

# Tree Parameter Evaluation Software User Guide

Version 1.1

MSpace

2023.09

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# 1. Introduction

The Tree Parameter Evaluation Software package is developed to evaluate the predicted tree parameters using the reference data. This guide introduces how to use the ‘Tree Parameter Evaluation’ software package.

The functions of this software include:

- to match trees between the predicted and reference positions based on 2D or 3D distance.
- to evaluate the predicted trees’ parameters according to references, including but not limited to positions, tree height, diameter at breast height (DBH) and stem curve.

More information:

Software name:	Tree Parameter Evaluation.
Project proponent:	MSpace members.
Software developer:	MSpace members.
Product user:	The software developers authorized entities and individuals, e.g., researchers, technicians, and developers.
MSpace webpage:	<a href="http://jszy.whu.edu.cn/liangxinlian/en/index/1350195/list/index.htm">http://jszy.whu.edu.cn/liangxinlian/en/index/1350195/list/index.htm</a>

## **2. Runtime Environment**

This section introduces the runtime environment required to this Parameter Evaluation package.

### **2.1. Hardware**

Require the hardware devices support the Windows 10 operating system.

### **2.2. Environment**

The required operating system: Windows 10.

### **2.3. Language**

The software package supports two languages: Chinese, English.

## 3. Operations Guide

This section introduces the interfaces and pipelines of basic operations: installation, individual parameter evaluation, and stem curve evaluation.

### 3.1. Installation

The software is installation-free. Unzip the package and double-click *Parameter Evaluation.exe* to launch the software.

The main interface is shown in Figure 1.

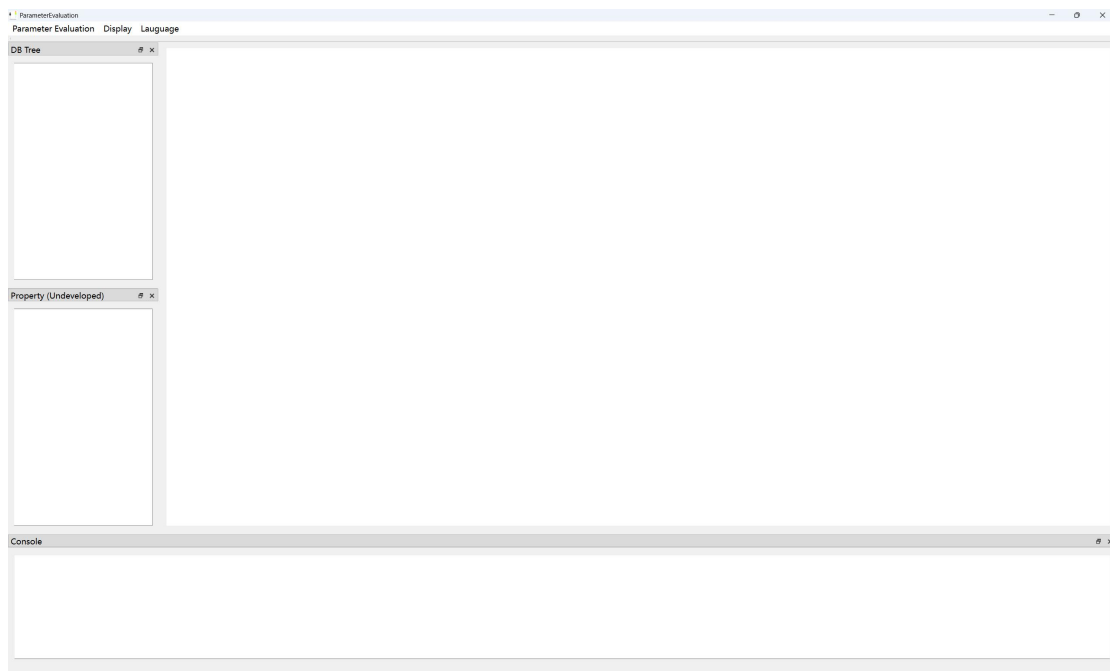

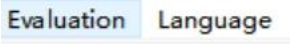


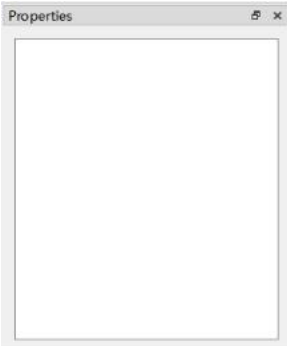


Figure 1. The main interface of the parameter evaluation software

## 3.2. Interfaces

Table 1 shows the information of interfaces.

