Research Square

Preprints are preliminary reports that have not undergone peer review.
They should not be considered conclusive, used to inform clinical practice,
or referenced by the media as validated information.

Improving quantitative structure models with an Huxley protocol based filter

Jan Hackenberg (jan.hackenberg@posteo.de)
Private Funded https://orcid.org/0000-0002-3462-3762

Jean-Daniel Bontemps
IGN: Instituto Geografico Nacional

Research Article

Keywords: Allometry, Trees, Forests, Pipe Model Theory, PMT, WBE

Posted Date: June 9th, 2023

DOI: https://doi.org/10.21203/rs.3.rs-2818844/v1

License: This work is licensed under a Creative Commons Attribution 4.0 International License.
Read Full License

Version of Record: A version of this preprint was published at Applied Geomatics on November 20th, 2023. See the published version at https://doi.org/10.1007/s12518-023-00537-4.

Improving quantitative structure models with an Huxley protocol based filter

PhD Jan Hackenberg 0000-0002-3462-3762[1*] and HDR Jean-Daniel Bontemps[2]

[1*] SimpleForest, Droehnenstr. 23, Hannover, 30455, Niedersachsen, Germany.
[2]Laboratoire d'Inventaire Forestier, IGN, 14 rue Giradet, Nancy, 54000, France.

*Corresponding author(s). E-mail(s): jan.hackenberg@posteo.de;
Contributing authors: jdbontemps.ign@gmail.com;

Abstract

Quantitative structure models (`QSMs`) are topological ordered cylinder models of trees which describe the branching structure up to the tips.

Methods: We present unpublished tree describing parameters which can be derived from a single Quantitative Structure Model (`QSM`). The parameters are used to build two `Radius` correction filters.
Results: For validation we use QSMs produced from an open point cloud data set of tree clouds with the SimpleForest software. We compare the QSM volume against the harvested reference data for 65 felled trees. We also found QSM data of TreeQSM, a competitive and broadly accepted QSM modeling tool. Our RMSE was less than 40 % of the TreeQSM RMSE.
For other error measures, the $r^2_{adj.}$ and the `CCC`, the relative improvement looked even better with reaching only 27 % and 21 % of the TreeQSM errors respectively.
Conclusions: In forest ecology we should use the here presented pipeline to build accurate `QSMs` for reasons of:
`Quality -` With the invention of the `QSM Radius` filter techniques we improve tree volume prediction capabilities utilizing `QSMs`.
`Quantity -` More data can be collected with `QSMs` than with traditional methods. Here we use models build on more than ten thousand measurements.

Keywords: Allometry, Trees, Forests, Pipe Model Theory, PMT, WBE

1 Introduction

Quantitative Structure Models (`QSMs`) [1–3] represent the Above Ground Biomass (`AGB`) of trees and consist of topological ordered cylinders following the branch structure from the root to the tips.

`QSMs` are build from 3d point clouds commonly recorded with Terrestrial Laser Scanners (`TLS`). The static `TLS` sensors provide in forest environments data which covers the surface of trees from the stem up to the branching structure. For the processing of the data 3d tree reconstruction algorithms have been developed [1, 2, 4–7]. The input `TLS` clouds tend to have a nearest neighbor distance in the order of approximately one `cm`. With such cloud densities the surface of a large mature tree can be covered with multiple millions of euclidean points. Because of the high automation level the human bias is low during both data collection and model computation.

The `QSMs` derived from such high resoluted clouds can consist of ten thousands up to hundred thousands cylinders [3]. Figure 1 shows a `QSM` representing a large *Acer pseudoplatanus* tree with more than 35 thousand cylinders.

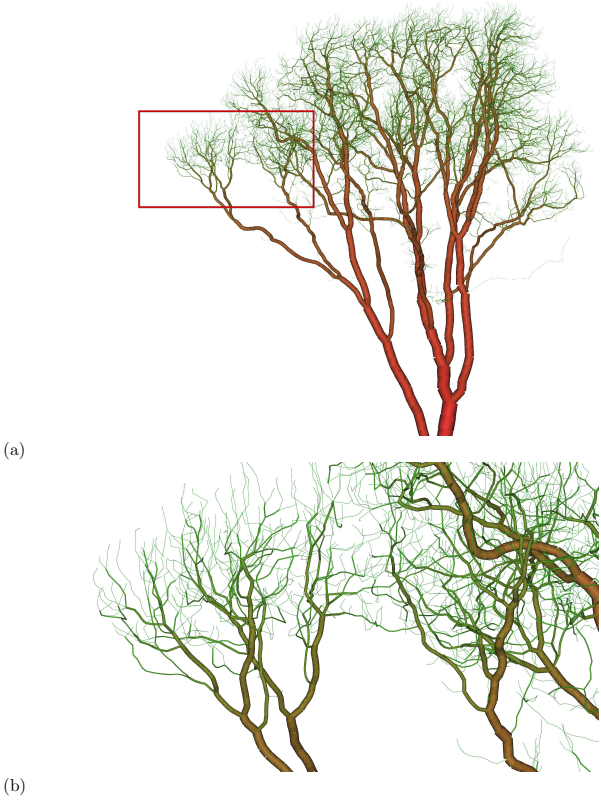


Fig. 1
(a) A QSM of an *Acer pseudoplatanus* [8, 9] with a DBH of $\sim$ 1.4 m containing approximately 25 m^3 of woody biomass. The QSM was modeled with Simple Forest [10]. The tree is located in Wytham Woods, UK. The QSM consists of more than 35 000 cylinders. (b) A zoom of the red bounding boxed area in (a).

Various software tools with the capability to compute `QSMs` have been published [11]. Licensed under copy left are the Computree [12] plugins SimpleTree [2, 13] and SimpleForest [10]. Also TreeQSM [1, 14] and 3dForest [15] are `QSM` building software tools which can be downloaded including their free source code.

The sum of the `QSM's` cylinder `Volumes` is an estimate for the above ground volume (`AGV`) of the scanned tree. If after scanning the `AGV` is additionally measured destructively reference data is collected for `QSM` accuracy analysis studies [14, 16–21].

