Automated matching of multiple terrestrial laser scans for stem mapping without the use of artificial references

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Terrestrial laser scanning has been widely used to analyze the 3D structure of a forest in detail and to generate data at the level of a reference plot for forest inventories without destructive measurements. Multi-scan terrestrial laser scanning is more commonly applied to collect plot-level data so that all of the stems can be detected and analyzed. However, it is necessary to match the point clouds of multiple scans to yield a point cloud with automated processing. Mismatches between datasets will lead to errors during the processing of multi-scan data. Classic registration methods based on flat surfaces cannot be directly applied in forest environments; therefore, artificial reference objects have conventionally been used to assist with scan matching. The use of artificial references requires additional labor and expertise, as well as greatly increasing the cost. In this study, we present an automated processing method for plot-level stem mapping that matches multiple scans without artificial references. In contrast to previous studies, the registration method developed in this study exploits the natural geometric characteristics among a set of tree stems in a plot and combines the point clouds of multiple scans into a unified coordinate system. Integrating multiple scans improves the overall performance of stem mapping in terms of the correctness of tree detection, as well as the bias and the root-mean-square errors of forest attributes such as diameter at breast height and tree height. In addition, the automated processing method makes stem mapping more reliable and consistent among plots, reduces the costs associated with plot-based stem mapping, and enhances the efficiency.

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1. Introduction

Terrestrial laser scanning (TLS) is a technology commonly used for accurate, repeatable, and highly detailed documentation and measurements of three-dimensional (3D) spaces in a variety of applications (Thies et al., 2004; Al-Durgham and Habib, 2014; Zhou et al., 2014; Kelbe, 2015). Placed on a fixed platform or tripod, a laser scanner produces digital representations of the 3D surfaces visible from the scanner. For forest inventories, TLS is often used to record detailed horizontal and vertical forest structures at the plot level (e.g., Thies et al., 2004; Henning and Radtke 2006; Rahl et al., 2014; Kelbe, 2015). Plot-wise stem mapping is a precise forest inventory technique for generating ground-truthed reference data that is used for calibrating large-scale forest sensing such as airborne laser scanning (ALS) and satellite imagery (Hilker et al., 2012; Wang et al., 2016).

Three data acquisition approaches have been reported for TLS-based forest inventories: single-scan, multi-scan and multi-single-scan (MSS) (Habib et al., 2010; Liang et al., 2016). Among the three approaches, the single-scan approach has the simplest data acquisition setting and the fastest speed. However, single-scan TLS has three challenges in terms of plot-wise stem mapping. First, laser scanning is a discrete sampling technology, and its point density is range-dependent (Jakubowski et al., 2013). These features mean that stems far from the scanner will be mapped at lower detail than those close to the scanner. Second, a single scan can only observe part of a stem; the points of a single scan cover at most half of the lateral section of a stem circle. When these points are used to model

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a circular stem, the geometry is unfavorable from a mathematical perspective, which causes errors in the estimation of stem radius and location. Third, natural occlusions limit the visibility of stems inside a plot. Trees may occlude each other; vegetation or terrain in the foreground may also occlude the line of sight to more distant objects. The occlusion effect increases with the distance from the scanner and with the forest density. Studies have shown that up to 40% of all trees in the sample plot are not detectable from the plot center when using the single-scan approach (Lovell et al., 2011). As a result, occluded stem sections or even full stems will fail to be mapped from a single scan. It is necessary to collect multiple scans from different standpoints, and match the point clouds acquired by different scans, so that multiple scans complement each other to attain a complete representation of the 3D scene within a unified reference coordinate system. A number of automated registration methods have been developed to register multiple scans (Besl and McKay, 1992; Rabbani et al., 2007; Henning and Radtke, 2008; Akca, 2010; Canaz and Habib, 2013; Kelbe, 2015). However, existing automatic registration techniques are usually suitable for engineered surfaces (Glira et al., 2015), and they cannot be directly used to match multiple TLS scans for stem mapping, which is the objective of this study, because of two reasons. First, when a small number of scans are taken, there are typically no adequate overlapping areas that cover tree stems from different standpoints (Liang et al., 2015). Additionally, even when two scans include overlapping view angles, parts of more distant stems may be occluded by closer stems. This occlusion reduces the overlapping area for a specific stem. Second, in the boreal forests where this study was conducted, most stems have a quasi-vertical orientation and similar geometry. In geometry, the correspondence between a pair of parallel cylinders does not provide adequate information for determining translation along their axial direction (Miralakkari et al., 2008; Al-Durgham and Habib, 2014). Normal vectors, which are often used as geometric features in previous methods, are nearly parallel for most of the stems. As a result, it is difficult to directly estimate the vertical translation between a pair of scans.

