallest structures were satisfactorily reconstructed by the skeletonization, and connection paths were correct despite the complexity of some structures. At tree scale, the trunk base reconstruction was not completely visually realistic because it only used one segment, but its estimated volume was probably close to reality. The estimated topology of the structures in the tree was also close to observations at this scale, which is particularly surprising considering there were no parameter except the number of nodes, and no manual corrections applied after the fully automatic reconstruction of the branch and tree.

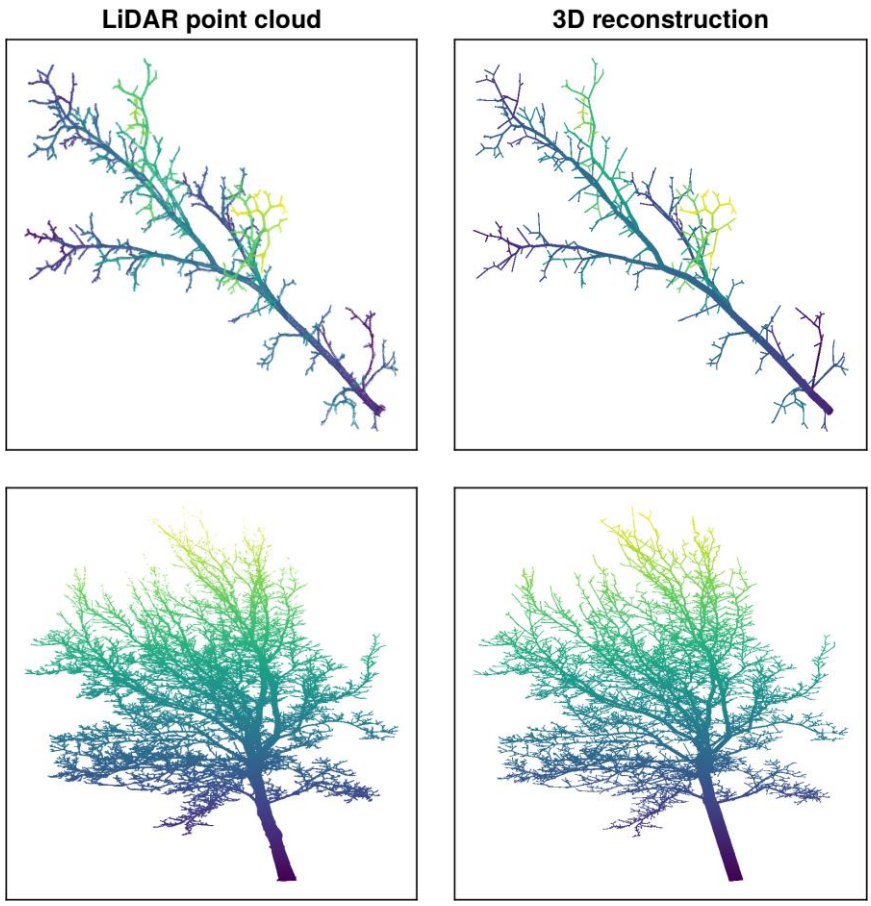

Figure 7. Co-registered LiDAR point-cloud (left panels) and 3D reconstruction using the structural model (right panels) of a sampled branch (top panels, 11-h) and a whole tree (bottom panels, 12). Note that the 3D reconstruction was done at the segment level, which implies that the trunk base has only one segment.

4. Discussion

Our first assumption was that we could improve on the method developed by Hu et al. (2021) by using the full extent of the LiDAR data for the estimation of the aerial woody biomass. It was based on the hypothesis that Plantscan3d was able to provide a correct estimation of the topology and length of all structures in the tree, including finer branches. Our results validated this assumption, showing that axis length estimations were close to the destructive measurements across the whole range of sizes with almost zero bias (0.2%), which is important when scaling-up to the tree or plot scale.

The main objective of this study was to design, train and evaluate a new approach for a more precise estimation of the aboveground woody biomass. As expected, our results showed that using the traditional approach of fitting the LiDAR point cloud to estimate the diameter of the structures gave unsatisfactory predictions of the biomass with a systematic overestimation (nRMSE: 92%, Figure 5, Table 3). This error can be explained by the noise in the point cloud induced by the significant footprint of the laser or the movements of the branches from wind and due to occlusion that lead to an insufficient sampling of some structures.