Studies binning the tree into different diameter compartments revealed that the the accuracy of `QSM` prediction capabilities decreased with smaller branch diameters [16, 22]. Small branching structure tends to be significantly overestimated both by the `TLS` clouds and the computed `QSMs`.

In earlier works [13] we introduced a `QSM` filter designed to reduce the overestimation problem. An allometric function between the `GrowthVolume` and the cylinder `Radius` allowed a statistical correction of overestimated `Radii` with equation 1:

$$Radius = a \times GrowthVolume^{b} \tag{1}$$

Modeling a `Radius` $\sim$ `Volume` relation with a power function is a common procedure in forestry, various `Volume` predicting functions have been published [23, 24]. In the traditional forestry approach just predictor and predicted change. Using power functions to model size relations is not limited to trees. The theory of allometric scaling relying on exactly that base function is a general biological theory, see equation 2 for the generalization.

$$Y_i = a \times X_i^{b} \tag{2}$$

A century ago Huxley analyzed size relations on the data of shore-crab bodies and realized he could linearize the problem by a simple log transform on predictor and predicted, as we can see in equation 3 [25]. The error ϵ_i follows a normal distribution with mean 0 and standard deviation σ^2. Huxley assumed an homoscedastic error constant over the full range of log transformed data, see equation 3.

$$ln(Y_i) = ln(a) + b \times ln(X_i) + \epsilon_i, \epsilon_i \sim N(0, \sigma^2) \tag{3}$$

After the linear fit the back transformation to the power function shown in equation 4 was performed by Huxley.

$$Y_i = a \times X_i^{b} \times exp(\epsilon_i), \epsilon_i \sim N(0, \sigma^2) \tag{4}$$

Our former published approach [13] does follow the so called Huxley protocol [26]. But the `GrowthVolume` filter has a significant design flaw. Being calculated from the sum of cylinders' `Volumes` it is indirectly relying on the cylinders' `Radii`. Unfortunately, we already know that the `Radii` predictions are not reliable for the thin branching structure. We conclude that our predictor `GrowthVolume` is error-prone and the computed model is supposed to deviate from the observed real world phenomenon.

In this manuscript we will build new filters which rely on other parameters which are much less error-prone.

2 Methods

In addition to the geometrical description also topological information is stored inside a QSM. Along each path from the tree root to one of the branch tips the parent child relation is added to the geometry parameters. In figure 2 we draw an idealized and simplified `QSM`.

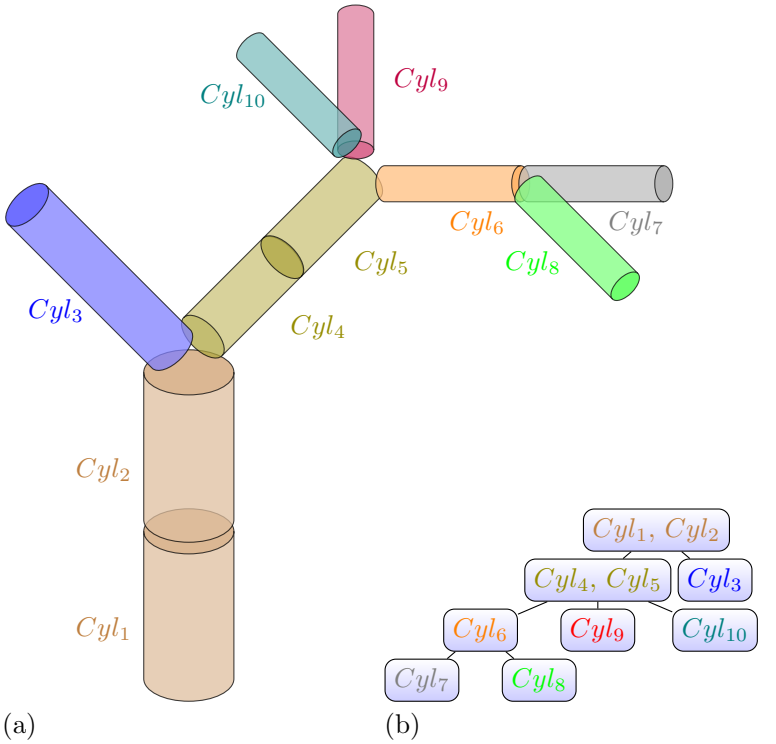


Fig. 2
(a) An artificial QSM consisting of ten cylinders `Cyl`$_n$. Each cylinder consists of two 3d points `start` and `end` as well as the `Radius`. The cylinders between two neighboring branch junctions are combined to a list structure called segment. Each segment is colored differently. The cylinder list of one segment is always ordered from closest to the root to farthest away from the root.
(b) We can see the topological order information from the QSM in (a). The segments are stored in the nodes. The root node is the segment which stores the root cylinder `Cyl`$_1$ at its begin.

First we define a few tree describing parameters, some relying on the topology only and others on the geometry of `QSM` cylinders as well. Then we will build two functions to predict the `Radius` of a cylinder. We will use both functions in `Radius` filters designed to improve the `Volume` prediction accuracy of `QSMs`.

2.1 Tree describing parameters

2.1.1 GrowthVolume

We defined in [13] the `GrowthVolume` of a cylinder recursively.

Definition 1 (GrowthVolume) The `GrowthVolume` of a cylinder is the cylinder's volume plus the `GrowthVolumes` of its children.

In other words the `GrowthVolume` is the sum of the `Volumes` of all cylinders with a child relation to the query cylinder, see figure 3.

