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Tree attributes estimation

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Content

1. Crown delineation
2. Tree location, H, and CA estimation
3. DBH estimation
4. Detected – measured tree matching
5. Accuracy assessment

Crown delineation by 2D convex hull polygons

Segmentation



Crown delineation

After tree segmentation, tree crowns were delineated by projecting the segmented point cloud on a 2D plane and fitting polygons around the points of each segmented tree.

Reference: Coomes et al., 2017



VirtualForests



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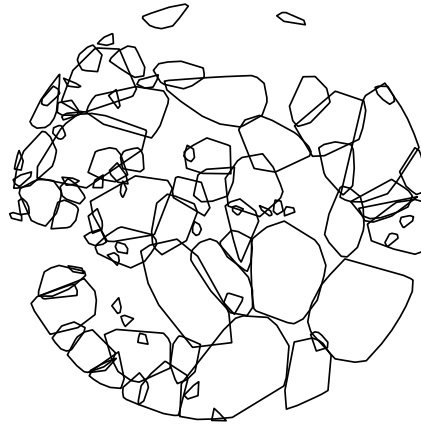
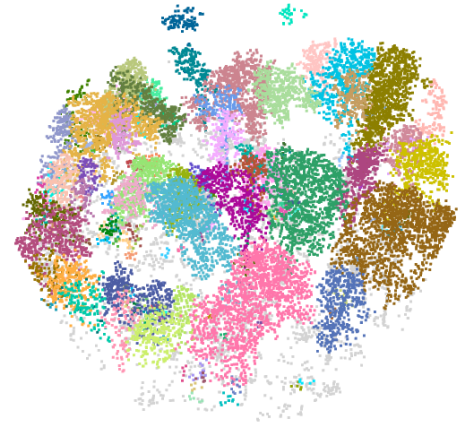
Crown delineation by 2D convex hull polygons

Segmentation



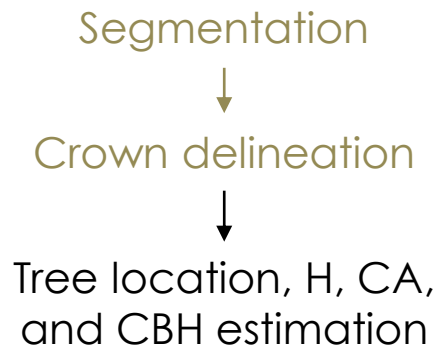
Crown delineation

Segmented
point cloud



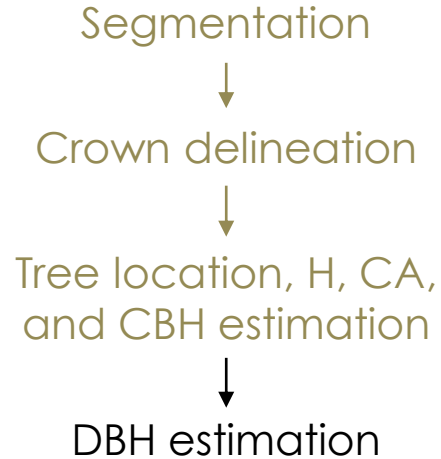
2D polygons

Tree attribute estimation



- Tree location was defined as the center of the X and Y coordinates of all points in a segmented tree.
- Tree height was derived from the Z value of the highest point within each segmented tree.
- Crown area was calculated as the area of the 2D crown polygons.

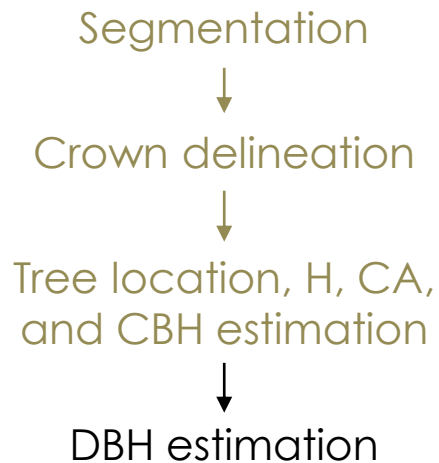
DBH estimation using allometric equation



