



City of Amsterdam – ITC UTwente

Individual tree delineation

Internship project

Jorges Nofulla

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Individual tree delineation

Introduction

Vegetations are a vital part of our daily lives and are crucial for urban planning and the continuity of ecosystems. Accurate identification and delineation of individual trees in point cloud data is an important task in a variety of fields, including forestry, urban planning, and environmental management. The information we get from individual trees is a critical aspect of forest stand knowledge, which constitutes a fundamental component of forest management (Wang et al., 2004). Individual tree delineation is a very popular and challenging topic in the field of point cloud analysis. Their complex and diverse characteristics make these objects very hard to delineate.

There are a number of methods and algorithms that have been developed for identifying and delineating individual trees, including the use of morphological image analysis (MIA) (Sarabia et al., 2020), mean shift segmentation (Xiao et al., 2019), and KD-trees. Several related works have explored the use of more complex models such as deep learning for aerial image analysis tasks, and one notable contribution in this area is the "Transformer for Tree Counting in Aerial Images" paper (Chen & Shang, 2022), which presents a novel approach for accurately counting trees using transformer-based models.

Previous research has also investigated neural network-based approaches for tree counting in UAV remote sensed images, such as the work by (Kestur et al., 2018) who proposed a spectral-spatial method for tree crown detection, delineation, and counting. Additionally, (Marques et al., 2019) proposed an automatic detection and monitoring system for chestnut trees using UAV-based remote sensing. These works demonstrate the potential of machine learning and remote sensing technologies for accurate tree counting and monitoring.

Recently, high-density point clouds have become more available, enabling more detailed studies to be conducted. An important characteristic of point clouds is their ability to penetrate through trees and capture their structure. Point cloud data can be collected using methods such as airborne laser scanning (ALS), terrestrial laser scanning (TLS), and structure from motion (SFM), which provide a dense, high-resolution representation of the surface of an object.

In addition to the works on tree counting from aerial images, there are also studies that have explored individual tree extraction and segmentation from LiDAR point clouds. For example, (Zhang et al., 2015) developed a method for individual tree segmentation from LiDAR point clouds in urban areas, aimed at facilitating urban forest inventory. Another study by (Hui et al., 2021) proposed a self-adaptive mean shift segmentation method for individual tree extraction from UAV LiDAR point clouds. These studies demonstrate the potential of LiDAR point clouds for accurate and efficient individual tree extraction and segmentation, which is crucial for forest management and conservation.

In this study, we have access to the Actueel Hoogtebestand Nederland (AHN) dataset, a publicly available high-resolution point cloud dataset generated by aerial laser scanning (ALS) throughout the Netherlands. This dataset also provides semantic labeling at the point level for four classes: "ground, water, buildings, and others." The dataset that we will be using

as the starting point for this study was previously labeled by the Amsterdam Intelligence team, with all tree points classified.

In this report, we present 2 different approaches for identifying individual trees. Both of the methods initial delineation is based on utilizing a KD-tree algorithm (Bentley, 1975) and vectors to make tree clusters. After we make these tree clusters :

The first method identifies local maxima within a designated region through analysis of point density in that area. The concept of using point density was inspired by Professor Sander Oude Elberink. He utilized it to represent high-density parts of the trees, which are often tree trunks since they typically have the highest point densities around them in the 2D plane. The process includes calculating each point's value based on how many other points are present in a 2D buffer around it.

The second method uses some parameters to further split or merge the clusters. These parameters are based on the average tree characteristics such as tree height, diameter and point cloud density. To get parameters as close to reality as possible, the data is first cleaned from all the outliers and categorized into small, medium and tall trees. Then in a decision tree type of algorithm, these parameters were used to delineate individual trees.

Methods and Results

Two different approaches were tested to delineate individual trees. The initial delineation is a common step for both of the methods. These methods are described below.

Initial delineation

To reduce the density of the raw point cloud data, the x, y, and z values of the LAS file were concatenated and converted to full integers using the NumPy library. This resulted in a flat voxel index, from which a subset of coordinates was selected by identifying a unique set of indices using the np. unique() function. The selected coordinates were sorted by their z value, and a list of "point" class objects was created for each set of coordinates. An ordered array was then generated with the size of the remaining coordinates, effectively reducing the number of points fed into the algorithm. This step was necessary to decrease the processing time and improve the efficiency of the algorithm.

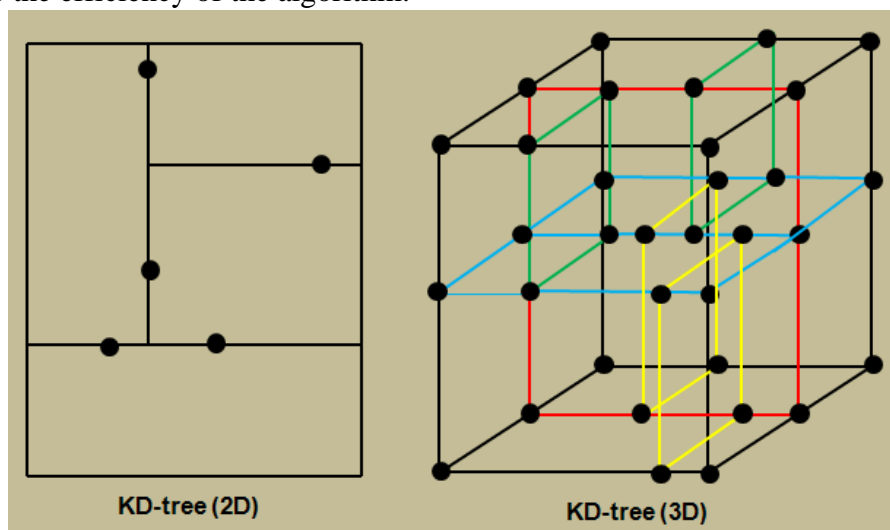


Figure 1 - KD-tree Algorithms (2D, 3D)

Available from: https://www.researchgate.net/figure/The-example-of-the-KD-tree-Algorithms-2D-3D_fig3_263937521
[accessed 9 Mar, 2023] (Park et al., 2010)

The radius used for clustering was manually selected based on the density and characteristics of the point cloud data. The KD-tree algorithm with nearest neighbors was then utilized to delineate trees, with the core functionality remaining the same as in the paper by (Hess et al., 2021). Our version of the code has been streamlined to enhance its efficiency and to better align with the specific requirements of our study, while still maintaining the core functionality.

