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Postprint: A Method for Extracting Cotton Phenotypic Parameters Using Multi-temporal LiDAR Point Cloud Data

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Abstract

Currently, achieving efficient and accurate measurement of crop phenotypic parameters and dynamic quantification of phenotypic parameters throughout the crop growth period represents one of the urgent challenges in phenotyping research and breeding. This study employs cotton as the research object, utilizing three-dimensional laser scanning LiDAR technology to acquire multi-temporal point cloud data of cotton plants. Based on the geometric characteristics of the cotton plant main stem, the Random Sample Consensus (RANSAC) algorithm combined with a linear model is utilized to complete main stem extraction, while region growing clustering is performed on the remaining point clouds to achieve segmentation of individual leaves. On this basis, estimation of trait parameters including plant volume, plant height, leaf length, and leaf width is accomplished. For multi-temporal cotton laser point cloud data, the Hungarian algorithm is adopted to complete alignment of adjacent temporal crop point cloud data and establishment of correspondence relationships between leaf organs. Simultaneously, the dynamic change process of various plant phenotypic parameters is quantified. This study, targeting point cloud data from four growth time points of three cotton plants, respectively completed main stem extraction, leaf segmentation, as well as phenotypic parameter measurement and dynamic quantification. Experimental results demonstrate that the main stem extraction and leaf segmentation methods adopted in this study can effectively achieve segmentation of cotton stems and leaves. The coefficient of determination between extracted phenotypic parameters such as plant height, leaf length, and leaf width and manual measurement values all approach 1.0. Furthermore, this study realized the dynamic quantification process of cotton phenotypic parameters, providing an effective method for the implementation of three-dimensional phenotyping technology.

Full Text

Preamble

Cotton Phenotypic Trait Extraction Using Multi-Temporal Laser Point Clouds

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Abstract: Efficient and accurate measurement of crop phenotypic parameters, along with dynamic quantification of these traits throughout growth stages, represents a critical challenge in phenomics research and breeding. This study focused on cotton as the research object, employing three-dimensional laser scanning technology to acquire multi-temporal point cloud data of cotton plants. Leveraging the geometric characteristics of cotton main stems, the Random Sample Consensus (RANSAC) algorithm combined with linear models was used for stem extraction, while region-growing clustering was applied to segment individual leaves from the remaining point clouds. Based on this segmentation, trait parameters including plant volume, height, leaf length, and leaf width were estimated. For multi-temporal cotton LiDAR data, the Hungarian algorithm was employed to align adjacent temporal point clouds and establish correspondence between leaf organs. The dynamic changes in various plant phenotypic parameters were subsequently quantified. This study processed point cloud data from four growth stages, completing stem extraction, leaf segmentation, phenotypic parameter measurement, and dynamic quantification for three cotton plants. Experimental results demonstrated that the proposed stem extraction and leaf segmentation methods successfully separated cotton stems and leaves. The coefficient of determination between extracted plant height, leaf length, leaf width and manual measurements all approached 1.0. Meanwhile, this study achieved dynamic quantification of cotton phenotypic parameters, providing an effective methodology for three-dimensional phenotyping technology.

Keywords: cotton phenotypic traits; LiDAR; stem extraction; leaf segmentation; point cloud registration; 3D phenotyping

1 Introduction

In recent years, with the advancement of crop phenomics and phenotyping technologies, three-dimensional phenotyping has attracted increasing attention from high-throughput phenotyping researchers due to its ability to capture one additional dimension of information compared to two-dimensional techniques. Light Detection and Ranging (LiDAR) technology overcomes limitations of traditional computer vision methods, such as high algorithmic complexity and time-consuming reconstruction processes, offering a novel approach for automated measurement of phenotypic parameters in three-dimensional space. Crops represent typical objects whose morphological structures continuously change over time. Continuous acquisition of point cloud data at different growth stages not only enables measurement of phenotypic parameters at specific time points but also facilitates investigation of dynamic changes in these parameters, providing valuable phenotypic data for breeders.