Table 1. The interfaces of the software

Widget	Name	Function Description
 Parameter Evaluation	Software Name	None
	Menu Bar	None
	DB Tree	Data Binary Tree for data management
	Console	Output information
	Properties	Data properties

## 3.3. Individual parameter evaluation

Select Evaluation \ Individual parameter evaluation.

Figure 2 presents the interface of Individual Parameter Evaluation.

Figure 2. The Interface of Individual Parameter Evaluation

The operations are:

- (1) Click **Select File** to select the path of prediction file. The format of the prediction file is detailed in Section 4.1.1 (1).
- (2) Click **Select File** to select the path of reference file". The format of the reference file is detailed in Section 4.1.1 (1).
- (3) If a matching relationship file exists, click **Select File** to select the path of matching relationship file and skip step (4). The format of the matching relationship file is shown in Section 4.1.1 (3).
- (4) If there is no matching relationship file, proceed to step (4).
- (5) Input the parameters of Column Index of Matching Feature, Coordinate Dimension and Search radius (m).
- (6) Click **Select File** to select the path to save the output of evaluation result. The output is shown in Section 4.3.1.
- (7) Select **Show Result**. The matching result will be displayed, as shown in Figure 3.
- (8) Click **OK** to evaluate.

The evaluate method and input parameters are described in Section 4.2.1.

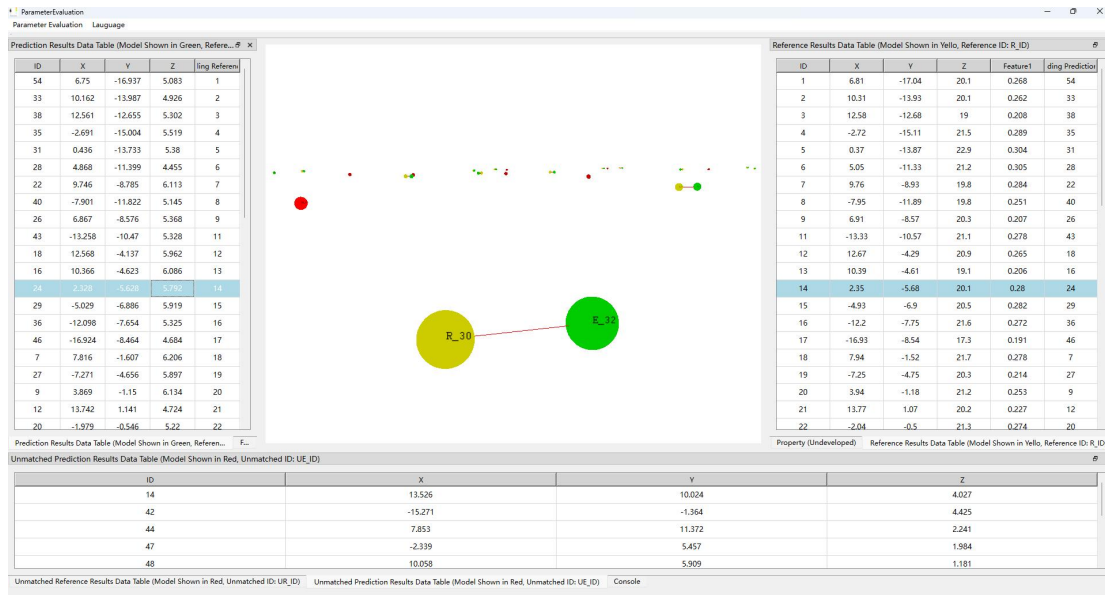


Figure 3. The Interface of displaying Matching results and graphs

The matched and unmatched data will be displayed in a floating window, which can be dragged to different places on the screen. The interface displays the coordinates of each tree by spheres, and the matched pairs will be connected by a line.

The matching results will be displayed in different colors:

- Green: a prediction with a matched reference.
- Yellow: a reference with a matched prediction.
- Red: a prediction without a match.