Allometry is the study of the relative change in proportion of an attribute compared to another one during growth (*BioMath:Allometry*)

“The study of allometry is extremely important in dealing with measurements and data analysis in the practice of forestry. Allometric relationships often are used to estimate difficult tree measurements, such as volume, from an easily measured attribute such as diameter at breast height (DBH)” (‘Tree Allometry’, 2022)

DBH estimation using allometric equation



Allometric relations in forestry

Tree level

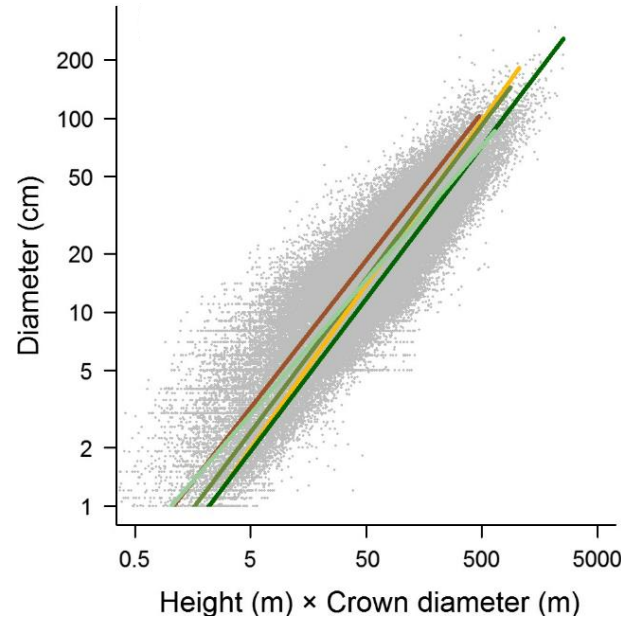
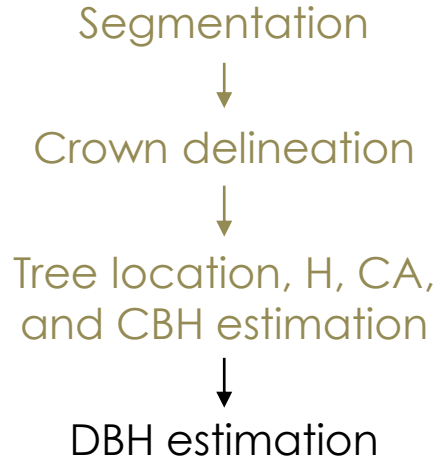
- DBH to height
- DBH to wood volume
- DBH to biomass
- DBH to crown diameter
- DBH to crown length
- DBH to crown volume
- DBH to leaf area
- ...

Stand level

- Height to biomass
- Height to basal area
- Basal area to biomass
- ...

Source: Nikolai., 2022 Introduction to allometry

DBH estimation using allometric equation

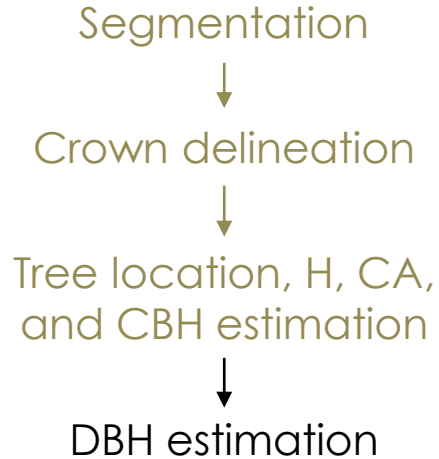


Jucker (2016) developed allometric equations to estimate DBH from tree height and crown diameter, using a global dataset of more than a hundred thousand individual trees

- Boreal forests
- Temperate coniferous forests
- Temperate mixed forests
- Savanna/woodlands
- Tropical forests