Currently, three-dimensional point cloud information of crops is primarily obtained through two approaches. The first involves computer vision-based image reconstruction methods, which have been applied to grapevines [?], tomatoes [?], soybeans [?], maize [?], and plant roots [?]. These image-based methods typically involve camera calibration, feature extraction, feature matching, and bundle adjustment, imposing constraints on image acquisition such as requiring high overlap between adjacent viewpoints. The quality of generated point clouds is highly dependent on the number of images. When crops lack sufficient features, structured light is often introduced to enrich texture characteristics for higher-precision point cloud data. Nguyen et al. [?] constructed a structured light system to acquire multi-view images of plants, obtained multi-view point clouds, completed registration between point clouds, and built complete three-dimensional plant models for measuring leaf number, plant height, leaf size, and internode distance. Ni et al. [?] used three cameras to capture 120 images of blueberry clusters, reconstructed point clouds and models, applied Mask-RCNN for individual blueberry segmentation and maturity detection on the two-dimensional images, and back-projected the segmentation results into three-dimensional space to extract phenotypic parameters.

The second approach utilizes LiDAR technology to directly acquire three-dimensional information. This method first obtains three-dimensional point clouds of crops from different viewpoints, then employs the Iterative Closest Point (ICP) algorithm for multi-view point cloud registration to generate complete three-dimensional models. LiDAR-based 3D phenotyping research can be summarized into two aspects: point cloud data processing methods and phenotypic parameter extraction methods. Based on crop scale, LiDAR technology can be applied to both individual plants and field crops to obtain phenotypic parameters at different scales. For field crops, extracted parameters primarily include average canopy height, projected area, plant density, and biomass. Jiang et al. [?] developed a 3D phenotyping technology for extracting harvest-related phenotypic parameters of blueberries from field LiDAR data,

including size and scale. Jin et al. [?] proposed a Median Normalized Vector Growth (MNVG) algorithm for stem-leaf segmentation of field maize, enabling measurement of leaf angle, stem height, and plant height. Sun et al. [?] applied density clustering methods to reconstructed field cotton plants at maturity stage to achieve cotton boll segmentation and counting for yield estimation. Liu et al. [?] constructed a Digital Plant Phenotyping Platform (D3P) to obtain three-dimensional canopy scenes of field wheat, recording green leaf area index, mean inclination angle, and scattered light interception rate, and simulated virtual LiDAR experiments to demonstrate the potential of LiDAR data for canopy light interception and structure analysis.

For individual plants, close-range or handheld laser scanning is primarily used to extract organ-level phenotypic parameters from leaves, stems, and even roots. Point cloud registration and segmentation are critical steps for obtaining three-dimensional models and extracting phenotypic parameters. Ma et al. [?] proposed a registration method based on geometric feature constraints of plant point cloud neighborhoods, selecting key points and estimating their support neighborhoods to calculate neighborhood geometric features for initial registration. Chaudhury and Barron [?] projected point clouds from different viewpoints onto two-dimensional planes to establish initial correspondence by locating node positions, with the prerequisite that linear features exist in the point cloud data. Point cloud segmentation is fundamental for phenotypic parameter acquisition. Three primary segmentation methods are applicable to crop organs: (1) Three-dimensional region-growing methods that utilize similarity attributes within point cloud regions to formulate appropriate growing rules, mainly applied to leaf segmentation in crops such as rapeseed [?], pothos, and monstera [?]; (2) Model-fitting based segmentation methods that employ typical geometric models such as lines, cylinders, and planes, commonly used for main stem segmentation in crops like sunflower [?] and maize [?]; (3) Machine learning-based methods, including clustering algorithms such as Support Vector Machine (SVM) and Mean Shift. Wahabzada et al. [?] used unsupervised clustering on plant models to complete leaf and stem segmentation for grape, wheat, and barley. Yu et al. [?] fused multi-dimensional features of point cloud data, used manually labeled data as samples, and combined SVM classifiers to separate branches and leaves in trees, representing a supervised classification approach.