### 3.4. Stem curve evaluation

Select Evaluation \ Stem Curve Evaluation.

Figure 4 presents the interface of Stem Curve Evaluation.

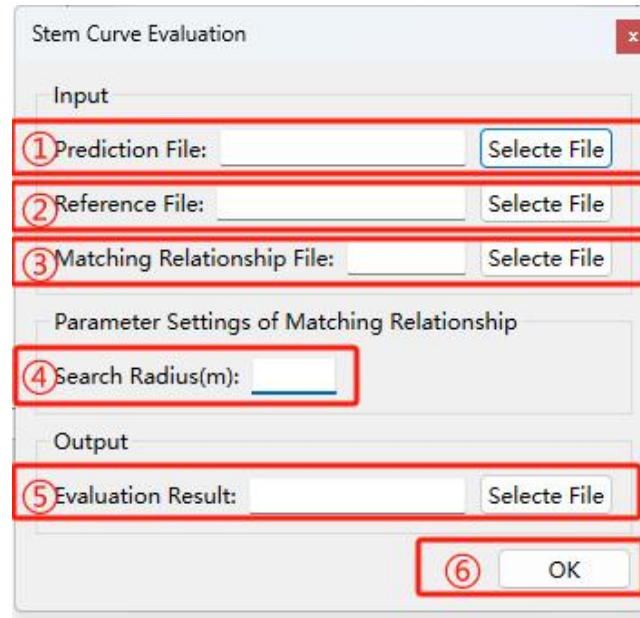


Figure 4. Dialog of "Evaluation of Stem Curve Prediction"

The operations are:

- (1) Click **Select File** to select the path of prediction file. The format of the prediction file is detailed in Section 4.1.1 (2).
- (2) Click Select **File** to select the path of reference file. The format of the reference file is detailed in Section 4.1.1 (2).
- (3) If a matching relationship file exists, click Select **File** to select the input path of matching relationship file and skip step (4). The format of the matching relationship file is shown in Section 4.1.1 (3).
- (4) If there is no matching relationship file, proceed to step (4).
- (5) Input the parameter of Search radius (m).
- (6) Click Select **File** to select the path to save the output for evaluation result. The output is detailed in Section 4.3.2.
- (7) Click **OK** to evaluate.

The evaluate method and input parameters are described in Section 4.2.2.

## 4. Function Description

This section introduces the inputs and the principle of individual parameter evaluation and stem curve evaluation.

### 4.1. Inputs

This section introduces the input for individual parameters evaluation and stem curve evaluation, including the input files and the input parameters.

#### 4.1.1. File

This section introduces the format of prediction, reference, and matching relationship files for individual parameters evaluation and stem curve evaluation.

##### 4.1.1.1. Files for the function of Individual Parameters Evaluation

The prediction and reference files are required for individual parameter evaluation. Table 2 represents the format of the file containing individual tree parameters.

Table 2. The format for the reference and prediction files

Field	ID	X(m)	Y(m)	Z(m)	Parameter 1	Parameter 2	...
Data Type	int64	double	double	double	double	double	...
Records	1						
	2						
	...						

Each row represents a piece of record:

- The first column is the unique ID;
- The second to fourth columns represent the coordinates, i.e., X, Y, Z, respectively;
- The subsequent columns, i.e., 5th onward, represent the one-dimensional parameters, such as: tree height, diameter at breast height, etc.

**Note:**

- The cell information of the data from the prediction and reference file with individual tree parameters should correspond to each other.

- If there are missing parameters in a file, please use "NaN" or "nan" to fill them. Individual items are separated by tab or space.
- The prediction and reference should be in the same coordinate system.

#### 4.1.1.2.Files of the function of Stem Curve Evaluation

Table 3 represents the format of the prediction and reference files for the Stem Curve Evaluation function.

Table 3. The format for the reference and prediction files

Field	ID	Data 1	Data 2	...
Data Type	int64	double	double	...
Stem Diameter (m)				
X(m)				
Y(m)				
Height (m)				

Each four rows represent a record of the stem curve of a tree:

- The diameter is in the first row, the X-/Y-/Z-coordinates are in the second, third, and fourth rows, respectively.
- The first column is an unique ID
- The subsequent columns contain the stem diameters, X-coordinate, and Y-coordinate at different heights, respectively.
- This file is a txt file. Please refer to Appendix II for a detailed example of the file format.