In forest inventory, the registration is usually accomplished using artificial reference objects that are placed in a scanning field (Holopainen et al., 2014). The process of manually placing artificial targets in the field and extracting their coordinates from acquired point cloud data strongly depends on the expertise of an operator. For example, field crews must carry the reference objects and tripods throughout field measurements and using them properly requires adequate knowledge (e.g., correctly locating these objects to create a good geometry). These pre-scanning tasks are often labor-intensive and time-consuming, and they greatly increase the cost of data collection. Furthermore, the accuracy and reliability of the registration may be degraded by imprecision or even mistakes during the manual process, even when accomplished by an expert. An automated solution that does not require artificial reference objects would increase the efficiency of fieldwork and post-processing. Such a technique would significantly enhance the applicability of TLS technology in forestry (Liang et al., 2012).

In this study, we present a complete processing procedure for plot-wise stem mapping that is based on automated matching of multiple scans. This automated matching method is developed by exploiting the natural geometric characteristics of trees within a plot, and it does not require the placement of artificial objects in the data acquisition field. This method can be used to match the point clouds of multiple scans within a unified coordinate system. The matched point cloud of multiple scans is then used for plot-wise stem mapping. We compare stem mapping performance using the matched point cloud of multiple scans with that of conventional single-scan based techniques in several respects. The results show that with the proposed method the mean correctness of tree detection in the test plots is improved by 3.1%, and mean stem mapping accuracy is improved by 2.3% to 9.2% for different parameters. More importantly, the proposed method presents in more robust and consistent stem mapping performance among different plots.

2. Study area and materials
2.1. Study area

The study area is a managed forest located near Evo, Finland (61.19°N, 25.11°E). The methods presented in this study were tested with ten plots of 32 × 32 m. As a reference for the plot attributes, field measurement data were collected in May–July 2014.

All trees with a diameter at breast height (DBH) greater than 5 cm were considered in the reference measurements. The breast height was defined as 1.3 m above the ground level in this study. The main tree species growing in these plots are Scots pine (Pinus sylvestris) and Norway spruce (Picea abies). One of the plots is a mixed forest where pine and spruce account for approximately 50% each; the other plots are either pine-dominated or spruce-dominated. The study plots’ densities range from 342 to 1191 stems/ha; 70% of the test plots are categorized as high-density based on a threshold number of 600 stems/ha (Watt and Donoghue, 2005).
Table 1

<table>
<thead>
<tr>
<th>Plot</th>
<th>Stem number (pc./ha)</th>
<th>BA (m²/ha)</th>
<th>DBH (cm)</th>
<th>Height (m)</th>
<th>Main species</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>All</td>
<td>Pine</td>
<td>Spruce</td>
<td>Mean +/- St. Dev.</td>
</tr>
<tr>
<td>1</td>
<td>342</td>
<td>22.5</td>
<td>0.0</td>
<td>18.8</td>
<td>27.7 +/- 8.4</td>
</tr>
<tr>
<td>2</td>
<td>596</td>
<td>17.8</td>
<td>17.2</td>
<td>0.0</td>
<td>19.0 +/- 4.2</td>
</tr>
<tr>
<td>3</td>
<td>596</td>
<td>22.7</td>
<td>0.0</td>
<td>18.5</td>
<td>20.9 +/- 7.2</td>
</tr>
<tr>
<td>4</td>
<td>615</td>
<td>21.2</td>
<td>20.0</td>
<td>0.3</td>
<td>20.6 +/- 4.1</td>
</tr>
<tr>
<td>5</td>
<td>625</td>
<td>33.2</td>
<td>0.0</td>
<td>28.7</td>
<td>24.4 +/- 9.1</td>
</tr>
<tr>
<td>6</td>
<td>635</td>
<td>21.9</td>
<td>21.5</td>
<td>0.2</td>
<td>20.1 +/- 6.0</td>
</tr>
<tr>
<td>7</td>
<td>664</td>
<td>24.4</td>
<td>0.0</td>
<td>20.5</td>
<td>21.1 +/- 4.9</td>
</tr>
<tr>
<td>8</td>
<td>713</td>
<td>26.4</td>
<td>11.7</td>
<td>13.4</td>
<td>17.9 +/- 12.4</td>
</tr>
<tr>
<td>9</td>
<td>947</td>
<td>23.3</td>
<td>19.8</td>
<td>0.1</td>
<td>15.5 +/- 8.6</td>
</tr>
<tr>
<td>10</td>
<td>1191</td>
<td>32.6</td>
<td>1.9</td>
<td>28.2</td>
<td>17.7 +/- 6.0</td>
</tr>
</tbody>
</table>

Fig. 2. Minimum, maximum and mean tree heights (H, in m) in each plot. Bars represent the mean H for each tree species, with whiskers showing the minimum and maximum values. The line shows the overall mean H per plot.