KD-trees are effective in identifying groups of points belonging to the same tree based on proximity to one another. The algorithm identified points within a certain distance from a given point in 3D space and calculated the centroid of the neighbors with higher elevation to determine the top of the tree. A link was then established to the neighbor closest to the centroid, and the resulting clusters were used to create geometric networks representing individual trees. Each point was assigned a label based on its network, which was later used to segment the trees. The approach demonstrated promising results in accurately segmenting deciduous trees in our study area, highlighting the potential of KD-trees and geometric networks in processing airborne lidar point clouds for tree segmentation. Finally, all points within a specified radius were clustered with their neighbors to create a group of points. The centroid of this group of points was calculated, and the neighbor closest to the centroid was selected as the parent point. This process was repeated until all points in the dataset were assigned a parent point. The output of the initial delineation step was saved as a NumPy array and then fed to both of our methods below.

Method 1 : Point density

The workflow of the first method is shown below (Figure 2). The code is available in this [GitHub Repo](#).

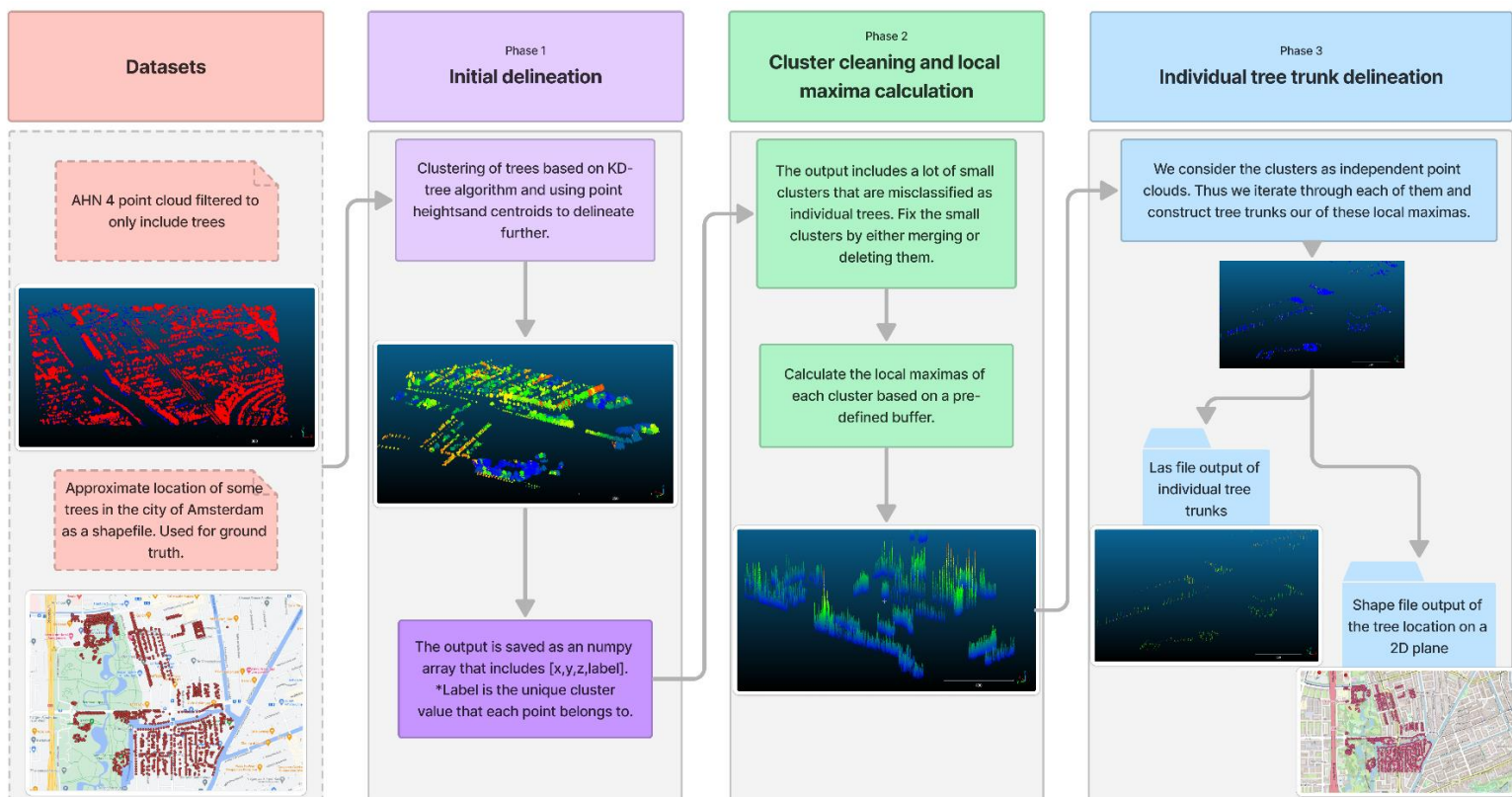


Figure 2 - The workflow of the first method

Cluster cleaning and local maxima calculation

Once the initial delineation process is complete, the resulting data may contain numerous small clusters erroneously identified as individual trees due to over-segmentation or incorrect labelling of small objects. To mitigate such errors, a threshold was established to filter out these clusters by either merging them with the nearest cluster, assuming they are branches of the same tree that were mistakenly classified separately, or deleting them if their size and location do not align with that of a tree.