#### Note:

- If there is any missing record, please use NaN or nan to fill it.
- Individual items are separated by tab or space.
- The prediction and reference should be in the same coordinate system.

#### 4.1.1.3.Matching Relationship File

Table 4 represents the format of the matching file.

Table 4. The format of the “Matching Relationship” file

Data Name	Prediction ID	Reference ID
Data Type	int64	int64
	6	1
Records	8	2
	⋮	⋮

Each row represents a pair of matching items:

- The first column represents the IDs of the prediction
- The second column represents the IDs of the reference.
- The file is txt file. The extension should be '.txt'.

Note:

- The matching relationship file is optional.
- Data should be separated by tab or space.

## 4.1.2. Parameters

This section introduces the input parameters for individual parameter evaluation and stem curve evaluation.

### 4.1.2.1. Search radius

This parameter is used for Matching Relationship for both functions of *Individual Parameter Evaluation* and *Stem Curve Evaluation*, i.e., to determine the searching neighborhood for each record in the prediction file. This parameter should be a positive value, and the unit is meter.

### 4.1.2.2. The index of the matching feature

This parameter is the input data for function of *Individual Parameter Evaluation*. The input data is a positive integer less than the number of records. This parameter aims to assign a specific parameter from the reference file as the matching features.

### 4.1.2.3. The Coordinate Dimension

This parameter is the input data for function of *Individual Parameter Evaluation*. The input data should be 2 or 3 to specify the coordinate dimension for neighborhood searching.

## 4.2. Evaluation Methods

The evaluation methods in this software package follow the methods in [1].

[1] X. L. Liang, J. Hyyppä, H. Kaartinen, M. Lehtomäki, J. Pyörälä, N. Pfeifer, M. Holopainen, G. Brogly, F. Pirotti, J. Hackenberg, H. B. Huang, H. W. Jo, M. Katoh, L. X. Liu, M. Mokros, J. Morel, K. Olofsson, J. Poveda-Lopez, J. Trochta, D. Wang, J. H. Wang, Z. X. Xi, B. S. Yang, G. Zheng, V. Kankare, V. Luoma, X. W. Yu, L. Chen, M. Vastaranta, N. Saarinen, and Y. S. Wang, “International benchmarking of terrestrial laser scanning approaches for forest inventories,” *ISPRS JOURNAL OF PHOTOGRAMMETRY AND REMOTE SENSING*, vol. 144, pp. 137-179, OCT, 2018.

### 4.2.1. Individual parameter evaluation

This function matches the predicted and reference records. The predicted parameters will be evaluated based on the matching relationship. The Figure 5 represents the function.