Acquiring point cloud data of crop objects at regular time intervals yields multi-temporal point cloud data containing spatiotemporal morphological change information. Research on multi-temporal crop point clouds provides powerful methods for dynamic analysis of phenotypic parameters and data foundations for constructing crop growth models. Su et al. [?] used laser scanners to obtain point clouds of maize at six growth stages, calculated three phenotypic parameters (plant height, leaf area, and projected leaf area), and investigated their dynamic trends. Chaudhury et al. [?] constructed a close-range vision system based on laser scanners, registered multi-view point clouds of wild Arabidopsis and barley plants, calculated area and volume through surface mesh generation,

and plotted continuous curves of area and volume changes from day 1 to day 22. Sun et al. [?] used LiDAR systems to extract phenotypic parameters throughout the entire growth period of field cotton and analyzed their dynamic changes in relation to yield. An et al. [?] conducted continuous 10-day acquisition of two-dimensional images of Arabidopsis, comparing differences in leaf phenotypic parameter measurements between 2D images and 3D models, with results indicating that 3D models yield higher-precision parameters than traditional 2D imaging.

Although these studies demonstrate progress in 3D phenotyping, data processing methods vary across different crops, indicating untapped potential. Cotton is one of China's four major economic crops and the primary raw material for the textile industry. Maximizing cotton yield is the primary goal of cultivation and breeding, significantly impacting China's agricultural economic development. Phenotypic parameters from each growth stage provide essential data foundations for achieving this goal. To further explore the potential of 3D phenotyping technology for individual cotton plants, this study focused on single cotton plants, using laser scanning to acquire multi-temporal point cloud data, investigating stem and leaf segmentation algorithms, and implementing calculations of phenotypic parameters including plant height, leaf length, leaf width, leaf area, and plant volume. Based on this, dynamic quantification of cotton phenotypic parameters was achieved, providing methodological support and data foundations for high-throughput 3D phenomics and crop growth modeling.

2 Materials and Methods

2.1 Point Cloud Data Acquisition

This study utilized a ZGScan handheld laser scanner (Wuhan Zhongguan Automation Technology Co., Ltd.) to acquire point cloud data from three cotton plants at 12 time points across four growth stages. Auxiliary scanning tools included laser scanning markers, brackets, and an HP laptop for data input and storage. Post-processing was performed on a Dell computer with a 64-bit Windows operating system, 16 GB RAM, and a 3.4 GHz Intel(R) Core i7-3770 CPU. [Figure 1: see original paper] shows the transplanted cotton plants and scanning equipment. Cotton plants were cultivated in the laboratory starting August 10, 2018, and transplanted to pots after reaching approximately 16 cm in height.

Point clouds were collected at four time points after transplantation: day 46, day 49, day 58, and day 63, yielding 12 datasets. As cotton plants grew, morphological changes included increasing height, emergence of new leaves, expansion of some existing leaves, shedding of older leaves, increasing leaf inclination angles, and slight increases in internode distance. Raw point cloud data were preprocessed using Geomagic Studio 2013 software to remove noise from pots and brackets. The preprocessed point cloud data for the three cotton plants are shown in [Figure 2: see original paper].

2.2 Cotton Organ Segmentation Method

To extract phenotypic parameters including plant height, leaf length, leaf width, and volume, and to quantify their dynamic changes, cotton plant point clouds must be segmented into organ-level subsets—disjoint point cloud subsets representing individual organs.

2.2.1 Main Stem Extraction As shown in [Figure 2: see original paper], cotton plant main stems tend to be straight. Therefore, based on cotton plant morphology and point cloud characteristics, a model-based detection method—the Random Sample Consensus (RANSAC) algorithm combined with linear models—was employed for stem extraction. RANSAC is an iterative method that estimates model parameters from observed data through random sampling. The process involves randomly selecting a subset of data, fitting a model, and iteratively optimizing model parameters. Upon reaching termination conditions, the model with the maximum number of inliers is selected as the final result.