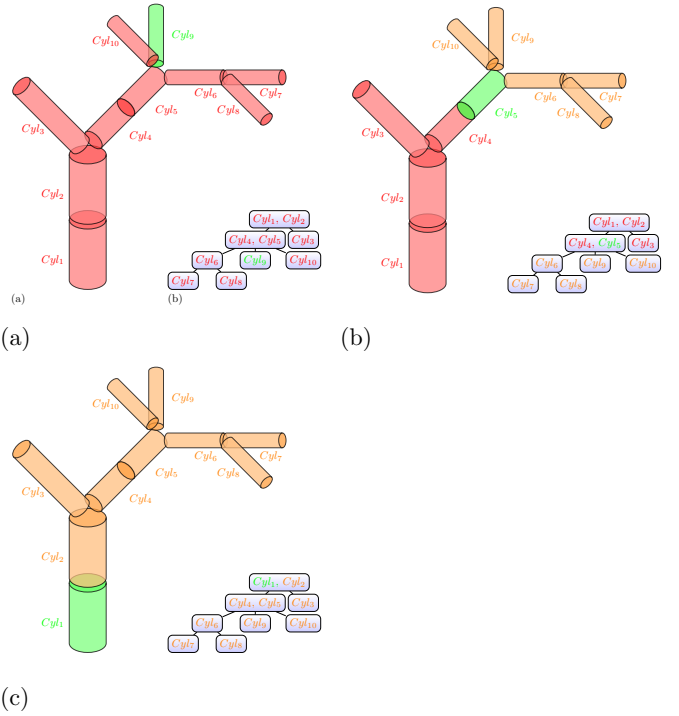


Fig. 3
We see a `QSM` colored in three different colors representing the concept of recursive child relation for a query cylinder. In green the query cylinder is highlighted. The query cylinder has a recursive child relation to itself. Orange are all cylinders which have additionally a recursive child relation to that query cylinder. Red are all cylinders colored which have no recursive relation to the query cylinder. Three border cases are depicted:
(a) The query cylinder Cyl_9 is a tip node and none of the other cylinders has a recursive child relation.
(b) Here the query cylinder Cyl_5 is located in the center of the `QSM`. The cylinders fullfilling the the child relation is the sub-branch which would be received when cutting the represented tree at the position between Cyl_4 and Cyl_5.
(c) The query cylinder Cyl_1 is the root cylinder of the `QSM`. All cylinders of the `QSM` have a recursive child relation to the root.

We used the `GrowthVolume` as a predictor for the radius in a radius correction filter [13], see equation 1.

Nevertheless this filter has a design flaw. Overestimated `Radii` of cylinders with a child relation to the query cylinder do influence those cylinders' `Volumes` and therefore also the `GrowthVolume`. Our predictor is distorted by the noisy attribute we want to get rid of.

2.1.2 GrowthLength

We can substitute the `Volume` with the `Length` in our previous definition to get a recursively defined `Length`.

Definition 2 (GrowthLength) The `GrowthLength` of a cylinder is the cylinder's `Length` plus the `GrowthLength` of its children.

The `GrowthLength` is not affected by the `Radius` prediction errors occurring during cylinder fitting. Therefore it is a robust ordering predicate for the child nodes at each branch junction in the topology structure. With this ordering we can extract the stem by following the left path in the `QSM` structure depicted in figure 2.

2.1.3 Reverse Branch Order

To define another meaningful order in the sense of diameter scaling we can read the reverse branch order from a tree.

Definition 3 (Reverse Branch Order) The `Reverse Branch Order` (`RBO`) of a cylinder is the maximum depth of the subtree of the segment's node. If we look at the real tree, the `RBO` denotes the maximal number of branching splits of the sub-branch growing out the segment.

The reverse branch order is depicted in the schematic QSM in figure 4.

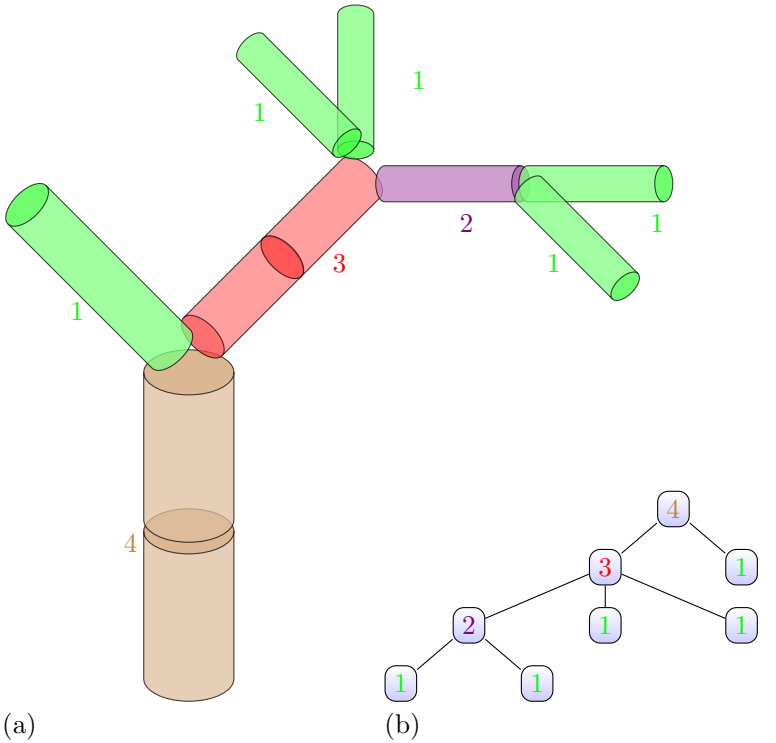


Fig. 4
(a) The artificial QSM of figure 2 labeled with the `RBO`.
(b) We can see the topological order information from the QSM in (a) and each node has the `RBO` displayed.

2.1.4 Reverse Branch Order Pipe Area

Definition 4 (Reverse Branch Order Pipe Area) We define the Reverse Branch Order Pipe Area (`RBOPA`): The West-Brown-Enquist (`WBE`) model states that the branching architecture is self-similar [27–32]. In a self-similar branching architecture the `Radius` as well as the cross sectional area of a tip is constant. The `RBOPA` is a tree specific area unit. By following the Pipe Model Theory (`PMT`) [33–35] the `RBOPA` of a cylinder at any location inside the QSM equals the number of supported tips. Supported tip cylinders always have a recursively defined parent relation to the query cylinder.

We can see the `RBOPA` depicted in the schematic `QSM` visible in figure 5.