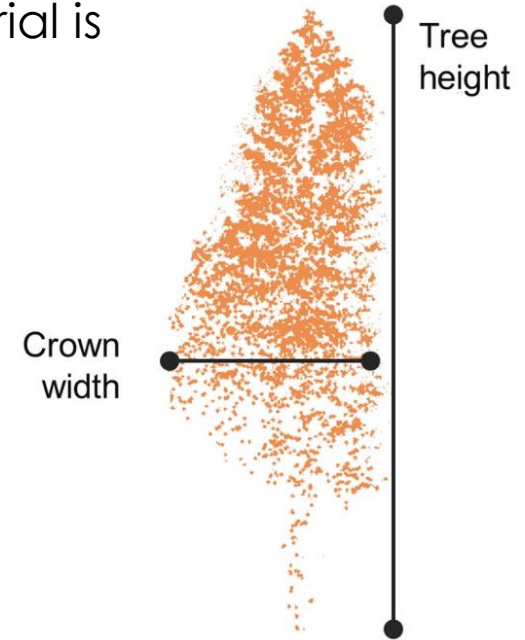
Source: Jucker et al., 2016 <https://doi.org/10.1111/gcb.13388>

DBH estimation using allometric equation



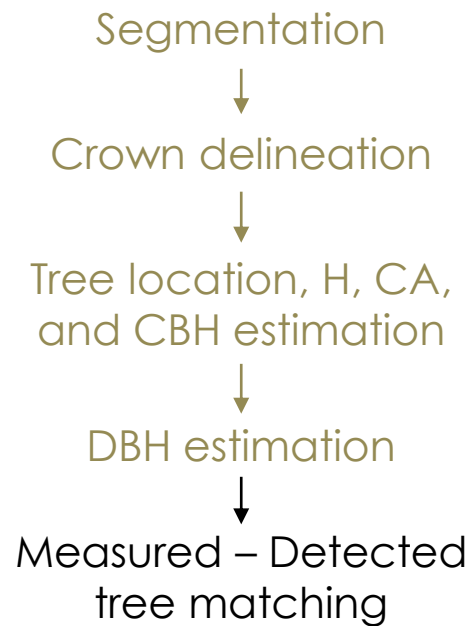
The equation used in this tutorial is specific to temperate mixed forests in the Palearctic realm (Jucker et al., 2016)

$$\text{DBH} = 0.708 \times (\text{H} \times \text{CD})^{0.753}$$



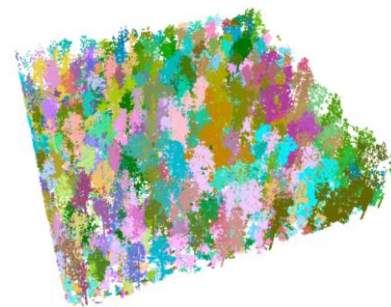
Source: Jucker et al., 2016 <https://doi.org/10.1111/gcb.13388>

Match inventory-measured trees to LiDAR-detected trees



Which tree in inventory is the tree detected from point cloud?

Detected trees



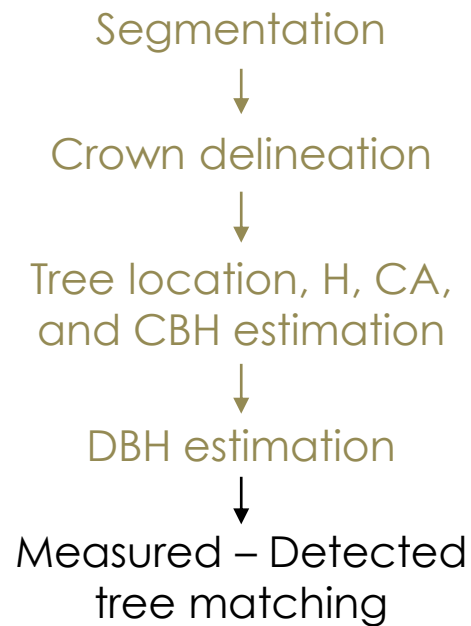
?