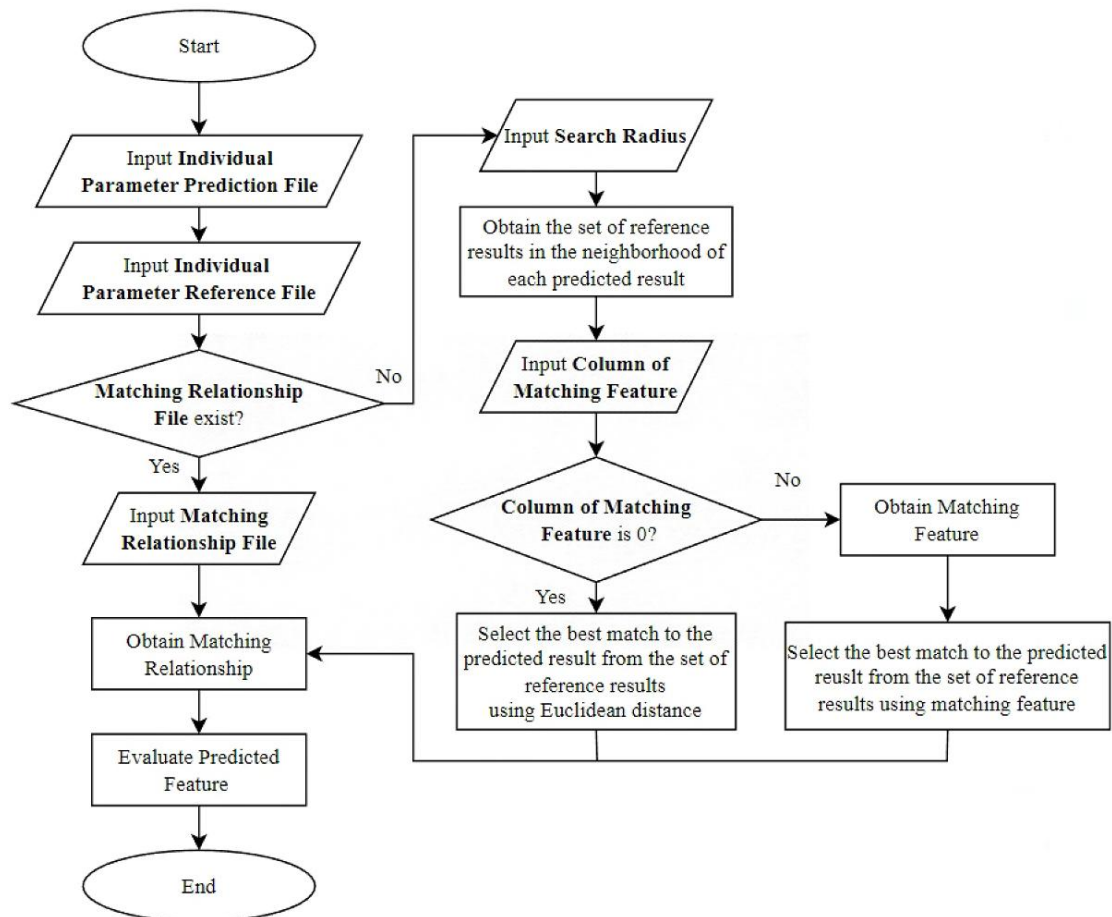


Figure 5. The flowchart of the evaluation of the individual parameters.

### 4.2.2. Stem curve evaluation

This function evaluates the extracted stem curve according to the references. The extracted stem curve can be evaluated according to the existing matching relationship, or by searching the matching relationship between the predicted and reference.

Figure 6 represents the function.

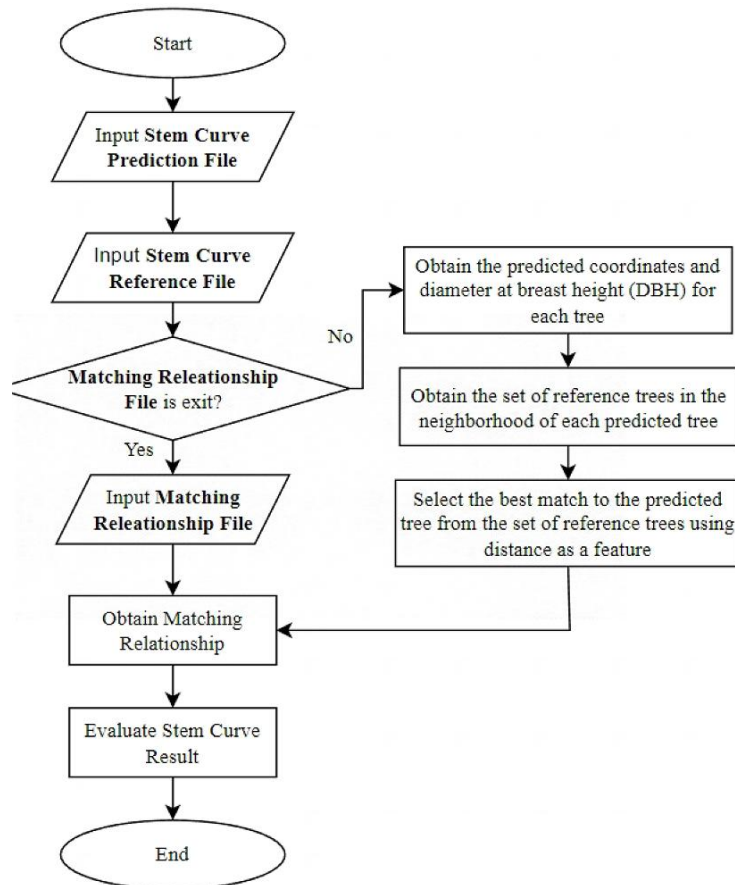


Figure 6. The flowchart of the evaluation of the stem curve

## 4.3. Output

### 4.3.1. Individual Parameters Evaluation

The software evaluates the matching results according to equations (1)-(6), the location according to the equation (7), and the individual parameters according to equations (8-11), respectively.