After the data is cleaned from these clusters, a buffer was constructed for every single point cloud and created a new feature. This new feature is called point density and it counts how many other points are inside this buffer in the 2D plane. The algorithm iterates through every point cloud in the file and saves the number of points in the buffer. The output array will look like this → [x, y, z, label, point_density].

Where:

- x, y and z are the coordinates of the point.
- label is the unique cluster number that this point belongs to (from the initial delineation).
- point_density is the number of points that are within the 2D buffer of this point.

The idea behind this point density is to use it when searching for trees centroids, instead of using the height value. Depending on their branch distribution, a tree can have multiple local maxima in height as seen in Figure 3.



Figure 3 - Image of a group of trees taken in Amsterdam

This occurrence is less common when using point density as the local maxima. Usually, the local maxima of point density will be on the tree trunks, as the location of the trunk has extra point clouds compared to other tree parts. Thus when searching in a 2D plane, it's almost certain that the peak will be on the tree trunk area.

Below is a visualization of trees using the point density value instead of height value (Figure 4). It's clear that the peaks are much more visible compared to a normal point cloud that uses Z value to represent trees height.

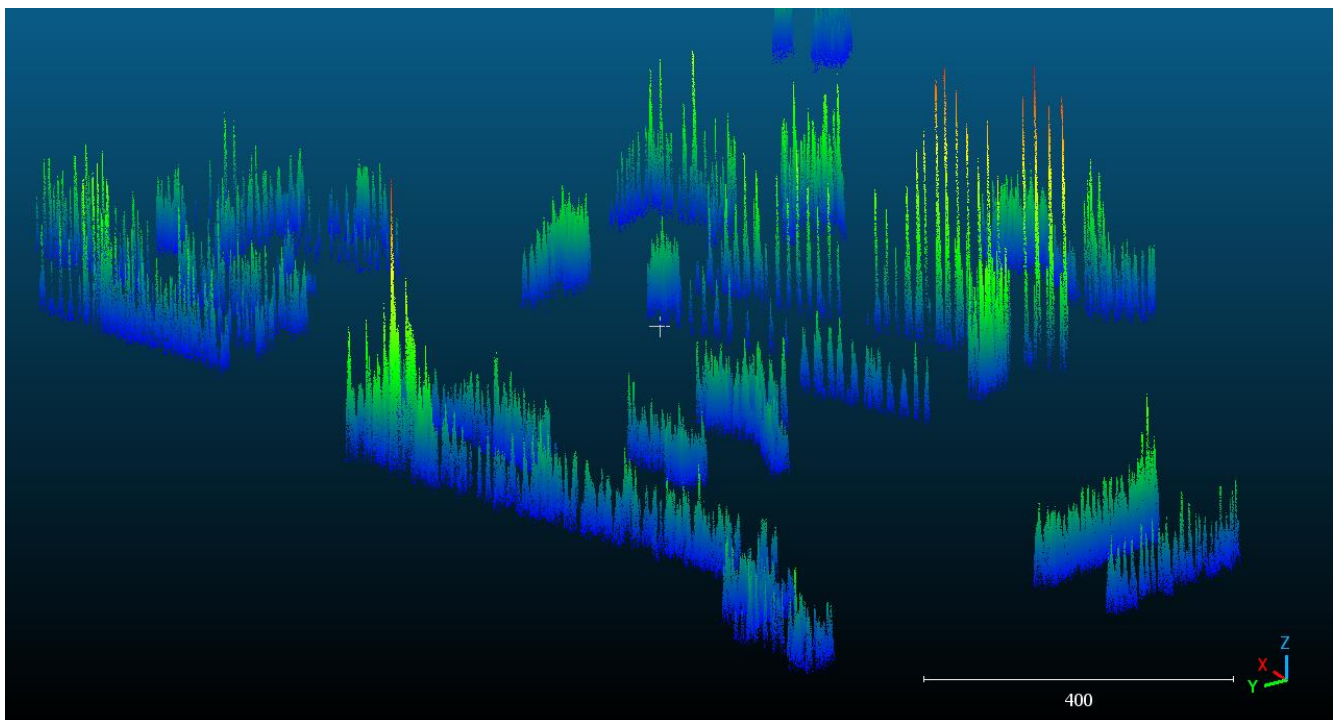


Figure 4 - Point cloud representation of a group of trees, using point density instead of height value

Individual tree trunk delineation

Point density calculation for the purpose of finding the local maxima can be also calculated in the entire dataset without pre-clustering but there are many problem and errors that come with it such as:

- Ignoring small trees that are next to tall trees, as the window size is static. The local maxima will be set on the tall trees, leaving small trees undetected.
- If we iterate through all the points instead of through the clusters, the time complexity is exponentially higher. It will be impossible to run it on a huge dataset, especially AHN4 which has a really high point density.

These are the reasons why we pre-cluster the data and then we iterate through the points of each cluster individually instead of the dataset as a whole. The concept behind this comes from "divide and conquer", which involve breaking down a larger problem into smaller, more manageable subproblems (Kleinberg & Tardos, 2006) (Béjar Alonso, 2013). This way we get a much faster algorithm and the boundaries of the cluster won't allow for a lot of false positive trunks or ignore small trees.

To further increase the accuracy, the code checks for minimum distance between 2 local maximas of the same cluster, as we can't have 2 trunks next to each other. The code assigns an

unique label to the peaks and then labels every points in a small 2D radius with the same label in order to visualize the whole trunk as show in the Figure 5. This unique label will represent them as individual tree trunks.