Measured trees

TreelD	Species	X	Y	DBH	H
1	RBU	419270.3	5851655	9.6	8.90000
2	RBU	419271.7	5851656	16.8	14.00000
3	RBU	419272.0	5851656	13.6	14.40000
4	RBU	419271.3	5851658	11.5	8.70000
5	GKI	419274.1	5851657	39.5	30.60000
6	RBU	419275.1	5851657	8.0	8.20000
7	GKI	419279.1	5851662	40.6	30.40000
8	GKI	419282.6	5851662	32.3	28.00000
9	GFI	419283.2	5851662	7.6	7.60000
10	RBU	419287.9	5851662	17.6	17.60000
11	RBU	419292.5	5851664	8.6	11.70000
12	GKI	419291.8	5851666	40.1	31.30000
13	GKI	419294.9	5851666	41.8	29.70000

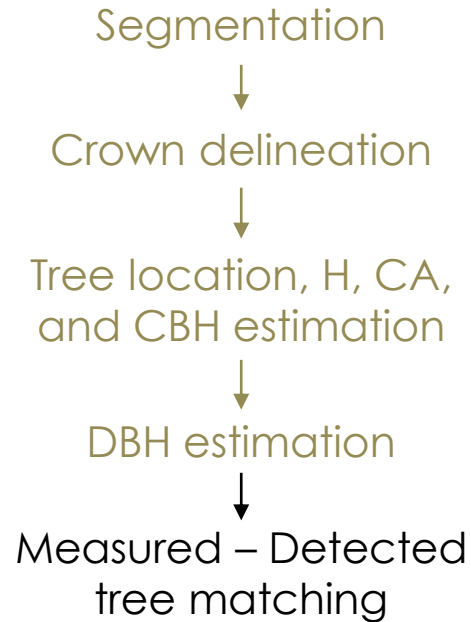
treelD	XTOP	YTOP	ZTOP	Z	npoints	cnvhl_
1	419347.1	5851575	26.0918	26.0918	1615	49.650
2	419341.4	5851574	10.2805	10.2805	128	5.056
4	419339.9	5851574	13.2852	13.2852	275	7.522
5	419327.4	5851568	9.2733	9.2733	134	4.938
6	419327.7	5851570	16.7855	16.7855	246	7.377
7	419329.6	5851571	28.2831	28.2831	418	15.765

Match inventory-measured trees to LiDAR-detected trees



To evaluate estimated and measured tree attributes at a single tree level, it is necessary to match the ALS-detected trees to field-measured trees. In other words, it is necessary to find which trees in the inventory data are the trees detected from the point cloud. After matching the data, it allows comparing estimated and measured tree attributes tree by tree.

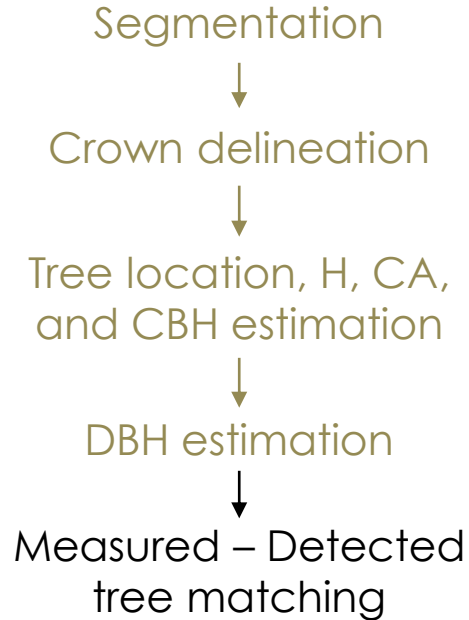
Match inventory-measured trees to LiDAR-detected trees



In this study, matching was performed based on two criteria:

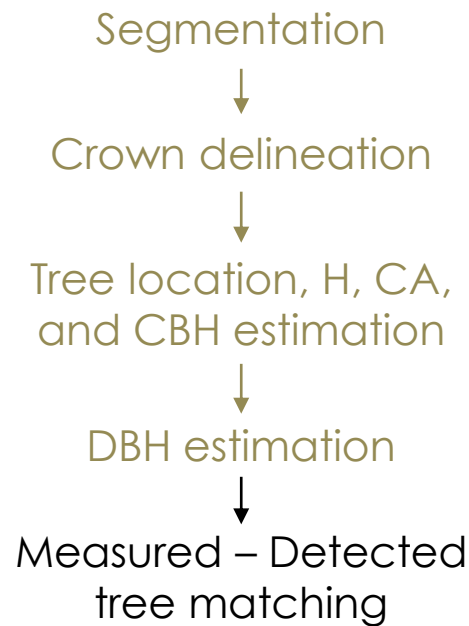
1. The distance between measured and detected trees below 4m. For each measured tree, searching for every detected tree within 4m, those trees are then marked as candidate trees for matching.