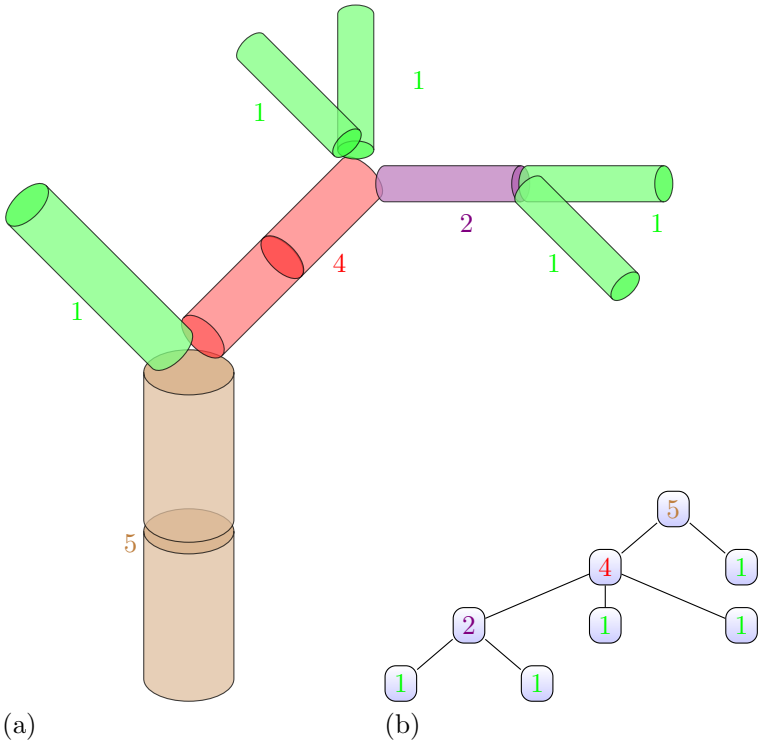


Fig. 5
(a) The artificial QSM of figure 1 labeled with the `RBOPA`.
(b) We can see the topological order information from the QSM in (a) and each node has the `RBOPA` displayed.

By its definition the `RBOPA` is a proxy for the sapwood area. To derive the true sapwood area measured in metrical units we need to simply multiply `RBOPA`$\times$ `AreaOfTip`. `AreaOfTip` is the expected cross sectional area of each tip of a tree.

2.1.5 Reverse Branch Order Pipe Radius

Earlier works have shown that small cylinders can represent the topology correctly, but their radius tends to be overestimated [16, 22]. By having a `Radius` independent proxy for the cross sectional area we can simply take its square-root to derive a proxy for the `Radius` of a cylinder.

Definition 5 (Reverse Branch Order Pipe Radius) We define the Reverse Branch Order Pipe Radius (`RBOPR`) as the square root of the `RBOPA`.

2.1.6 ProxyVolume

As the RBOPA is a proxy for the area of active vessels which pass the cylinder we can also model a proxy for the volume occupied by vessels in a cylinder.

Definition 6 (ProxyVolume) The ProxyVolume of a cylinder is calculated by multiplying the Length with the RBOPA as shown in equation 5. By definition the ProxyVolume is not relying on correctly modeled Radii.

$$ProxyVolume = RBOPA \times length \tag{5}$$

2.1.7 VesselVolume

We had defined the GrowthVolume of a cylinder in a recursive manner. We used the GrowthVolume in earlier works [13] as a predictor for a corrected radius of each cylinder utilizing a simple power function fit. In similar manner to the GrowthVolume we can define the VesselVolume, but utilizing instead of cylinders' Volumes their ProxyVolumes.

Definition 7 (VesselVolume) The VesselVolume of a cylinder is it's ProxyVolume plus the VesselVolume of the cylinder's children.

2.2 QSM Filters

We are about to present two filters with Radius prediction capabilities. We pre-filter first the QSM data. We want to remove cylinders with overestimated Radii in the afterwards presented fitting routines. As over-fitting during the QSM generation is more likely to happen within the tip regions [16, 22], we can simply create one filter to get rid of overestimated cylinders by thresholding the RBO. For example requesting the the RBO of valid cylinders has to be larger one removes all tip segments' cylinders.

The remaining cylinders can then be piped through a statistical outlier filter based on the cylinder's distance to the aligned TLS sub-cloud.

2.2.1 Linear RBOPR filter

We will build the RBOPR filter to correct overestimated Radii with equation 6.

$$Radius = a \times RBOPR \tag{6}$$

We only correct Radii if they differ by more than a user selected percentage deviation threshold from their predicted Radii.

2.2.2 Non linear VesselVolume filter

Similar to the `GrowthVolume` approach we can try to predict the `Radius` from the `VesselVolume` by a simple non linear power fit. So we will use equation 7 to correct cylinders `Radii` and will refer to as the `VesselVolume` filter.

$$Radius = a \times VesselVolume^{b} \tag{7}$$

To get appropriate initial parameters required for non linear solvers we use the Huxley method on log transformed data [25].

To be in agreement with the geometrical relation between a `Volume` and a `Length` we expect b close to the cube root $\frac{1}{3}$.

The solver can still fail, if too large residuals are contained in the fitting data. Non linear fitters are less robust as they can find false, local minima instead of global minima in the error space. To get robust against such failures we recommend to first apply the Filter based on the `RBOPR` with a large deviation threshold. The linear correction will be applied to the cylinders with the largest errors, but a lot of unmodified cylinders are still usable to predict the `VesselVolume` power function parameters.

The allowed deviation between measured and predicted is user selected.

2.3 Data

The author's of [21] destructively harvested 65 individuals of the species *Fagus sylvatica*, *Larix decidua*, *Pinus sylvestris*, *Fraxinus excelsior*. From `AGB` measurements and density analysis `Volume` reference data was derived. Then the authors produced 65 QSMs with TreeQSM version 2.4.1 [36]. For TreeQSM models a tapering filter [17] relying on a parabolic function to correct overestimated leaves was applied. Both TreeQSM models as well as input cloud data is published at Zenodo [37].

`QSMs` have been produced as well with SimpleForest v 5.3.1 [10, 38]. We applied the following pipeline on the input clouds:

1. apply a statistical outlier filter on the input clouds [39],
2. produce `QSMs` with the SphereFollowing method wrapped in an automated parameter search [13, 40],
3. apply the `RBOPR` filter,
4. apply the `VesselVolume` filter.

2.4 Software

Statistical results have been produced with R-Software [41] and for the plots we used ggplot [42].