The PMT, another standard method that only rely on the topology and diameter estimated at the base, was also tested and gave acceptable results with an nRMSE of 31% and a bias of -27%. The results are particularly impressive giving that no parameters were used for this method except for the diameter at the base and the number of nodes from base to main axis tip. We propose that this model should be used in a first approximation of the biomass when no further data is available.

The new method presented in this paper showed that including structural-based knowledge to the modelling process significantly improved the estimation of the diameters. The structural

model predicted segments diameters with only 1% nRMSE, and gave satisfactory results when applied to the branch scale for the prediction of the woody biomass, with a significantly lower error (13% nRMSE) and bias (-5%) compared to the other methods. Furthermore, the error was primarily driven by one branch (13-h) and was already observed on the prediction of the cross section (Figure 4) of one of the widest axis for both the PMT and the structural model. Knowing the process of estimation of both models, this indicates that the error most probably came from the high number of broken structures in this branch, which hinders a proper estimation due to a loss of information about the variables used in the model, and most notably the number of terminal segments and the total length of the subtree.

For comparison, Calders et al. (2015) reported whole-tree nRMSE of 16.1% and 9.68% nBias using TreeQSM. Kunz et al. (2017) measured whole tree volumes and used TreeQSM for the reconstruction with average nRMSE of 22.7% and 6% nBias, and Burt et al. (2021) showed only 2.8% relative error using TreeQSM on whole trees. It is important to note that those reported errors would most probably be higher if reported only for the twigs as they are in this study, because most of the error comes from structures with lower diameters, which represented 21% of the total biomass in this study. Demol et al. (2022) showed for example that 80-83% of the bias from their whole-tree reconstruction originated from the structures with a diameter lower than five centimeters, and the structures below or equal 10 cm diameter had errors of *c.a.* 139%, when we report errors of only 20% with our method.

The structural model allowed for a better estimation of the branches biomass with very little bias, which is required for computations at the tree or plot level. However, it requires data for training, unlike the simple PMT or the biased mean point distance algorithm. In our study, two people were able to measure one branch per day, including cutting, measuring biomass of the whole branch and of the secondary axis, full topology, and segments diameter and length. The model is trained once, and can be applied without further parameterization. This is particularly

true when considering that Plantscan3d does not require any complex parameters to reconstruct tree topology and spatial arrangement. This allows for fast estimations of the aboveground woody biomass at larger scale, or repeated estimations for the monitoring of growth and development.

One of the most interesting result of this study is how the structural model is generic enough to predict the cross-sectional area of all structures in the tree, although trained only over two branches per tree. The application of the structural model to the whole tree showed that structures with a diameter lower than 5 cm represented 22% of the tree aerial woody biomass. These results indicate that a substantial portion of the biomass can be lost if not properly used or handled.

The 3D reconstruction of the trunk base at tree-level is slightly unrealistic because only one segment was used. This issue can be easily corrected using the mean point distance algorithm from Plantscan3d for the structures with largest diameters instead. These bigger structures are not prone to the issues presented in this paper, so algorithms using the LiDAR point cloud to compute the diameters should be sufficient. The quality of the whole-tree reconstruction shows that the skeletonization algorithm from Plantscan3d is highly suitable for this task, especially considering that it only uses one parameter (*i.e.* the total number of nodes between the base and the tip of the main axis) on which it has little sensitivity. For comparison, TreeQSM uses more than twenty parameters, and its reconstructions were shown to be highly sensitive to the parameter values (Demol et al., 2022).

The new method presented in this study is promising but need further applications on other conditions. Further work may investigate the minimal and optimal set of data needed to define and parameterize the architectural model giving an acceptable prediction error. The method was also found sensitive to a high number of broken structures, which means that the estimation of the aerial woody biomass of highly pruned trees must be done with caution, unless trained

specifically on such data. In any case, further improvements to the method should include a way of accounting for pruned structures, by *e.g.* using the LiDAR-derived diameters as a first approximation to identify were the structure deviate from the PMT, and mark those nodes as potential pruning sites.