Match inventory-measured trees to LiDAR-detected trees



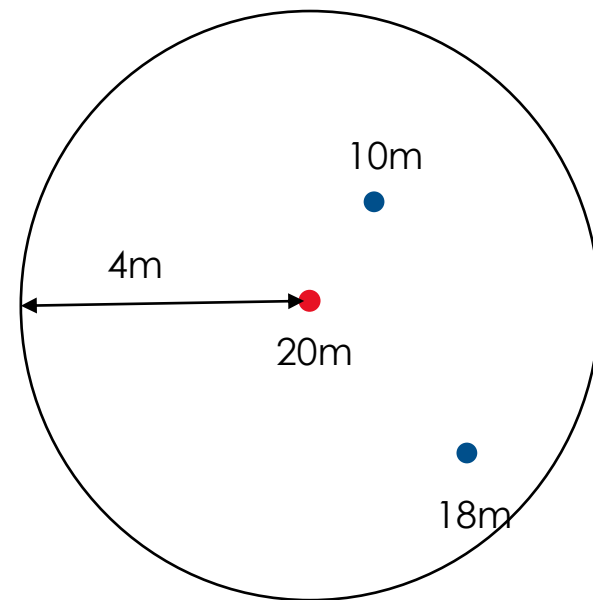
2. The difference in height between measured and detected trees does not exceed 20% of the height of measured trees. After candidate tree searching, the H error is calculated by taking the absolute value of the difference between the detected and measured tree H. The detected tree with the lowest H error was examined to see if this error was below 20% of the measured tree H. If the criterion is fulfilled, the trees get matched. After tree matching, H and DBH can be evaluated further.

Match inventory-measured trees to LiDAR-detected trees

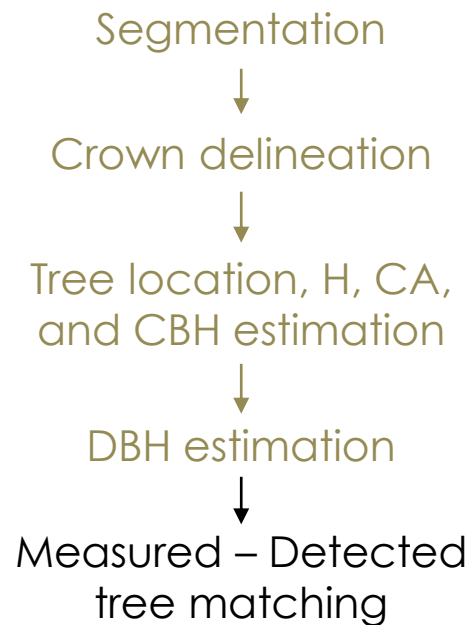


The detected 18m tree gets matched. Because it is within 4m-distance of the measured tree and has the lowest H error

- Measured tree
- Detected tree



Match inventory-measured trees to LiDAR-detected trees



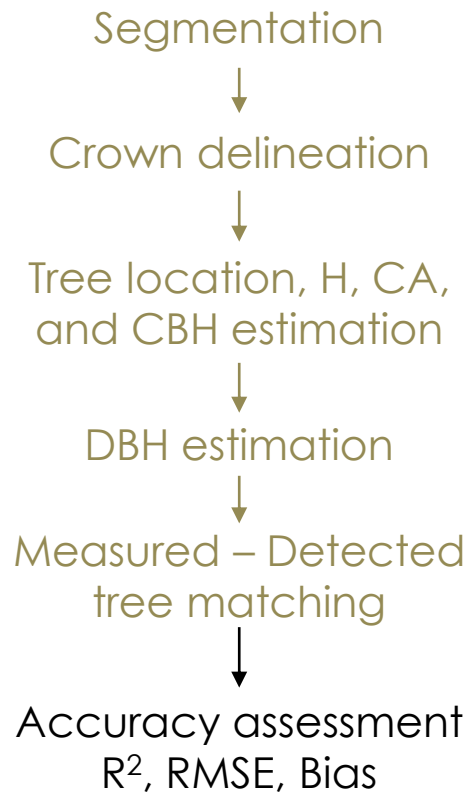
After matching the data, it is possible to compare predicted and measured tree attributes tree by tree