The trees in the plots represent various stages of growth, including both small and large trees. Their DBHs range from 5 cm to 45 cm, and the standard deviations (STDs) vary between 4.1 cm and 12.4 cm among the plots. The tree heights range from 2 m to 35 m, and the STDs vary between 2.4 m and 8.5 m. The basal areas of the plots range from 17.8 m²/ha to 33.2 m²/ha. Descriptive statistics of the plots are summarized in Table 1 and Figs. 1 and 2.

2.2. Terrestrial laser scanning data acquisition

The TLS data used in this study were collected in May–July 2014 using a Faro Focus³D X 330 scanner (Faro, USA), which has a full field-of-view scanning capability of 360° in the horizontal direction and 300° in the vertical direction. The scanner employs a continuous wave at 1550 nm to measure distances with a range accuracy of +/- 2 mm (Kaartinen et al., 2015). Each plot was measured using five scans; one was located in the central part of the plot (called the center scan). The others were located in four quadrants, to the northwest, northeast, southeast, and southwest of the center scan; these were called side scans, as shown in Fig. 3. Before scanning, the scanner was leveled using the leveling instrument on the scanner, and this operation simplified the matching process of multiple scans. Fig. 4 shows the TLS point clouds of trees from a number of single scans taken from different perspectives.

3. Method of automated matching of multiple scans for stem mapping

The automated matching of several scans in forest areas typically involve three steps: feature detection, initial parameter estimation and the matching of several scans (Liang et al., 2013; Zhou et al., 2014). Fig. 5 presents a complete procedure for TLS stem mapping that automatically matches multiple scans without requiring artificial references. The procedure includes 1) stem curve reconstruction using the point cloud of individual scans, 2) stem matching between scans at the feature level, 3) registering point clouds of multiple scans, and 4) stem mapping using the matched point cloud from multiple scans.

3.1. Stem mapping from single-scan TLS data and from multi scans using the multi-single-scan approach

For comparisons, the test plots are also mapped using the single- and multi-single-scan approaches, which are shown in grey in Fig. 5. The mapping methods are briefly discussed in this section.

The stems in the individual single-scan data are mapped using the robust stem modelling method (Liang et al., 2012). A tree stem is divided into a series of small curves along the stem profile and the stem curves are reconstructed from the clustered points of the stem. Each curve is fit to a 3D cylinder, and its parameters, including diameter and location, are estimated using the point cloud. Stem parameters such as DBH and stem height, are extracted from the points and reconstructed stem.

The MSS approach merges the stem mapping results of multiple scans of a same plot at the feature and decision levels (Liang et al., 2013). The MSS method establishes matching pairs of trees using the horizontal locations of the mapped stems in different scans; it coarsely determines the transformations between different scans.
on a two-dimensional (2D) plane using horizontal location-based matching. Individual stem maps are transformed into the coordinate system of the central scan using the estimated transformation parameters. Finally, the MSS method generates “multi-scan” stem mapping results, which are a collection of single-scan stem mapping estimates of different scans for the trees in the plot. The MSS method does not estimate stem curves from aligned point cloud of multiple scans. Instead, it selects the “best” single-scan estimates of specific stem attributes of the trees in a plot according to defined decision rules and combined these estimates to create the final “multi-scan” results. This method does not require artificial reference targets to be placed on the field and it improves plot-wise stem mapping in comparison with the single-scan approach.

3.2. Automated scan matching

The MSS method coarsely registers different scans in the horizontal plane, leaving the vertical translation unresolved. This study uses the natural geometry of the tree stems in a plot to align the different scans.

A plot is assumed to be a volumetric space and the point clouds of different scans in a plot are considered to be different representations of the plot space. The stems in a plot are used as tie objects to align the different representations of the plot. Because of mapping errors, the reconstructed stems in each specific scan are considered to be a deformed instance of the tie objects. Two types of geometric primitives are utilized to describe the deformation between different scans: the diameters of the stem curves and the geometric distances between the stem curves in a set of trees, as shown in Fig. 6. Within a single scan, these two types of geometric primitives are independent of the defined coordinate system. When two scans are not aligned, these geometric primitives of different scans disagree due to the misalignment between coordinate systems and the estimation errors associated with the geometric variables. The registration process aims to find transformation parameters that minimize disagreement. For this purpose, a single figure of merit (FoM), i.e., the deformation energy, is constructed based on a concept of a mechanical deformation model. A searching process is used to determine the minimum FoM value. This process uses tree stems in the plots as features, and artificial objects of reference are not required.