3 Results

3.1 The Huxley protocol

First we run the `RBOPR` filter on all `QSMs`. We then filtered out all cylinders which had been modified with the `RBOPR`. That left us with more than 12'000 cylinders which were directly fit into the point cloud and never statistically modified after the geometry fit. On the remaining cylinders of each `QSM` a normalization was performed so `Radius` and `VesselVolume` both range from 0 to 1. Lastly a log transformation was performed. We then pooled the 12'000 measurements species wise and fitted four linear models. The $\texttt{r}^2_{\texttt{adj}}$.s of the species wise linear models range from 0.96 to 0.97 and the slopes of the fitted lines are quite similar in a range of 0.34 to 0.36, see figure 6.

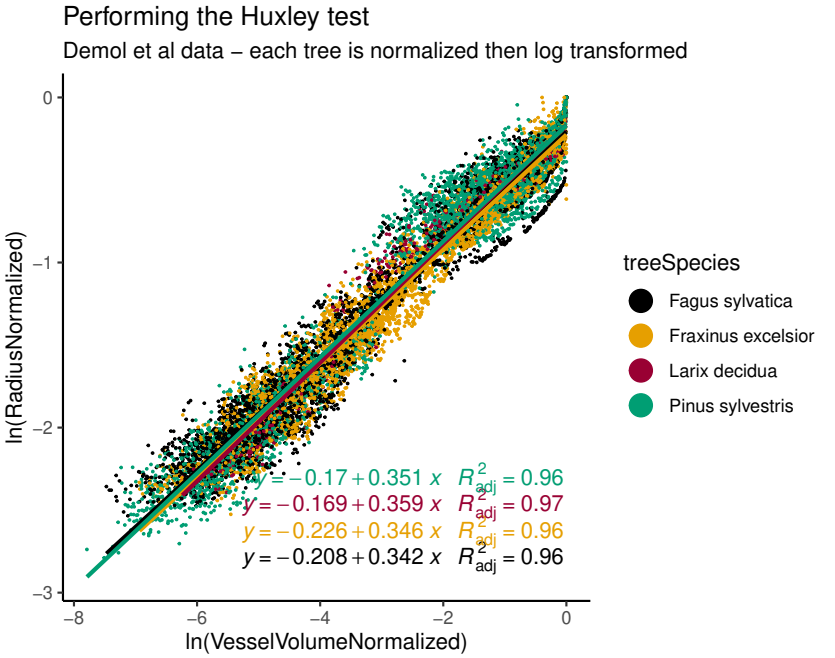


Fig. 6
All 65 `QSMs` have been filtered with the `RBOPR` method. We extracted 12352 cylinders which had not been modified by the filter. All of those are cylinders fitted into the point cloud [2] without any further statistical processing. First we normalize each `QSM` so both `Radius` and `VesselVolume` range between 0 and 1. Then we log transform the data, cluster by species and lastly fit a linear model for each cluster.

3.2 Volume accuracy

As we have destructively collected reference `Volume` data [37] we can analyze the accuracy of QSM `Volume` predictions. In figure 7 we use SimpleForest QSMs which have been improved by either the linear `RBOPR` filter (a) or the

non-linear `VesselVolume` filter (b). We plot as well the results produced with TreeQSM as published [37] (c).

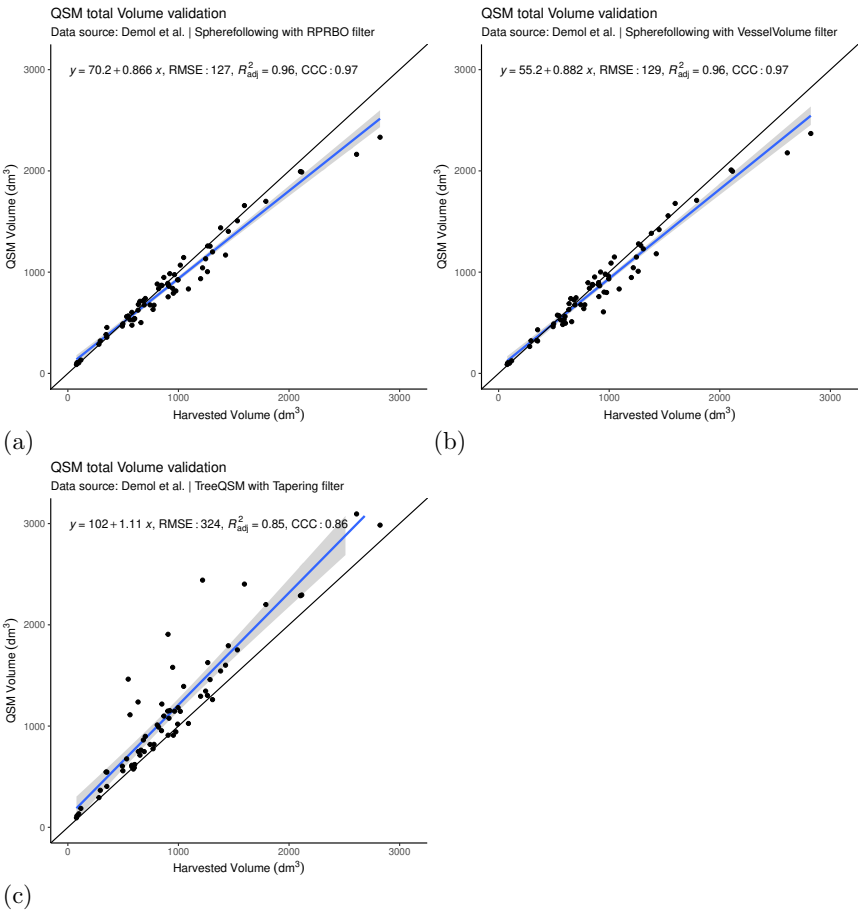


Fig. 7 We use free accessible data of tree point clouds, those trees' destructively collected `Volume` ground truth data and TreeQSM computed `Volume` data [11].
(a) SimpleForest QSMs filtered with the `RBOPR` filter have their `volumes` compared to destructive ground truth measurements.
(b) Similar to (a), but this time the `VesselVolume` filter was applied to SimpleForest QSMs.
(c) We also show the scatter plot of QSMs stored in the data base. Those have been modeled with TreeQSM algorithm [1] and then filtered by the TreeQSM tapering method [17].