crownID	x_pred	y_pred	H_pred	crownArea_pred	TreeID	x	y	DBH	species	H
3728	419275.1	5851657	29.7474	28.976	5	419274.1	5851657	39.5	GKI	30.60000
3941	419279.3	5851661	29.6039	44.808	7	419279.1	5851662	40.6	GKI	30.40000
3875	419291.7	5851667	28.9234	28.678	12	419291.8	5851666	40.1	GKI	31.30000
4008	419295.7	5851663	18.1610	27.186	14	419295.3	5851663	16.9	GFI	19.10000
4207	419302.2	5851668	20.1824	21.719	16	419302.7	5851666	15.6	RBU	16.30000
4707	419305.3	5851669	17.3382	22.126	18	419306.0	5851667	19.4	RBU	15.30000
4048	419304.4	5851670	27.3816	25.460	19	419303.1	5851670	35.2	GKI	27.90000
4106	419309.4	5851670	28.8888	26.030	20	419307.3	5851670	42.3	GKI	29.00000
4705	419310.5	5851667	15.9627	16.998	21	419309.4	5851668	10.4	RBU	8.40000
4187	419313.3	5851670	17.4916	19.995	26	419313.6	5851670	19.6	GFI	19.10000
4186	419313.9	5851669	15.8481	23.307	27	419314.8	5851672	33.5	GKI	29.50000

Predicted attributes

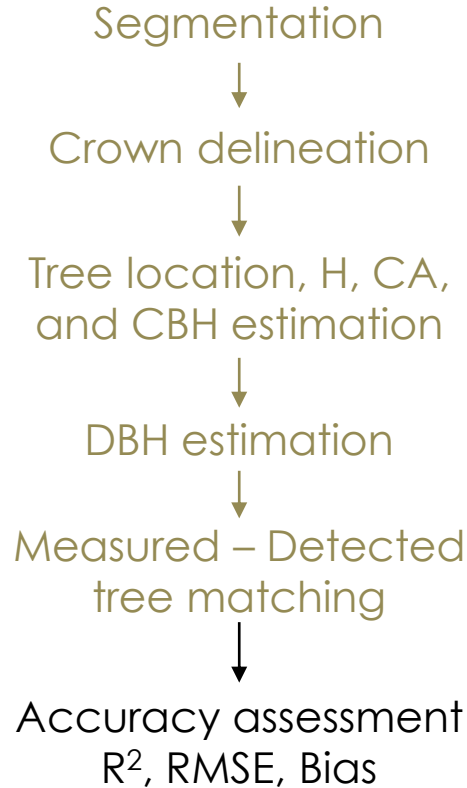
Measured attributes

Accuracy assessment of H and DBH estimation



Some goodness-of-fit measurements can be calculated to assess the accuracy at tree level of the estimated H and DBH for trees matched with the inventory data. These indicators are RMSE, bias, and R^2 which were calculated as follow:

Accuracy assessment of H and DBH estimation



$$\text{RMSE} = \sqrt{\frac{1}{n_{\text{match}}} \sum_{i=1}^{n_{\text{match}}} (x_i - y_i)^2}$$

$$\text{Bias} = \frac{1}{n_{\text{match}}} \sum_{i=1}^{n_{\text{match}}} (x_i - y_i)$$

$$R^2 = 1 - \frac{\sum_1^{n_{\text{match}}} (y_i - x_i)^2}{\sum_1^{n_{\text{match}}} (y_i - \bar{y})^2}$$

Where, n_{match} is the number of matched trees; x_i is the estimated value of tree i ; y_i is the measured value of tree i and \bar{y} is the mean of the measured values



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¡Thank you for your reading!



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