3.2.1. Estimation model

We consider a general deformation energy model defined based on the Euclidean space $\mathbb{R}^d$. For a solid object, the deformation energy mainly includes contributions from the bending of thin-shell surfaces and local stretching within the object (Mio et al., 2007; Botsch and Sorkine, 2008). According to differential geometry (Carmo, 1976), the first and second fundamental forms $I$ and $II$ can be used, respectively, to measure the geometrically intrinsic (i.e., parameterization independent) properties of a solid object $S$ such as areas (diameters) and lengths (distances). The change
in these fundamental forms yields a measure of the deformation energy due to stretching and bending (Terzopoulos et al., 1987), as shown in the following equation:

\[
E[f] = \int_{D \in \mathbb{R}^2} (k_1 ||f' - f||^2 + k_2 ||f'' - f||^2) \, df
\]  

(1)

where \( f' \) and \( f'' \) are the fundamental forms of the deformed status \( S' \), \( || \cdot ||_F \) denotes a weighted Frobenius norm, and \( k_1 \) and \( k_2 \) are stiffness factors in the mechanical context. The energy calculated in (1) is invariant under rigid motion (rotation and translation).

For forest inventories, the deformation is represented by the discrepancies between the geometric primitives of stems reconstructed in different scans. The reconstructed stem curves are the minimum discretization elements, the geometric primitives of which are compared between different scans to quantify the deformation. Each reconstructed stem consists of a set of curves, and each curve is represented by the coordinate of its central point \((x, y, z)\) and its radius \(r\) in the equation \( T = (S) = \{x_1, y_1, z_1, r_1\} \), where the coordinate \((x, y, z)\) is defined locally in a scan-specific coordinate system. Among the five scans of each plot, the central scan \((X0)\) is chosen as the reference scan and the other scans \((X1, X2, X3, X4)\) are aligned with the reference scan using the registration process. In other words, the curve coordinates of the side scans are transformed into the coordinate system of the central scan so that all scans are matched into the unified coordinate system \((X^3)\).

We let \( A = \{A_1, A_2, \ldots, A_m\} \) be the \( M \) matched stems between two scans; \( \{A^1, A^2, \ldots, A^m\}^T \) be the stems reconstructed from the first scan (the central scan); and \( \{A^b, A^b, \ldots, A^b\} \) be the stems from the second scan (one of the side scans). Thus, the set of curves of \( M \) matched stems are represented as follows:

\[
x_1 \ y_1 \ z_1 \ r_1 \\
x_2 \ y_2 \ z_2 \ r_2 \\
\vdots \ \vdots \ \vdots \ \vdots \\
x_n \ y_n \ z_n \ r_n \\
A^b_k = \begin{bmatrix} x_k \\ y_k \\ z_k \\ r_k \\ \vdots \\ \vdots \\ x_n \\ y_n \\ z_n \\ r_n \end{bmatrix} \quad |k = 1, \ldots, M|; \quad b = I, II; \quad n = \sum_{m=1}^{M} l_m
\]  

(2)

A sliding search process is operated in the vertical direction to find the vertical translation that minimized the deformation energy. Given the maximum tree height \( H_{\text{max}} \) in the plot, which can be retrieved from the stem mapping results of single scans, the search range is defined as \([-H_{\text{max}}, H_{\text{max}}]\). The searching step is half of the length of every curve \((d/2)\); the curve length \(d\) is defined as \(2\) cm in this study. A given search candidate is assumed to be the vertical translation between two scans and it is applied to

**Table 2:** The search scheme for registration.

| Field operation of data acquisition | The laser scanner is placed vertically on top of a tripod using a leveling marker so that the different scans have parallel vertical axes. |
| Search range | \([-H_{\text{max}}, H_{\text{max}}]\), where \(H_{\text{max}}\) is the maximum stem height in both scans. \(d/2\)cm, where \(d\) is the length of the stem curves. Here, \(d = 2\) cm. |
| Searching step length | 1. A search candidate of vertical translation is given from the search range. |
| Search procedures | 2. Correspondences of curves are established. |
| | 3. Deformation energy is calculated with Eq. (3). |
| | 4. Steps 1–3 are repeated for all search candidates. |
| | 5. The coordinate transformation parameters that minimize the deformation energy are identified. |