(1) Evaluation of Matching

$$Recall = \frac{TP}{TP + FN} = \frac{\hat{n}_T}{\hat{n}_T + n_F} \quad (1)$$

$$Precision = \frac{TP}{TP + FP} = \frac{\hat{n}_T}{\hat{n}_T + \hat{n}_F} \quad (2)$$

$$Mean Accuracy = \frac{TP}{TP + FP + FN} = \frac{\hat{n}_T}{\hat{n}_T + \hat{n}_F + n_F} \quad (3)$$

$TP$  represents the True Positive and  $\hat{n}_T$  represents the number of matched trees pair between the prediction and reference ;  $FN$  represents False Negative and  $n_F$  represents the number of references which are not matched with any prediction ;  $FP$  represents the False Positive and  $\hat{n}_F$  represents the number of predictions which were not matched with any reference.

(2) Evaluation of Location

$$RMSE_{loc} = ||\hat{L} - L||_2 = \sqrt{\frac{1}{n_{match}} \sum_{i=1}^{n_{match}} (\hat{L}_i - L_i)^2} \quad (4)$$

$RMSE_{loc}$  represents the Root Mean Square Error of the location.  $\hat{L}$  and  $L$  represents the prediction and reference locations, respectively.  $n_{match}$  represents the number of matched trees between the prediction and reference.

(3) Evaluation of Individual Parameters

$$RMSE_f = ||\hat{F} - F||_2 = \sqrt{\frac{1}{n_{match}} \sum_{i=1}^{n_{match}} (\hat{F}_i - F_i)^2} \quad (5)$$

$$Bias_f = \frac{\sum_{i=1}^{n_{match}} (\hat{F} - F)}{n_{match}} \quad (6)$$

$$RMSE_f\% = \frac{RMSE_f}{\bar{F}} \times 100\% = \sqrt{\frac{1}{n_{match}} \sum_{i=1}^{n_{match}} (\hat{F}_i - F_i)^2} \times 100\% \quad (7)$$

$$Bias_f\% = \frac{Bias_f}{\bar{F}} \times 100\% = \frac{\sum_{i=1}^N (\hat{F} - F)}{\frac{1}{n_{match}} \sum_{i=1}^{n_{match}} F_i} \times 100\% \quad (8)$$

$RMSE_f$  represents the Root Mean Square Error (RMSE) of the prediction of basic tree parameters.  $Bias_f$  represents the bias of the prediction of basic tree parameters.  $RMSE_f\%$  represents the Relative Root Mean Square Error (RMSE) of the prediction of basic tree parameters,  $Bias_f\%$  represents the Relative Bias of the prediction of basic tree parameters.  $\hat{F}$  represents the predicted basic tree parameters.  $F$  represents the reference basic tree parameters.  $n_{match}$  represents the number of matched trees between prediction and reference without parameter missing.

The output file is a xlsx file, as shown in Figure 7.

The Corresponding Index of Trees		Evaluation of Matching Results		Positional Precision		Evaluation of Basic Feature Prediction for Group1		Evaluation of Basic Feature Prediction for Group2	
Index of The Extracted Tree	Index of The Reference Tree	TP(True Positive)	FP(False Positive)	RMSE of Distance		RMSE		RMSE	
1	0	1	1	0.229129		0.1		0.1	
2	0	1	1			8.88178E-16		-2.22045E-16	
3	1	0	0			0.788954695		1.60642E-103	
4	2	1	0			7.00732E-15		-3.56698E-15	
5	3	1	0						
6	3	1	0						
		Recall	1.000000						
		Matching Precision	1.000000						
		Mean Accuracy	0.888889						

Figure 7. Output result of the individual parameter evaluation

### 4.3.2. Stem Curve Evaluation

The software uses to evaluate the stem curve according to equations (9)-(14).

#### 4.3.2.1.Evaluation of Matching

The evaluation method is the same as the Evaluation of Individual Parameters.

#### 4.3.2.2.Evaluation of Location Precision

The evaluation method is the same as the Evaluation of Individual Parameters.