All results are written with their root mean squared error (`RMSE`), their $\mathtt{r^2_{adj}}$. and their Concordance Correlation Coefficient (`CCC`) into table 1.

Table 1 Numerical validation of QSM volume measures compared to harvested reference volume measures.

Software `Filter`	RMSE(dm^3)	$r^2_{adj.}$	CCC
SimpleForest `VesselVolume`	129	0.96	0.97
SimpleForest `RBOPR`	127	0.96	0.97
TreeQSM `Tapering`	324	0.85	0.86

4 Discussion

4.1 Filter Reasoning

4.1.1 RBOPR filter

The `RBOPR` filter was build on theoretical grounds. From the `WBE` model follows the assumption of a constant tip cross sectional area. And with the `PMT` we can correlate the `Radius` at any position with the number of supported tips. Our equation 6 is the mathematical realization of the two conceptual properties originated from two well established ecology theories.

4.1.2 VesselVolume filter

The second filter was build on a revealed pattern during data analysis and not build on forest ecology theories. So here we reason numerically.

The relation `Radius` $\sim$ `VesselVolume` is expected to have an exponent value close to $\frac{1}{3}$. The slope of the fitted models in figure 6 deviates with values between 0.34 and 0.36 only by 0.01 up to 0.03. So the used relation reflects the fit of a `Length` to a `Volume`.

The $r^2_{adj.}$ is close to one for all four fitted functions.

4.2 QSM Volume Accuracy

We imported here in our analysis results [21, 37] which have been produced with TreeQSM. The TreeQSM pipeline which was utilized by Demol et al. uses an algorithm which has been discussed in detail [1, 3, 14] embedded within a traditional optimization algorithm [13]. The `QSMs` then were filtered with the tapering method [17].

Importing the same clouds we also produced SimpleForest [10] `QSMs` relying on the same parameter optimization technique [13] but utilizing a different algorithm - the spherefollowing algorithm [2]. The output QSMs have then been filtered with the here proposed allometric theory based filters. We fitted linear models into the ground truth `Volume` vs QSM `Volume` predictions, see figure 7 and table 1.

Our results produced data where the `RMSE` is 39 % of the TreeQSM error. The devation of the $\mathtt{r^2_{adj.}}$ value from the best score 1.0 is for SimpleForest only 27 % of the TreeQSM derived deviation. For the `CCC` the deviation is only 21 % of the TreeQSM deviation.

We conclude that the analyzed tree species can be modeled with the here presented allometric scaling theory based filters. Using our introduced allometric relations performes better than previously published `QSM` filtering methods [13, 17]. This should help to rise the acceptance to rely on `TLS` scans and `QSM` modeling [43].

4.3 Bias

We can see an underestimation of the prediction by SimpleForest, 12 % for `RBOPR` and 13 % for `VesselVolume` filtering. The bias is of roughly the same magnitude like the TreeQSM overestimation (11 %) bias. A partial explanation might have been the statistical outlier filtering [39] of the input clouds before building the `QSMs`. While getting rid of noise points improves the optimization results we potentially also lost a significant part of the thin branching structure.

Another explanatory hypothesis is that in the year of recording less leave growth did happen. Less growing units - the tips which we count - leads to an underestimation of both `RBOPR` and `VesselVolume`.

Time series data recorded under temporal changing weather and climate conditions might open here a complete new field. In hot dry years we might observe underestimation as the sapwood `Radius` and sapwood `Volume` which we use as a predictors are less than in humid and mild years.

5 Conclusions

5.1 Impact on QSM usage

We recommend the usage of one of the two the here presented filtering protocols when working with QSMs. To our knowledge no national forest inventory decided to use QSMs to build `Volume` functions from it up to date. This work provides a significant boost for the `Volume` prediction capabilities of QSMs so we recommend a reevaluation of QSM usage potentials. The computation of linear models is more stable compared to the computation of non linear models. Linear model solvers do not rely on good starting parameters and are always guaranteed to find the global minimum. Therefore we recommend the usage of the `RPOBA` filter over the `VesselVolume` filter.

Generalization of the results should be handled with care. We analyzed here data recorded in leave-off conditions with multiple scans with state of the art equipment and protocols [21]. Only if similar scanning conditions are faced, the accuracy of the results can be expected of the same order as discussed.

Prooning campaigns which are designed to influence a tree's growth pattern to produce the maximal amount of merchantable wood might result in tree individuals following growth patterns not fulfilling of the here applied Huxley protocol [25]. How well this work performs on either conifers or large evergreen trees needs to be analyzed as well.

5.2 Impact on forest ecology theories

The RBOPA we interpreted as a proxy for the area of sapwood at any given point in the tree. Of course we could also think of multiplying the RBOPA with the expected number of leaves on a new growth unit and derive the total number of leaves. So the RBOPA can be seen as a proxy for the area leave index as well.

With open QSM data bases [14, 16–21] tree modelers have from now on a much more convenient way to collect data.

acknowledgements

We would like to acknowledge Matthias Disney for providing the SimpleForest development with constructive feedback over the last decade via emails and manuscript reviews.

Declarations

Funding

All development of SimpleForest software including the presented research results have been private funded by Jan Hackenberg. The authors declare that no funds, grants, or other support were received during the preparation of this manuscript. No Artificial Intelligence Language Model [44] was used during the manuscript's writing process.

Conflict of interest/Competing interests

The authors declare no conflict of interest.

Availability of data and materials

The TLS clouds and the TreeQSM results can be downloaded [37].

Code availability

We use for the computation in addition to the mentioned data the persistent SimpleForest release v5.3.1 [38]. Here a precompiled windows executable exists.

The code of SimpleForest can also be downloaded from the Git repository https://gitlab.com/SimpleForest/computree/.

SimpleForest QSMs as well the R scripts for the statistical analysis and plots are embedded in the manuscript repository https://gitlab.com/SimpleForest/allometricscalingpaper.