For multi-branched plant types, RANSAC can be applied multiple times until all linear stem-like structures are extracted. The ideal outcome separates petioles from the main stem, minimizes noise in the stem portion, and maintains leaf counts matching manual observations. During stem extraction, the distance threshold parameter significantly affects results: too small a threshold yields incomplete stems, while too large a threshold incorrectly extracts non-stem points. Insufficient iterations prevent optimal inlier detection, whereas excessive iterations increase computational time. With fixed iteration count (2000), distance thresholds of 1.0 mm, 6.0 mm, and 18.0 mm were tested. Optimal results were achieved with thresholds between 5.0–10.0 mm, as shown in [FIGURE:3(a)] and .

2.2.2 Leaf Segmentation After stem extraction, the remaining point cloud contains multiple leaves that require clustering. Euclidean clustering segmentation was applied to the residual point cloud to obtain individual leaves. The algorithm proceeds as follows: (1) Create a K-D tree for input point cloud dataset P ; (2) Construct an empty cluster list C and a point queue Q for verification; (3) Randomly select point P_i from dataset P , add it to queue Q , and for each point in Q , search for neighboring points within radius $r < d_{th}$. For each neighbor not yet processed, add it to Q . After processing all points in Q , add them to cluster C and reset Q ; (4) Terminate when all points in P are processed and assigned to clusters.

Three parameters require configuration: nearest neighbor search radius, minimum cluster size, and maximum cluster size. Minimum and maximum cluster sizes exclude noise and prevent errors from improper radius settings. Based on leaf point cloud distribution, maximum cluster size typically exceeds half the total point count, while minimum cluster size remains below 10%. The nearest neighbor radius relates to mean inter-point distance: excessive radius prevents segmentation, while insufficient radius causes fragmentation. Through system-

atic testing, optimal parameters were identified as: minimum cluster size = 800 points, maximum cluster size = 155,000 points, and nearest neighbor radius = 120 mm. As shown in [FIGURE:3(b)], a minimum cluster size of 100 incorrectly segmented non-leaf noise, while a radius of 80 mm fragmented leaves because it was smaller than the average inter-point distance within leaf regions. Increasing minimum cluster size to 800 eliminated noise, and increasing radius to 120 mm integrated leaves with petioles.

2.3 Registration of Adjacent Growth Stage Point Clouds and Leaf Correspondence

To investigate growth changes and dynamic phenotypic variations in the same plant, point clouds from adjacent growth stages must be registered and leaf correspondence established.

2.3.1 Coarse Registration Point cloud registration comprises coarse and fine registration stages. Coarse registration estimates an approximate transformation matrix when initial relative positions are unknown. A representative algorithm is the Sample Consensus Initial Alignment (SAC-IA), which randomly selects geometrically consistent point pairs rather than exhaustively testing all combinations, calculating optimal transformations from these pairs [?].

First, Fast Point Feature Histograms (FPFH) are computed for each point, forming multi-dimensional histograms that describe geometric properties of a point's K-neighborhood by parameterizing spatial differences between query points and neighbors. After FPFH computation, SAC-IA performs coarse registration: (1) Select n sample points from source cloud S with pairwise distances exceeding a minimum threshold to ensure distinct FPFH features; (2) In target cloud R , find points with similar FPFH features to each sample point and randomly select one as the correspondence; (3) Compute transformation matrices between correspondences and evaluate performance using the Huber error function:

$$H(l_i) = \begin{cases} |l_i| & \text{if } |l_i| < m_l \\ |l_i - m_l| & \text{if } |l_i| > m_l \end{cases}$$

where m_l is a predefined value and l_i is the distance difference after transformation for the i -th correspondence pair. The optimal transformation minimizes this error function.