These labeled clusters can help reveal patterns or trends in the data, and can be further analyzed to extract useful information. The algorithm is flexible and can be adapted to fit the needs of a particular analysis, making it a valuable tool for data exploration and analysis.

The parameters are made easily to change in order for the user to have a more personalized code for specific uses.

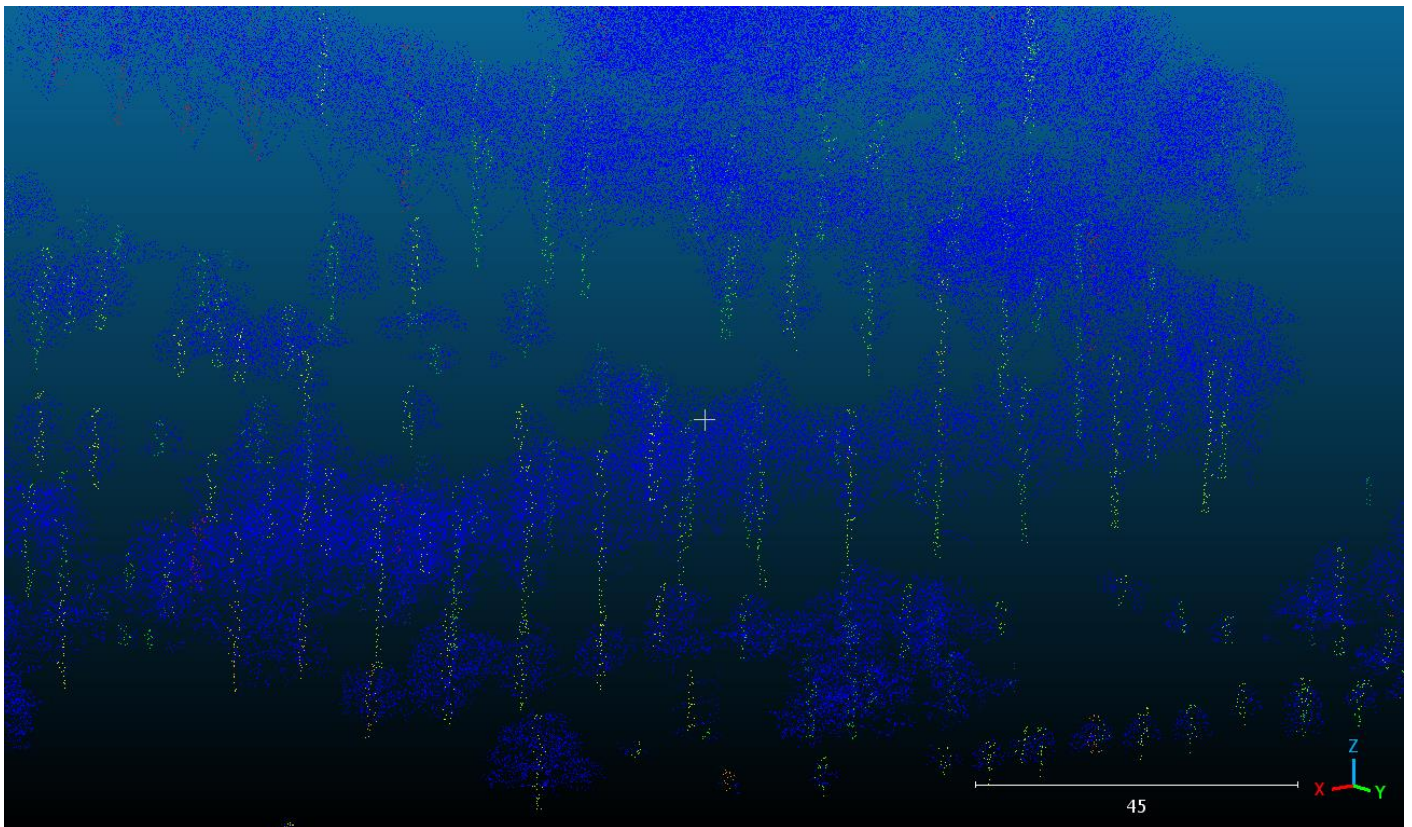


Figure 5 - Output of the first method where individual tree trunks are highlighted

Method 2 : Parametric

The flowchart of the second method is shown below in Figure 6:

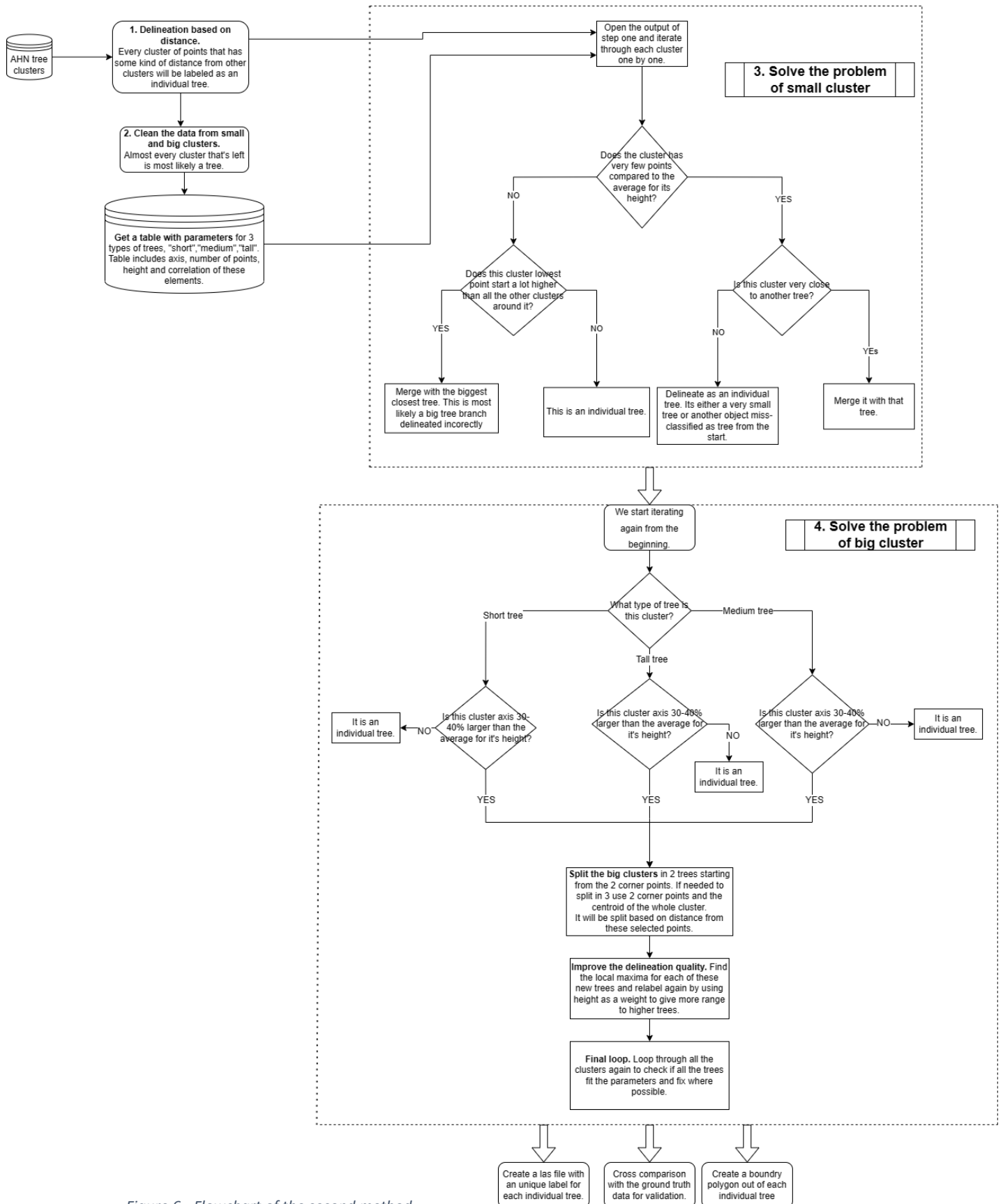


Figure 6 - Flowchart of the second method

Extracting tree parameters

Using the primary delineation obtained in the first step, small and large clusters are removed upon a threshold. The threshold of removing these clusters is decided by data distribution (Figure 7).

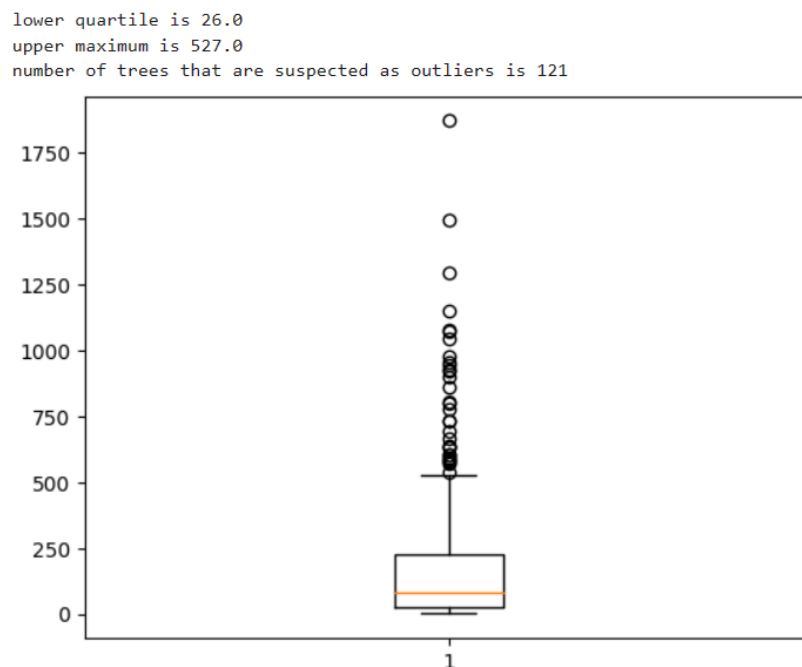


Figure 7 - BoxPlot of the number of points per cluster

This step is necessary to eliminate noise and improve the accuracy of the final delineation. As we can see from Figure 7, most of the correct trees should be between 26-527 points and there are 121 trees that are suspected as outliers (In this specific case, in another dataset these numbers will change). We remove the all the “lower and upper quartile +20%” clusters and the remaining clusters, which are mostly correctly delineated trees, are then split into three groups: small, medium, and tall.

From the 3 groups of trees, height, axis, the number of points, and correlations are obtained . This set of parameters was extracted from clusters of points in the data, and later

Tree type	Height	Major axis	Number of points	Height/Major axis
Short	3.0	5.3	49.74666667	0.63
Medium	6.4	7.7	134.8657718	0.98
Tall	11.1	11.2	300.3066667	1.09

Table 1 - Average parameters for each tree type

(on the next step) they are used to segment clusters into individual trees(Maas et al., 2008). All of these parameters are saved in a txt file for later use (Table1).

Final delineation

The Las file saved in the first step is loaded, and the first problem to solve is small clusters. Small clusters can be difficult to accurately identify as individual trees, as they may not contain enough points or have a clear shape. To address this problem, we checked these characteristics:

1. The cluster is small. This can be determined based on the number of points in the cluster or the size of the bounding box surrounding the cluster.
2. The cluster is very close to another big tree. This can be determined based on the distance between the centers of the clusters.
3. The cluster's lowest point starts from a much lower elevation than other clusters around it. This can be determined based on the height of the lowest point in the cluster relative to the surrounding clusters.