Authors' contributions

Jan Hackenberg developed the SimpleForest software as well as the methods and algorithms. He did the statistical analysis and the writing of the first

version of the manuscript. Jean-Daniel Bontemps participated in improving the allometric methods of SimpleForest and did the review of this manuscript.

References

[1] Raumonen, P., Kaasalainen, M., Akerblom, M., Kaasalainen, S., Kaartinen, H., Vastaranta, M., Holopainen, M., Disney, M., Lewis, P.: Fast automatic precision tree models from terrestrial laser scanner data. Remote Sensing **5**(2), 491–520 (2013). https://doi.org/10.3390/rs5020491

[2] Hackenberg, J., Morhart, C., Sheppard, J., Spiecker, H., Disney, M.: Highly accurate tree models derived from terrestrial laser scan data: A method description. Forests **5**, 1069–1105 (2014)

[3] Markku, Å., Raumonen, P., Kaasalainen, M., Casella, E.: Analysis of geometric primitives in quantitative structure models of tree stems. Remote Sensing **7**(4), 4581–4603 (2015). https://doi.org/10.3390/rs70404581

[4] Xu, H., Gossett, N., Chen, B.: Knowledge and heuristic-based modeling of laser-scanned trees. ACM Transactions on Graphics **26**(4), 19 (2007). https://doi.org/10.1145/1289603.1289610

[5] Côté, J.-F., Fournier, R.A., Egli, R.: An architectural model of trees to estimate forest structural attributes using terrestrial LiDAR. Environment Modelling Software **26**, 761–777 (2011)

[6] Lau Alvaro, M.C.S.A.B.H.R.P.M.Y.J.T.H.M. Bentley Lisa Patrick: Quantifying branch architecture of tropical trees using terrestrial LiDAR and 3D modelling (2018). https://doi.org/10.1007/s00468-018-1704-1

[7] Ye, N., van Leeuwen, L., Nyktas, P.: Analysing the potential of UAV point cloud as input in quantitative structure modelling for assessment of woody biomass of single trees. International Journal of Applied Earth Observation and Geoinformation **81**, 47–57 (2019). https://doi.org/10.1016/j.jag.2019.05.010

[8] Disney, M.I., Boni Vicari, M., Burt, A., Calders, K., Lewis, S.L., Raumonen, P., Wilkes, P.: Weighing trees with lasers: advances, challenges and opportunities. Interface Focus **8**(2) (2018). https://doi.org/10.1098/rsfs.2017.0048

[9] Calders, K., Origo, N., Burt, A., Disney, M., Nightingale, J., Raumonen, P., Åkerblom, M., Malhi, Y., Lewis, P.: Realistic forest stand reconstruction from terrestrial lidar for radiative transfer modelling. Remote Sensing **10**(6) (2018). https://doi.org/10.3390/rs10060933

[10] Hackenberg, J., Calders, K., Demol, M., Raumonen, P., Piboule, A., Disney, M.: SimpleForest - a comprehensive tool for 3d reconstruction of trees from forest plot point clouds. bioRxiv (2021). https://doi.org/10.1101/2021.07.29.454344

[11] Demol, M., Verbeeck, H., Gielen, B., Armston, J., Burt, A., Disney, M., Duncanson, L., Hackenberg, J., Kükenbrink, D., Lau, A., Ploton, P., Sewdien, A., Stovall, A., Takoudjou, S.M., Volkova, L., Weston, C., Wortel, V., Calders, K.: Estimating forest above-ground biomass with terrestrial laser scanning: Current status and future directions. Methods in Ecology and Evolution **00**(n/a) (2022). https://doi.org/10.1111/2041-210X.13906

[12] Othmani, A., Lew Yan Voon, L.F.C., Stolz, C., Piboule, A.: Single tree species classification from Terrestrial Laser Scanning data for forest inventory. Pattern Recognition Letters **34**(16), 2144–2150 (2013). https://doi.org/10.1016/j.patrec.2013.08.004

[13] Hackenberg, J., Spiecker, H., Calders, K., Disney, M., Raumonen, P.: Simpletree — an efficient open source tool to build tree models from tls clouds. Forests **6**, 4245–4294 (2015)

[14] Raumonen, P., Casella, E., Calders, K., Murphy, S., Åkerblom, M., Kaasalainen, M.: Massive-scale tree modelling from tls data. ISPRS Annals of the Photogrammetry, Remote Sensing and Spatial Information Sciences **II-3/W4**, 189–196 (2015). https://doi.org/10.5194/isprsannals-II-3-W4-189-2015

[15] Trochta, J., Krůček, M., Vrška, T., Král, K.: 3d forest: An application for descriptions of three-dimensional forest structures using terrestrial lidar. PLOS ONE **12**(5), 1–17 (2017). https://doi.org/10.1371/journal.pone.0176871

[16] Hackenberg, J., Wassenberg, M., Spiecker, H., Sun, D.: Non destructive method for biomass prediction combining tls derived tree volume and wood density. Forests **6**(4), 1274–1300 (2015). https://doi.org/10.3390/f6041274

[17] Calders, K., Newnham, G., Burt, A., Murphy, S., Raumonen, P., Herold, M., Culvenor, D., Avitabile, V., Disney, M., Armston, J., Kaasalainen, M.: Nondestructive estimates of above-ground biomass using terrestrial laser scanning. Methods in Ecology and Evolution **6**(2), 198–208 (2015). https://doi.org/10.1111/2041-210X.12301

[18] Kunz, M., Hess, C., Raumonen, P., Bienert, A., Hackenberg, J., Maas, H., Härdtle, W., Fichtner, A., Von Oheimb, G.: Comparison of wood volume estimates of young trees from terrestrial laser scan data. iForest: Biogeosciences and Forestry **10**(2), 451–458 (2017)

[19] Momo Takoudjou, S., Ploton, P., Sonké, B., Hackenberg, J., Griffon, S., de Coligny, F., Kamdem, N.G., Libalah, M., Mofack, G.I., Le Moguédec, G., Pélissier, R., Barbier, N.: Using terrestrial laser scanning data to estimate large tropical trees biomass and calibrate allometric models: A comparison with traditional destructive approach. Methods in Ecology and Evolution **9**(4), 905–916 (2018) https://arxiv.org/abs/https://besjournals.onlinelibrary.wiley.com/doi/pdf/10.1111/2041-210X.12933. https://doi.org/10.1111/2041-210X.12933