5. Conclusion

The Plantscan3d software was able to reconstruct the branches topology and axis lengths with high accuracy. Visual evaluations showed it also performed correctly at the whole-tree level, even for finer branches. Our results confirm that LiDAR point-clouds can be used for accurate reconstructions of trees, except for the estimation of finer branches diameters.

In this study, we present a new method for the estimation of the diameters and woody biomass of trees. It outperformed the two standard approaches of adjusting cylinders to the LiDAR point-cloud or using the pipe model theory. The method is designed to use most of the information extractable from the LiDAR point cloud, while controlling the effect of under-sampling (*i.e.* occlusions), light winds or laser footprint. The structural model was applied at the whole-tree level, and showed that 96% of the length and 21% of the biomass were located in the finer branches with a diameter lower than 5 cm. These results indicate that most of the studies that do not account for finer branches could miss a substantial part of the biomass in the trees.

The structural model approach could pave the way for a better assessment of whole-tree aboveground woody biomass using LiDAR, with very low need for destructive sampling for model training and validation, while controlling errors induced by wind, low sampling and laser footprint.

Conflicts of interest

None.

Acknowledgements

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Authors' Contributions

RV and MM wrote the manuscript, MM, AB, JD and RV did the field work with the experimentation team, JD and RV made the LiDAR scans with the help of Merlin Ramel, RV developed the code, trained the models and made the visualizations, RV, MM, AB, and JD analysed the results.

Appendix A

The estimation of the woody biomass from the structural model used the dimensions of the segments and an average wood density. The error coming from this estimation can be computed using only the destructive measurements. We can compare the reference fresh biomass measured using a scale with the biomass estimated from the average fresh wood density and the volume computed from the segment dimensions (*i.e.* diameter and length) measured by hand.

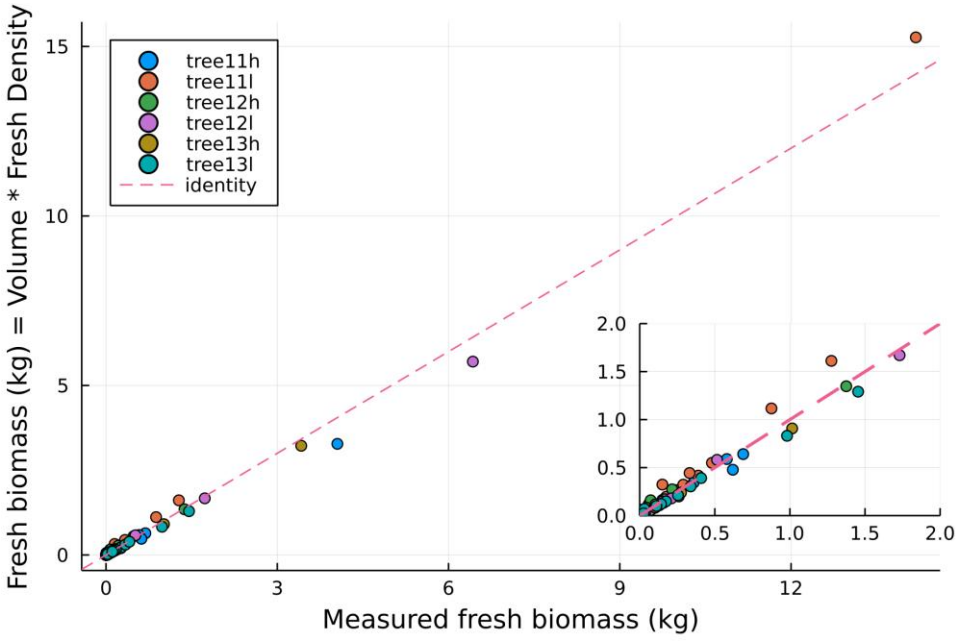

Figure A 1. Fresh biomass measured with a scale on the field (x) compared to its calculation using an average branch fresh wood density and segment volume estimated with the segment's radius and length (y). Each point is an axis on the branch. First order axis biomass is defined as the sum of its segments biomass, excluding higher order axis, and second order axis biomass is defined as the sum of all segments it bears. RMSE: 105.81g, nRMSE: 1%, EF: 0.99.

The results show that the computed axis biomass from its volume and an average wood fresh density was close to the scale measurement, with a low nRMSE of 1% and a modelling efficiency close to one.

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