align these scans by correcting the vertical coordinate \((Z\text{-axis})\) of a side scan with this translation value. Next, corresponding curves that belong to the same tree are recognized from each pair of matched stems in two scans. For a given pair of matched stems, when the vertical coordinate of the curve of one stem have a difference of less than the searching step \((d/2)\) from the curve of the paired stem, the two curves are considered to be a pair of correspondences. The set of curve correspondences is established for all curves and matched stems. This establishment process suffers from the complex changes in visibility between two scans. For example, a stem or part of a stem might be mapped in one scan but not in another scan. After all of the curve correspondences are determined, the coordinate transformation parameters between the two scans are estimated based on the center coordinates of the corresponding curves using the computation method presented in Appendix A. Finally, the differences between the curve diameters, curve-to-curve distances and transformed coordinates of the curve correspondences are calculated for the set of curve correspondences. These are used to calculate the deformation energy. In practice, the deformation energy is calculated using Eq. (3). It is normalized by the number of correspondences in each searching step because the number of correspondences varies based on differences in occlusion and visibility. A vertical translation that minimizes the deformation energy is found after completion of the searching process. The entire scheme is summarized in Table 2.
Finally, the scanner is placed horizontally using the leveling instrument. The Z-axis of each scan-specific coordinate system is in the vertical plane and it is parallel in the different scans. Thus, the rotations around the X- and Y-axes can be assumed to be zero. Additionally, the scale parameter is considered to be of unit length because the same scanner is used for data acquisition of the different scans. Therefore, the number of transformation parameters to be estimated is reduced from seven to four, remaining the translations in the X, Y, and Z directions and the rotation angle around the Z-axis.

3.3. Evaluation measures

The registration accuracy of the proposed method is evaluated in two ways. During the field measurement, artificial balls (198.8 mm in diameter) were placed in the plots for the purpose of benchmarking. These balls and their center coordinates in individual scans were manually extracted from the point cloud data of single scans using the commercial software “Faro Scene 5.2.1.” The ball centers are used as the tie points for manual registration of multiple scans. Registration parameters (Pball) are calculated using the tie points and the calculation routine for coordinate transformation parameters described in Appendix A. Using the resulting transformation parameters, the residual 3D errors of the ball coordinates are less than 4 mm in all ten plots. It is worth to note that the artificial balls are only used to evaluate the accuracy of the proposed method, but they are not utilized in the proposed automated matching method. Finally, the errors (e) associated with the estimated registration parameters (P) of the proposed method are calculated based on the difference with respect to the artificial ball-derived parameters (Pball) as follows:

\[ e = P - P_{\text{ball}} \]  

(6)

The performance of the automated registration of several scans is also evaluated through stem-mapping results. Registration of multiple scans enables us to combine the point clouds of individual scans into a unified coordinate system. The matched point cloud of all scans can be used for stem mapping with improved performance. Compared to the individual scans, the combination of multiple scans has two advantages for stem mapping. First, all stems in a plot are included in the combined point cloud, and the occluded parts of one scan are complemented by the other scans. Second, a more comprehensive point cloud using different perspectives improves the mapping accuracy, even although the same algorithm used for the individual scans is applied to the combined point cloud from multiple scans. Two measures, completeness and correctness, are used to describe the performance of tree mapping, which are defined in Eqs. (7) and (8). Completeness measures the percentage of all reference trees that are found by the mapping process; correctness measures the percentage of all detected trees that are matched correctly with the reference trees (Yao et al., 2014).

\[ \text{Completeness} = \frac{n_{\text{match}}}{n_{\text{ref}}} \]  

(7)

\[ \text{Correctness} = \frac{n_{\text{match}}}{n_{\text{extr}}} \]  

(8)

where \( n_{\text{match}} \) denotes the number of matched trees (correct detections), \( n_{\text{ref}} \) denotes the total number of reference trees, and \( n_{\text{extr}} \) denotes the total number of extracted trees.

4. Results

4.1. Matching accuracy

Because the scanner is leveled at the beginning of the scanning process, only four registration parameters have to be evaluated.
Fig. 7. Comparison of the completeness values of stem mapping using matched multiple scans, the MSS method, and the single center scan.

Fig. 8. Comparison of the correctness values of stem mapping using matched multiple scans, the MSS method, and the single center scan.

(translation in the three dimensions and rotation around the vertical (Z) axis); the remaining three parameters remained constant (scale factor and rotation around the horizontal (X, Y) axes). Table 3 presents the estimation errors of horizontal and vertical translation and rotation around the vertical axis, which are calculated by subtracting the estimation values of the proposed method from the benchmarking values derived manually with the artificial balls. Table 3 shows that RMS errors of horizontal and vertical translations are 1.63 cm and 13.14 cm, respectively, and rotation RMS error is 4.38°. Several scans have outlier errors that contribute significantly to the RMS errors. For example, 4 scans (10% of the total side scans) have horizontal and vertical translation errors greater than the RMS values. Excluding these outlier scans reduces the RMS errors of horizontal and vertical translations to 0.87 cm and 5.02 cm. The causes of the outlier errors and their impacts on stem mapping of the matched point clouds will be discussed in the discussion section.