If these conditions are met, the cluster is merged with the nearest big tree. Otherwise, it is considered a small tree. More detailed on the flowchart of the workflow (Figure 6).

The second problem is trees that are merged together into a single large cluster. This can occur when multiple trees are very close together and their crowns overlap. To solve this problem, a major axis check can be done, in order to find the trees that have unusually large axis (Sarabia et al., 2020). The following steps are taken in the code:

1. Iterate through each individual cluster.
2. Determine if the cluster is a small, medium, or tall tree based on the criteria established in Table 1.
3. Apply the following rules to each cluster, according to its category: If the axis is bigger than the average axis for the tree category (small, medium, tall), or the point cloud number is higher than the average for the tree category, it means that this cluster is not a single tree, the cluster is split in multiple trees, depending on how much larger than the average are these values. More detailed on the flowchart of the workflow (Figure 6).

Balance the newly delineated trees.

After the "Final delineation" step, every cluster that has doesn't fit the Table 1 parameters is either split or merged. But the split is always equally done for each cluster. However, this should not be the case when a tall and small tree are merged, as tall trees should have more points and are bigger than small trees. In this case, to solve this problems we first find the centroids and local maxima of each newly split tree. The different weights are applied to different heights. For example, the highest tree will get a larger weight than the lowest tree.

In the end we loop through all the clusters again and check if the parameters fit each new tree cluster. If not, we apply small adjustments.

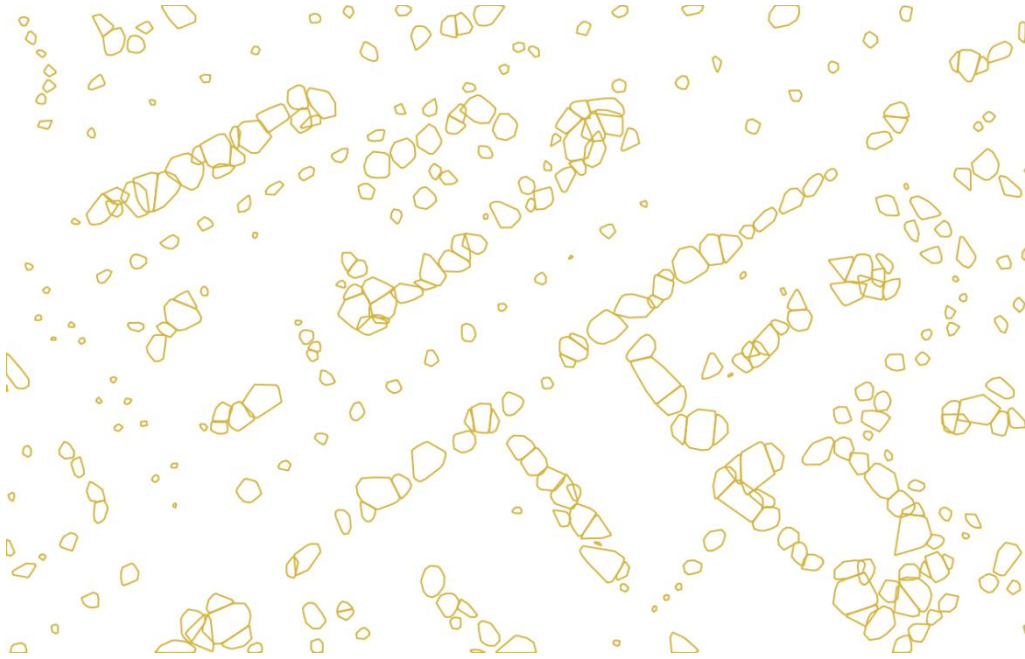


Figure 8 - Output of the second method. 2D polygons of delineated trees.

Load and compare

The initial and modified delineations are loaded and compared to ensure the code is functioning as intended. Ground truth data is used to validate the results. For better visual inspection a 2D polygon of each individual tree border is created(Figure 8).

Results and Limitations (Method 1)



Figure 9 - Accuracy assessment of a cluster of trees in the city of Amsterdam

Figure 9 illustrates the occurrence of false positives and false negatives in a city cluster, highlighting the algorithm's chances to misidentifying trees. False positives refer to the algorithm incorrectly delineating a tree, and false negatives occur when a tree should be identified but is not.

However, assessing the effectiveness of a clustering algorithm requires a consideration of both its accuracy and limitations. One significant limitation is the algorithm's sensitivity to the initial parameters and settings, as varying settings can produce different results and make it challenging to compare performance across different algorithms or even different runs of the same algorithm. Therefore, it is crucial to carefully select initial parameters and settings and test the algorithm's sensitivity to these choices. Additionally, the quality of input data is another significant limitation, as noise in point cloud data can negatively impact clustering results.

In the case of our study, the complexity and irregularity of tree distribution and patterns in urban areas also pose a challenge for accurate tree identification using tree parameters. It is worth noting that while tree parameters are effective in tree plantations as shown in the study made by (Sarabia et al., 2020), where trees follow a regular pattern, their effectiveness in urban areas is limited.