2.3.2 Leaf Correspondence Across Adjacent Growth Stages Quantifying dynamic phenotypic changes requires establishing one-to-one correspondence between leaves after coarse alignment. For a plant at time T_i with m leaves and at time T_{i+1} with n leaves, two scenarios exist:

Case 1 ($m = n$): Calculate the centroid of each leaf at both time points. Construct an $m \times n$ adjacency matrix M where $M(i, j)$ represents the 3D Euclidean

distance between the i -th leaf centroid at T_i and the j -th leaf centroid at T_{i+1} . With both point clouds in the same coordinate system, apply the Hungarian algorithm to matrix M to minimize the sum of distances, yielding optimal leaf matching. As shown in , bold values indicate matched leaf pairs.

Case 2 ($m < n$): When leaf counts differ due to new leaf emergence or senescence, supplement the T_i leaf set to n leaves by adding $n - m$ virtual leaves with zero distance to all T_{i+1} leaves. Construct an $n \times n$ matrix and apply the Hungarian algorithm. The m leaves at T_i are matched to m leaves at T_{i+1} , while the remaining $n - m$ leaves at T_{i+1} without correspondences are identified as newly emerged.

3 Experiments and Results Analysis

3.1 Cotton Stem and Leaf Segmentation Results

RANSAC stem extraction ideally separates petioles from stems, minimizes stem noise, and preserves leaf counts matching manual observations. Parameter selection critically affects results. With fixed iteration count (2000), distance thresholds of 1.0 mm, 6.0 mm, and 18.0 mm were evaluated ([FIGURE:3(a)]). Optimal results were achieved with thresholds of 5.0-10.0 mm ().

For multi-branched plants, RANSAC can be iteratively applied until all linear stem structures are extracted. Visual evaluation criteria require that extracted stems reflect actual plant height. Quantitative evaluation compares the ratio of extracted stem length to manually measured length, with ratios approaching 1.0 indicating higher accuracy.

Euclidean clustering ideally produces segments matching manual leaf counts with complete leaf preservation. Three parameters require optimization: nearest neighbor radius, minimum cluster size, and maximum cluster size. Minimum and maximum sizes exclude noise and prevent errors from improper radius settings. Based on leaf point distribution, maximum cluster size typically exceeds half the total points, while minimum size remains below 10%. The neighbor radius relates to mean inter-point distance: excessive radius prevents segmentation, while insufficient radius causes over-segmentation. Optimal parameters were: minimum cluster size = 800 points, maximum cluster size = 155,000 points, radius = 120 mm. As shown in [FIGURE:3(b)], minimum cluster size of 100 incorrectly segmented non-leaf noise, while radius of 80 mm fragmented leaves. Increasing minimum size to 800 eliminated noise, and increasing radius to 120 mm integrated leaves with petioles.

3.2 Establishment of Leaf Correspondence

The method described in Section 2.3 was applied to establish correspondence between leaves at different growth stages. [Figure 4: see original paper] shows the distance matrix for Plant 1 between days 46 and 49. After Hungarian algorithm optimization, shaded cells indicate matched leaf pairs. Leaf #9 at

T_{i+1} had no correspondence at T_i , identifying it as a newly emerged leaf. [Figure 5: see original paper] visualizes leaf correspondence across four time points for three plants, with each leaf rendered in a consistent color. New leaves at the top and senesced leaves at the bottom are clearly distinguishable.

3.3 Phenotypic Parameter Extraction and Accuracy Evaluation

3.3.1 Plant Height and Volume Plant height was measured from extracted stems by calculating the Euclidean distance between the lowest and highest stem points. Accuracy was evaluated by comparing point cloud-derived parameters with manual measurements using absolute error, relative error, and coefficient of determination (R^2). Relative error is calculated as:

$$E_R = \frac{|Y - L|}{L} \times 100\%$$

where E_R is relative error, Y is the point cloud-derived value, and L is the manual measurement.

R^2 measures correlation between point cloud-derived and manual measurements:

$$R^2 = \frac{\sum_{i=1}^n (Y_i - \bar{Y})^2}{\sum_{i=1}^n (Y_i - \bar{Y})^2 + \sum_{i=1}^n (Y_i - \hat{Y}_i)^2}$$

where n is the number of samples, Y_i are manual measurements, \bar{Y} is the mean manual measurement, and \hat{Y}_i are point cloud-derived values.