4.2. Performance of stem mapping using the matched point cloud of multiple scans

Figs. 7 and 8 show the completeness and correctness values of stem mapping using the matched point cloud compared to the single-scan method and the MSS method. The results from the center scan are used to represent the single-scan method, and the MSS method selects the best results from each separate scan. Figs. 7 and 8 show that the MSS method has high completeness but a little bit lower correctness compared to the results from the matched scan, meaning that the MSS method detects more trees, but with some false detection. Matching multiple scans enhanced the completeness and correctness because of the full coverage of the point cloud. For the single center scan, the MSS method, and the matched multiple scans, the mean completeness and correctness of the ten plots are 0.700 and 0.942; 0.808 and 0.909; 0.731 and 0.972, respectively. For specific plots, the improvement of correctness may be up to 10.3% compared to the single-scan method and 17.7% compared to the MSS method. More importantly, the matched multiple scans yields more consistent completeness and correctness among the plots. This improvement is more noticeable for plots in which single scans have lower completeness or correctness, such as plots 3, 4, 6, and 10 in Fig. 7, and plots 1, 3, 4, and 10 in Fig. 8. In particular, outlier errors associated with the registration do not degrade the completeness and correctness of stem mapping, such as in plots 1, 3, and 10. Some plots (such as plot 8) have lower completeness values because of the presence of a number of small trees. The detection of small trees is more sensitive to matching errors. Plot 8 is dominated by both pine and spruce and has many small trees, as shown in Table 1 and Fig. 3. It remains challenging to detect small trees.

We compare also the accuracy of stem mapping among the three approaches. Tables 4 and 5 present the bias and RMS errors of the mean DBH and stem height for the ten plots estimated using the matched multiple scans; the results using the single center scan and the MSS method are also shown. Overall, matching multiple scans reduces the mean relative RMS error from 8.66% and 8.56% to 6.38% for the DBH and from 29.93% and 26.31% to 20.70% for the tree
Table 4
Accuracy of the predicted DBHs in the ten plots using the matched multiple scans, the MSS method, and the single center scan.

<table>
<thead>
<tr>
<th>Plot ID</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
<th>9</th>
<th>10</th>
</tr>
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<tbody>
<tr>
<td>Bias (cm)</td>
<td>1.75</td>
<td>1.23</td>
<td>0.89</td>
<td>0.84</td>
<td>1.51</td>
<td>0.73</td>
<td>1.80</td>
<td>1.52</td>
<td>1.04</td>
<td>1.80</td>
</tr>
<tr>
<td>Bias (%)</td>
<td>0.50</td>
<td>0.62</td>
<td>0.84</td>
<td>0.84</td>
<td>1.51</td>
<td>0.73</td>
<td>1.80</td>
<td>1.52</td>
<td>1.04</td>
<td>1.80</td>
</tr>
<tr>
<td>RMS (cm)</td>
<td>2.70</td>
<td>2.83</td>
<td>3.49</td>
<td>3.49</td>
<td>3.49</td>
<td>3.49</td>
<td>3.49</td>
<td>3.49</td>
<td>3.49</td>
<td>3.49</td>
</tr>
</tbody>
</table>

Table 5
Accuracy of the predicted tree heights in the ten plots using the matched multiple scans, the MSS method, and the single center scan.

<table>
<thead>
<tr>
<th>Plot ID</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
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<td>Bias (m)</td>
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<td>5.00</td>
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<td>RMS (%)</td>
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<td>13.69</td>
<td>23.07</td>
<td>22.90</td>
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Fig. 9. Relative RMS errors associated with DBH estimation using the matched multiple scans, the MSS method, and the single center scan.

Fig. 10. Relative RMS errors associated with stem height estimation using the matched multiple scans, the MSS method, and the single center scan.

height. In most cases, the relative RMS errors of the DBH and stem height estimates are improved significantly by using the matched multiple scans, as shown in Figs. 9 and 10. When the registration parameters have notable horizontal errors (such as in plots 1 and 3), the relative bias and RMS errors of the predicted DBH increased slightly by 1–4%. In cases where the registration parameters have outlier vertical errors of several decimeters (such as in plot 10), the relative RMS errors of the predicted DBH are slightly reduced by 1–4% and the relative RMS errors of the predicted stem height were reduced by a greater amount of 5–12%. Fig. 11 shows that the location errors associated with stem mapping are comparable between the matched multiple scans and the single scans. This result indi-
Fig. 11. Errors associated with the estimated horizontal tree locations using the matched multiple scans, the MSS method, and the single center scan.

cates that the center positions of the mapped stem curves derived from the matched multiple scans did not change notably, although there are horizontal and vertical matching errors.