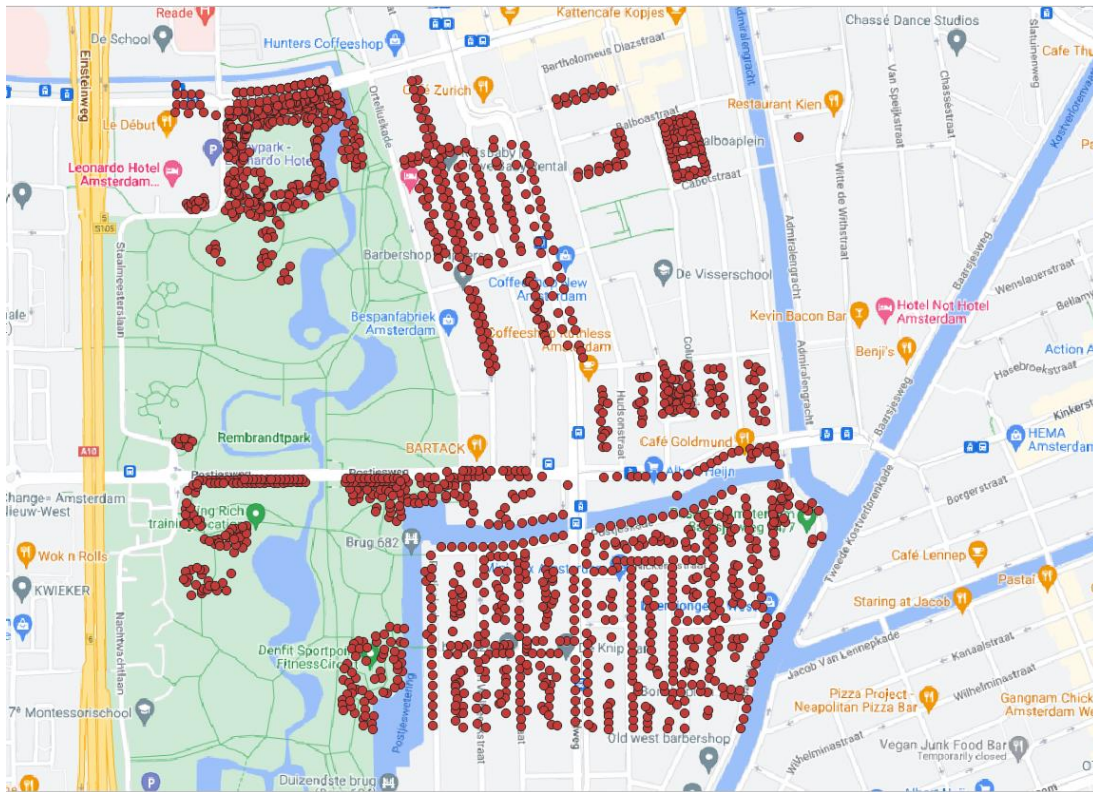


Figure 10 – Ground truth

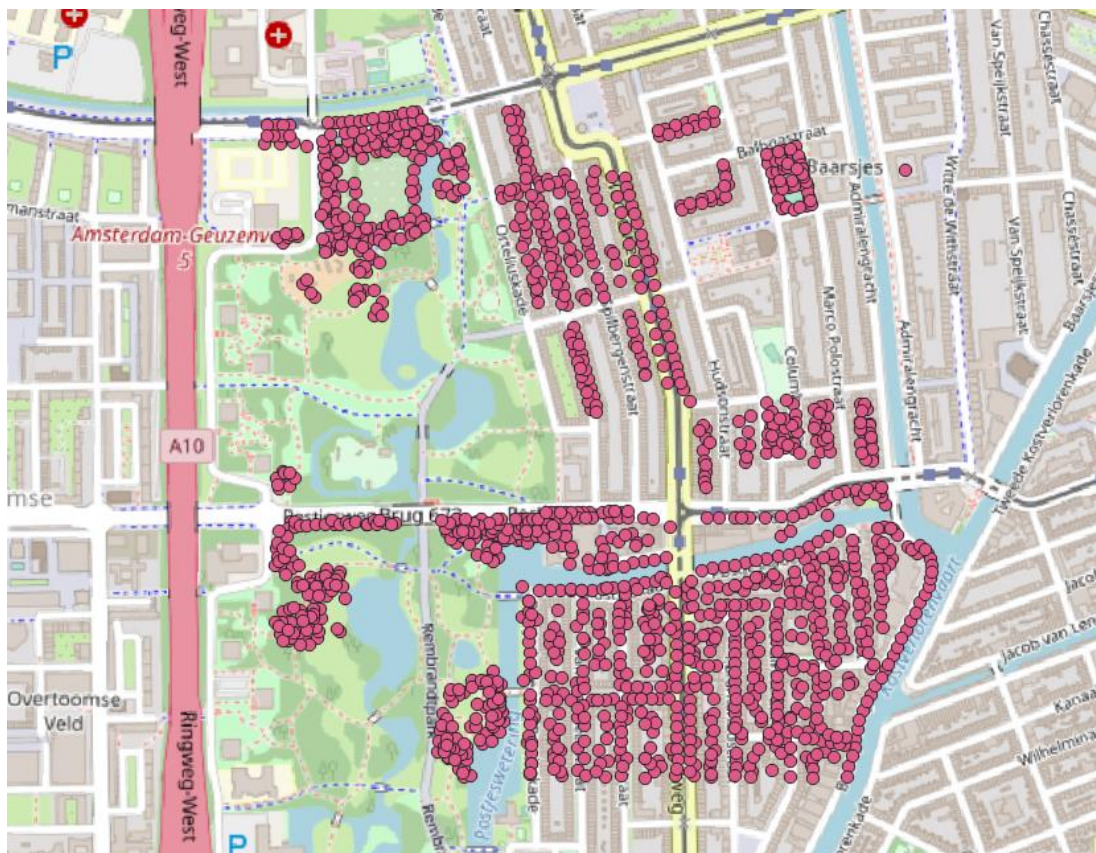


Figure 11 - Our output for the same area as the ground truth



Figure 12 - Comparison with the existing tree count method

The algorithm's validation process involved utilizing data from the municipality's current algorithm. The results of this analysis were particularly promising, given that the assessments were completed using default parameters, and the algorithm was not yet fine-tuned for our specific area. Even more encouragingly, our manual inspection of the outliers revealed that the algorithm correctly identified some areas even though they had anomalies with the previous algorithm, further indicating the accuracy of the system.