[Figure 7: see original paper] presents accuracy assessment for plant height, leaf length, and leaf width across 12 cotton plants. All three traits showed high correlation with manual measurements, with R^2 values of 1.0000, 0.9964, and 0.9993, respectively, approaching 1.0. This demonstrates that 3D laser scanning can obtain high-precision phenotypic parameters, attributed to: (1) high scanning accuracy (0.03 mm) of the close-range system, and (2) the additional dimension of information compared to 2D imaging methods.

Plant volume was calculated using convex hulls—the smallest convex polyhedron containing a point set. The convex hull generation is closely related to point cloud distribution, making it suitable for representing plant volume. Inputting raw plant point cloud data into MATLAB automatically computed the convex hull volume ([FIGURE:6(a)]).

3.3.2 Leaf Length, Width, and Area Estimation Cotton leaves exhibit curvature, making direct Euclidean distance between endpoints unsuitable for length measurement. This study employed an iterative approximation method [?]. Given leaf endpoints $A(X_A, Y_A, Z_A)$ and $B(X_B, Y_B, Z_B)$ with distance L_{AB} ,

the midpoint C is calculated. Distances l_{AC} and l_{BC} are computed, and $l_{AB} = l_{AC} + l_{BC}$ is compared to L_{AB} . If $|l_{AB} - L_{AB}| < d$ (where d is a threshold), l_{AB} is accepted as leaf length; otherwise, the process iterates on segments AC and BC . Leaf width was measured using the same approach.

For leaf area, each segmented leaf point cloud was meshed using Geomagic Studio 2013, and the sum of all mesh facets was calculated as leaf area. Mesh quantity and distance constraints affect accuracy: more facets yield finer surfaces and more accurate area estimates. This study used 2,500,000 facets with zero distance value, ensuring sufficient mesh quantity for high-precision area estimation ([FIGURE:6(c), 6(d)]).

3.3.3 Dynamic Estimation of Phenotypic Parameters Multiple acquisitions of cotton point clouds enabled temporal comparison of phenotypic parameters, visualizing growth dynamics for breeding and genetic research. [Figure 8: see original paper] shows dynamic trends for three plants across four time points. Plant height and volume exhibited steady increases. Volume growth correlated strongly with height. Older leaves showed minimal area changes, while new leaves demonstrated significant area expansion (e.g., top three leaves of Plant 1 in [FIGURE:5(a)], rendered in purple, dark blue, and blue-green). Leaf area and length showed consistent trends due to their strong correlation.

From data acquisition to phenotypic parameter output, total processing time was approximately 30 minutes per plant: 15-20 minutes for scanning (dependent on complexity), <30 seconds for stem extraction and leaf clustering, ~11 seconds for volume calculation, and ~30 seconds per leaf for area estimation.

4 Conclusion and Discussion

To explore LiDAR applications in crop phenomics, this study acquired multi-temporal 3D laser point clouds of cotton, enabling extraction and dynamic quantification of plant height, leaf length, leaf width, leaf area, and volume in 3D space. Key results include:

1. RANSAC with linear models successfully extracted stems from 12 point cloud datasets of three cotton plants. Euclidean clustering segmented individual leaves, enabling calculation of leaf length, width, area, plant height, and volume. Comparison with manual measurements showed high correlation (R^2 approaching 1.0), overcoming limitations of traditional destructive and subjective methods, providing foundations for yield-related studies.
2. Multi-temporal point clouds from different growth stages were co-registered, and leaf correspondence was established and visualized. Dynamic quantification of phenotypic parameter changes was achieved based on organ correspondence, providing precise information for analyzing individual cotton organ development and reliable data for constructing crop growth models.

Limitations include incomplete coverage of the full growth period, preventing whole-season dynamic analysis. Future work will utilize full-growth-period cotton point clouds for comprehensive dynamic visualization and deep data mining. The proposed methodology is also applicable to other crops with linear stem structures, such as maize and rapeseed.

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