[20] Gonzalez de Tanago, J., Lau, A., Bartholomeus, H., Herold, M., Avitabile, V., Raumonen, P., Martius, C., Goodman, R.C., Disney, M., Manuri, S., *et al.*: Estimation of above-ground biomass of large tropical trees with terrestrial lidar. Methods in Ecology and Evolution **9**(2), 223–234 (2018)

[21] Demol, M., Calders, K., Krishna Moorthy, S.M., Van den Bulcke, J., Verbeeck, H., Gielen, B.: Consequences of vertical basic wood density variation on the estimation of aboveground biomass with terrestrial laser scanning. Trees **35**, 671–684 (2021). https://doi.org/10.1007/s00468-020-02067-7

[22] Demol, M., Wilkes, P., Raumonen, P., Moorthy, S.M.K., Calders, K., Gielen, B., Verbeeck, H.: Volumetric overestimation of small branches in 3D reconstructions of Fraxinus excelsior. Silva Fennica **56**(1), 1–26 (2022). https://doi.org/10.14214/sf.10550

[23] Henry, M., Bombelli, A., Trotta, C., Alessandrini, A., Birigazzi, L., Sola, G., Vieilledent, G., Santenoise, P., Longuetaud, F., Valentini, R., Picard, N., Saint-André, L.: Globallometree: international platform for tree allometric equations to support volume, biomass and carbon assessment. iForest - Biogeosciences and Forestry (6), 326–330 (2013) https://arxiv.org/abs/http://www.sisef.it/iforest/pdf/?id=ifor0901-006. https://doi.org/10.3832/ifor0901-006

[24] Zianis, D., Muukkonen, P., Mäkipää, R., Mencuccini, M.: Biomass and Stem Volume Equations for Tree Species in Europe. FI, ??? (2005). https://doi.org/10.14214/sf.sfm4.

[25] Huxley, J.S.: Constant differential growth-ratios and their significance. Nature **114**(2877), 895–896 (1924)

[26] Packard, G.C.: Julian huxley and the quantification of relative growth. Zoomorphology **139**, 131–140 (2019). https://doi.org/10.1007/s00435-019-00466-0

[27] West, G.B., Brown, J.H., Enquist, B.J.: A general model for the origin of allometric scaling laws in biology. Science **276**(5309), 122–126 (1997)

[28] West, G.B., Brown, J.H., Enquist, B.J.: The fourth dimension of life: fractal geometry and allometric scaling of organisms. science **284**(5420), 1677–1679 (1999)

[29] West, G.B., Brown, J.H., Enquist, B.J.: The origin of universal scaling laws in biology. Scaling in biology, 87–112 (2000)

[30] West, G.B., Enquist, B.J., Brown, J.H.: A general quantitative theory of forest structure and dynamics. Proceedings of the National Academy of Sciences **106**(17), 7040–7045 (2009) https://arxiv.org/abs/https://www.pnas.org/doi/pdf/10.1073/pnas.0812294106. https://doi.org/10.1073/pnas.0812294106

[31] Enquist, B.J., West, G.B., Brown, J.H.: Extensions and evaluations of a general quantitative theory of forest structure and dynamics. Proc. Natl. Acad. Sci. U. S. A. **106**(17), 7046–7051 (2009)

[32] Brummer, A.B., Savage, V.M., Enquist, B.J.: A general model for metabolic scaling in self-similar asymmetric networks. PLOS Computational Biology **13**(3), 1–25 (2017). https://doi.org/10.1371/journal.pcbi.1005394

[33] Shinozaki, K., Yoda, K., Hozumi, K., Kira, T.: A quantitative analysis of plant form – the pipe model theory. i. basic analyses. Japanese journal of ecology **14**(4), 97–105 (1964)

[34] Shinozaki, K., Yoda, K., Hozumi, K., Kira, T.: A quantitative analysis of plant form-the pipe model theory: Ii. further evidence of the theory and its application in forest ecology. Japanese journal of ecology **14**(4), 133–139 (1964)

[35] Lehnebach, R., Beyer, R., Letort, V., Heuret, P.: The pipe model theory half a century on: a review. Annals of botany **121**(5), 773–795 (2018)

[36] Raumonen, P.: TreeQSM code repository. https://github.com/InverseTampere/TreeQSM. [Online; accessed 16-July-2022] (2022)

[37] Demol, M., Gielen, B., Verbeeck, H.: QSMs, Point Cloud and Harvest Data from a Destructive Forest Biomass Experiment in Belgium Using Terrestrial Laser Scanning. https://doi.org/10.5281/zenodo.4557401. https://doi.org/10.5281/zenodo.4557401

[38] Hackenberg, J.: SimpleForest Source Code and Documentation - v5.3.1. Zenodo (2021). https://doi.org/10.5281/zenodo.5138255. https://doi.org/10.5281/zenodo.5138255

[39] Rusu, R.B., Cousins, S.: 3D is here: Point Cloud Library (PCL), Shanghai,

China (2011)

[40] Donati Sarti, G., Busa, M., Garnero, G., Magnani, A., Rossato, I.: An open-source approach to modelling and analysing a tree detected with a mobile laser scanner. In: Italian Conference on Geomatics and Geospatial Technologies, pp. 275–286 (2022). Springer

[41] R Core Team: R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria (2022). R Foundation for Statistical Computing. https://www.R-project.org/

[42] Wickham, H.: Ggplot2: Elegant Graphics for Data Analysis. Springer, ??? (2016). https://ggplot2.tidyverse.org

[43] Stovall, A.E., Vorster, A., Anderson, R., Evangelista, P.: Developing non-destructive species-specific tree allometry with terrestrial laser scanning. Methods in Ecology and Evolution (2022)

[44] Floridi, L., Chiriatti, M.: Gpt-3: Its nature, scope, limits, and consequences. Minds and Machines (2020). https://doi.org/10.1007/s11023-020-09548-1

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- snmathphys.bst
- snjnl.cls
- snbibliography.bib