Our analysis also revealed that the majority of errors fell within a range of +1 and -1 tree per cluster, as demonstrated by the Figure 13. The initial results demonstrate great potential for the algorithm's effectiveness, and we anticipate even more impressive outcomes once the algorithm is calibrated to more specific parameters for each distinct area.

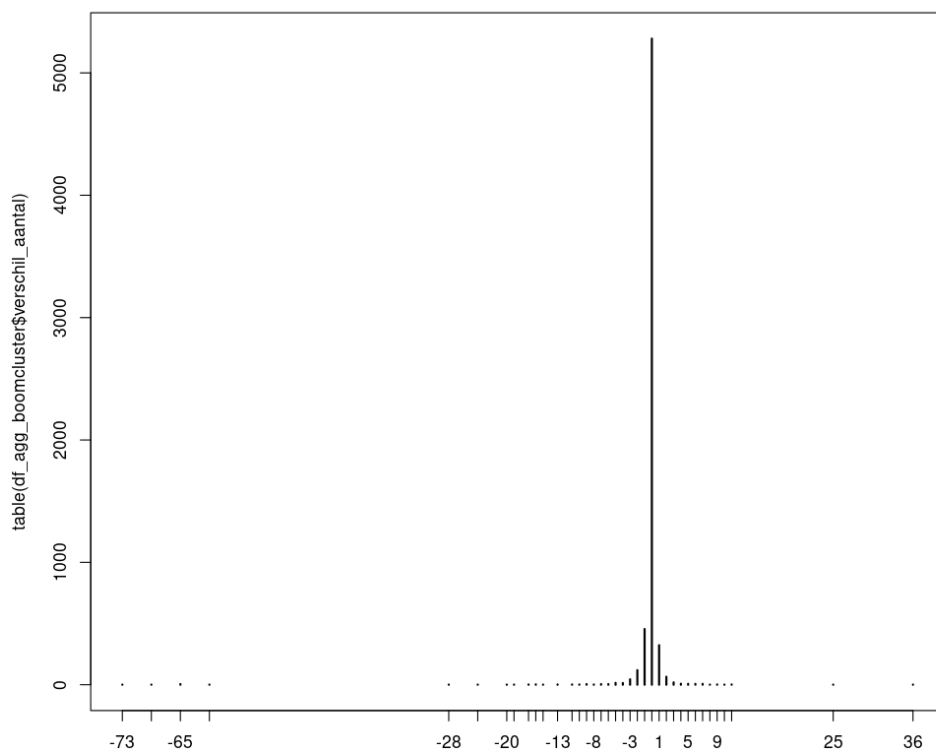


Figure 13 - Quantifying the Differences: Tree Count Disparities Between Our Algorithm and the Existing Approach

Discussions and Conclusions

Both of the proposed methods show promising result when explored in relatively small datasets and they appear to be effective when counting the total number of trees in clusters that contain just one or a few trees. The situation is different when giving the algorithm larger point cloud tiles and more complex tree clusters.

The point density method is quicker than the parametric method since fewer computations are required for each tree. There is no need to extract any pre-calculated parameters from the data; instead, the utilized feature is retrieved by iterating over the points, making the technique quicker and more versatile.

The parametric approach does delineate the entire tree, whereas the point density method only finds the tree trunks. The primary issue with the parametric method was that tree parameters were not as easily generalized as first anticipated. Since trees differ so significantly, they cannot be generalized into a finite number of types. The algorithm attempts to delineate trees using the dataset parameters, however balancing this delineation proved to be an incredibly difficult process.

The deeper we go into the data and structure of tree clusters, the clearer it becomes that trees in cities are quite distinct and unique, since they do not follow any particular pattern, especially in various regions of the city. For example, trees that are located alongside streets have dissimilar traits when compared to the trees in parks, and there can be variations in characteristics even among trees within the same vicinity. Figures 15 and 16 demonstrate the heterogeneous and unpredictable nature of tree diversity.



Figure 14 - An image of a cluster of trees taken from a distance in the city of Amsterdam

While the trees in Figure 14 appear to have a pattern and are fairly divided, a closer inspection reveals that things are really different (Figure 15 and 16).



Figure 15 - A closer look into a tree cluster of the city of Amsterdam



Figure 16 - A closer perspective into another cluster of trees in the city of Amsterdam

The point density method works around this diversity because, despite their differences, trees all have one thing in common: they all have a trunk that has more points given to it than any other section of the tree. This approach also performs significantly better in densely packed clusters. Looking for trunks was more successful than relying on how a tree should look.

When parameters were applied to the parametric method, many large trees were split unnecessarily since they simply did not meet the "average" specifications for their height; consequently, this method is not the solution we want. The point density technique is also superior since it is much easier for the user to grasp and is more adaptable to manual modifications because it does not rely on automatic parameters derived from the dataset.

To enhance the code's performance, several improvements can be made, including making the sliding window dynamic to adapt better to various tree cluster sizes. The restriction distance between two trunks can also be made dynamic, depending on the expected density of the area, and ensuring that the delineated tree trunk is not too close to any corner of the cluster can also improve accuracy. Also we can use the fact that the lowest point of each trunk is significantly lower than the rest of the points of the tree. Therefore, in a cluster where many "trunks" are found, we can restrict a group of points to be called a "trunk" only if they have a

minimal distance close to this lowest point per each individual cluster. To further enhance the algorithm's functionality, it could be upgraded to detect not only the trunk's position but also the entire tree and its type.

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