5. Discussion

The method presented in this study exploits the anisotropic properties of the natural geometry of stems in a plot. When the stems of a plot have different orientations, the anisotropy of the trees is strong, which is favorable for the proposed method to achieve high accuracy in the vertical direction. In contrast, when the stems are oriented parallel to one another and the anisotropic properties are weak, the method may obtain inferior accuracy in the vertical direction. This occurs in scan 4 of plot 10 (Table 3), in which all matched stems have a quasi-vertical orientation; this geometry is not sensitive to the misalignment in the vertical direction. As a result, the error associated with vertical translation exceeds 70 cm. Fortunately, in this geometric condition, the vertical errors have a relatively small impact on stem mapping because of the parallel orientation of the stems. This is shown by the results of matched stem mapping in Tables 4 and 5 and Figs. 7–11. In boreal forests where the dominant tree species is Scots pine or Norway spruce, an error of 10 cm in the stem direction causes a bias of no more than 6 mm in the estimation of stem diameter, as shown in Fig. 12. Typically, the maximum rate of change in diameter is approximately 5.5 mm per 10 cm of height change at breast height, and the rate of change in diameter is less than 2 mm per 10 cm for the remainder of the stem.

The precision of single-scan stem mapping, including the estimates of curve diameters and central positions, has a direct impact on the registration accuracy of the proposed method because the estimated curve diameter and central position values are used to calculate the geometric primitives. Therefore, it is necessary to reject outlier estimates from individual scans. The robustness measures introduced in Section 3.2.2 improve the accuracy and reliability of the proposed method. Integrity monitoring of stem mapping of specific curves is required so that outlier curves could be rejected more effectively based on the specific integrity of each curve; this results in less frequent removal of correct curves. A larger number of accurately mapped curves improve the matching.

Because the center points of the curves are used as tie points for the coordinate transformation, a shorter curve length causes smaller discretization error. However, shorter curve lengths lead to smaller step lengths of searching, and increase the computation time. For example, when the curve length (d) is 5 cm, the RMS errors of registration are almost twice the current values in Table 3; these include extra errors of curve discretization, although the computation time is only one third of the value for a curve length of 2 cm. When the curve length is reduced to 1 cm, the search time is more than doubled compared to a curve length of 2 cm; however, the accuracy does not improve significantly. When the curve length is relatively small, the errors of curve discretion become secondary and the stem mapping errors of single scans have a dominant impact. An appropriate searching step (d/2) should correspond to the overall amount of stem mapping errors, and a smaller curve length does not improve registration accuracy after a certain point.

Previous studies have considered simultaneous registration of multiple views to be optimal (Bergevin et al., 1996; Jokinen and Haggren, 1998; Kelbe, 2015); this is shown to improve registration results compared to a pair-wise approach (Henning and Radtke, 2008). However, simultaneous registration of multiple views requires significant overlap between adjacent scans and a much larger number of scans are needed per plot. For example, graph-based registration requires 25 scans for each 20 × 20 m plot in Kelbe (2015). Therefore, the process necessitates more field measurements and increases the cost. In this study, we only use 5 scans for each 32 × 32 m plot; there are notable changes in the scene contents of different scans. There is limited overlap between each set of two side scans and the overlapping areas are far from the scanner. Single-scan stem mapping of these overlapping areas would likely have outlier errors associated with the estimates of center positions and diameters (Liang et al., 2012); this would decrease the overall accuracy of a simultaneous registration approach. In this study, we combine all the scans and create a global registration for this composite scan. Our results demonstrate that this global registration has worse accuracy than pair-wise registration for over half of the plots. Therefore, we adopt pair-wise registrations between each side scan and the center scan, which has the most significant overlap.

After the point clouds from multiple scans are combined using the derived registration parameters, we use the same stem mapping routine for integrated stem mapping as the single-scan cases. In the future, the method could be improved by implementing a quality check at the point level given that the number of points in the matched multiple scans is several times greater than in a sin-
gle scan; additionally, the combined point cloud covers complete stems rather than the partial stems represented by single scans. Consequently, more sophisticated algorithms could be applied to the redundant points to increase the reliability and precision of stem mapping. For example, surface points that deviate substantially from the assumed cylinder of stem curves could be identified and filtered out. In addition to stem mapping, combined point clouds with full coverage of tree stems could enable new applications based on the comprehensive horizontal and vertical structure of forests. One such application is the analysis of standing timber quality, which is in highly demand in forestry industry.

6. Conclusions

In this study, we present a method for plot-wise stem mapping using automated matching of multiple scans. The method involves a stem mapping algorithm using a set of TLS points and an automated matching method that aligns multiple scans without the use of artificial references. Classic automated registration methods cannot be directly applied to forested scenes because of the difficulty associated with defining correspondence primitives during registration; additionally, forest conditions give rise to complex occlusion and visibility situations. The registration method proposed in this study exploits the geometry of tree stems in a plot, which is a natural characteristic of the trees and independent of the defined coordinate system. Point clouds from multiple scans are combined into a unified coordinate system and the set of points from multiple scans are used for integrated stem mapping. For most of cases, the proposed matching method improves the performance of plot-wise stem mapping in terms of the correctness of tree detection and estimation bias and RMS errors of stem attributes DBH and tree height. A large horizontal matching error may increase slightly the bias and RMS errors of DBH estimation by 1–4%. More importantly, the proposed method produces more robust and consistent performance of stem mapping among different plots, compared to single-scan approaches. Therefore, the improvements due to the automated matching are especially significant for plots where single scans perform poorly. Automated matching of multiple scans could be used to generate a high-precision forest inventory reference dataset at the plot level. In the future, automatically derived stem curves could be used to calculate stem volume and aboveground biomass with higher accuracy.

Acknowledgments

This work was funded by the Academy of Finland, based on its support for the projects “Interaction of Lidar/Radar Beams with Forests Using Mini-UAV and Mobile Forest Tomography” (No. 259348) and “Centre of Excellence in Laser Scanning Research (CoELaSR)” (No. 272195).

Appendix A. Calculation of coordinate transformation parameters

Given a number of correspondences between two scans, coordinate transformation parameters can be estimated based on the concept of the tensor of inertia, which yields information about how the mass is distributed in a rigid object (Bakker et al., 1995; Meriam and Kraige, 2012). The tensor of inertia of an object is defined with respect to a specific coordinate system. However, there always exist three mutually orthogonal coordinate axes relative to a given rigid body such that all products of inertia are simultaneously zero. These orthogonal coordinate axes are known as principal axes; they can be found by resolving the eigenvalue problem of the inertia tensor. The principal axes of a rigid body can be calculated using the coordinates of a set of mass points (e.g., correspondence points in two TLS scans), though they are independent of the specifically defined coordinate system. Thus, the derived principal axes are equivalent for the same set of mass points, even though they have different coordinate values in different coordinate systems. Thus, the principal axes can connect two coordinate systems, allowing calculation of the transformation parameters of the two systems.

In the present context, the corresponding curves of two scans form the distribution of mass points. Given the coordinate values \(X_i\) and \(X_j\) of the corresponding curves in the two scans, the computation of coordinate transformation parameters proceeds in the following manner:

1. The center of mass of all points \(X_c = \{x_c, y_c, z_c\}\) is computed as follows:

\[
x_c = \frac{1}{n} \sum_{k=1}^{n} x_k, \quad y_c = \frac{1}{n} \sum_{k=1}^{n} y_k, \quad z_c = \frac{1}{n} \sum_{k=1}^{n} z_k
\]

2. The center of mass is subtracted from the original point coordinates as follows:

\[
X_{(k)} = X_k - X_c
\]

3. The symmetric inertia tensor \(I\) is calculated by computing the sum of products and cross products of the coordinates \(X_{(k)}\) of the following points:

\[
I = \begin{bmatrix}
\sum (y^2 + z^2) & -\sum x' y' & -\sum x' z' \\
-\sum x' y' & \sum (x'^2 + z'^2) & -\sum y' z' \\
-\sum x' z' & -\sum y' z' & \sum (x'^2 + y'^2)
\end{bmatrix}
\]

The normalized eigenvectors \(a_1, a_2, a_3\) of the inertia tensor \(I\) represent the body axes, and they form a matrix \(R = \{a_1, a_2, a_3\}\).

4. The radius of gyration is calculated as follows:

\[
s = \frac{1}{n} \sum_{k=1}^{n} \left( x_k^2 + y_k^2 + z_k^2 \right)
\]

5. The above steps A1–A4 are performed for the coordinates \(X_1\) and \(X_2\) of the corresponding curves of the two scans. The transformation parameters are determined as follows:

\[
\lambda = \frac{s_1}{s_2}, \quad A = R_1 R_2^{-1}, \quad T = x_2^1 - \lambda \times A \times x_1^2
\]

References