#### 4.3.2.3.Evaluation of Stem Curve Prediction

$$RMSE_i = \sqrt{\frac{1}{m_i} \sum_{j=1}^{m_i} (\hat{d}_i(\hat{z}_{i,j}) - d_i^{interp}(\hat{z}_{i,j}))^2} \quad (9)$$

$$MAE_i = \frac{1}{m_i} \sum_{j=1}^{m_i} |\hat{d}_i(\hat{z}_{i,j}) - d_i^{interp}(\hat{z}_{i,j})| \quad (10)$$



$$Bias_i = \frac{1}{m_i} \sum_{j=1}^{m_i} (\hat{d}_i(\hat{z}_{i,j}) - d_i^{interp}(\hat{z}_{i,j})) \quad (11)$$

$i$  is the index of the tree and  $j$  is the index of the diameter in the  $i$ -th tree.  $RMSE_i$  represents the Root Mean Square Error (RMSE) of the parameters of stem curve of the  $i$ -th tree.  $MAE_i$  represents the Mean Absolute Error (MAE) of the parameters of stem curve of the  $i$ -th tree.  $m_i$  represents the number of diameters extracted from the  $i$ -th tree.  $\hat{d}_i(\hat{z}_{i,j})$  represents the predicted diameters at the height  $\hat{z}_{i,j}$ .  $d_i^{interp}(\hat{z}_{i,j})$  represents the diameter at height  $\hat{z}_{i,j}$  generated by interpolation based on the reference data.

For the plot-level evaluation, the stem curve is evaluated according to the equations (12)-(14):

$$\overline{RMSE} = \frac{1}{n_{match}} \sum_{i=1}^{n_{match}} RMSE_i \quad (12)$$

$$\overline{MAE} = \frac{1}{n_{match}} \sum_{i=1}^{n_{match}} MAE_i \quad (13)$$

$$\overline{Bias} = \frac{1}{n_{match}} \sum_{i=1}^{n_{match}} Bias_i \quad (14)$$

$\overline{RMSE}$  represents the Average Root Mean Square Error (RMSE) of all matched trees,  $\overline{MAE}$  represents the Average Mean Average Error (MAE) of all matched trees,  $\overline{Bias}$  represents the Average Bias of all matched trees and  $n_{match}$  represents the number of matched trees between prediction and reference without any missing parameter.

The output is a xlsx file, as shown in Figure 8.

A		B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	
The Corresponding Index of Trees		Evaluation of Matching Results		Positional Precision		Evaluation of Stem Curve Precision (All Trees)		Evaluation of Stem Curve Precision (The Trees)		Evaluation of Stem Curve Precision (The Trees)		Evaluation of Stem Curve Precision (The Trees)		Evaluation of Stem Curve Precision (The Trees)		Evaluation of Stem Curve Precision (The Trees)	
Index of The Extracted Tree	Index of The Reference Tree	TP(True Positive)	FP(False Positive)	FN(False Negative)	Recall	Matching Precision	Mean Accuracy	RMSE of Diameter	MAE of Diameter	Bias of Diameter	Mean of RMSE	STD of RMSE	Mean of RMSE	Mean of MAE	Mean of Bias	Mean of RMSE	
0	0	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
1	1	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
2	2	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
3	3	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
4	4	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
5	5	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
6	6	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
7	7	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
8	8	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
9	9	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
10	10	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
11	11	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
12	12	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
13	13	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
14	14	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
15	15	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
16	16	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
17	17	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
18	18	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
19	19	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
20	20	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
21	21	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
22	22	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
23	23	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
24	24	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
25	25	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
26	26	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
27	27	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
28	28	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
29	29	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
30	30	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
31	31	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
32	32	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
33	33	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
34	34	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
35	35	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
36	36	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
37	37	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
38	38	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
39	39	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
40	40	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
41	41	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
42	42	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
43	43	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
44	44	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
45	45	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
46	46	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
47	47	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
48	48	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
49	49	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
50	50	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
51	51	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
52	52	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
53	53	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
54	54	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
55	55	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
56	56	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
57	57	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
58	58	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
59	59	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
60	60	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
61	61	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
62	62	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
63	63	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	
64	64	1	0	0	1.000000	1.000000	0.888889	0.265111	0.15	-7.22045E-16	0.15	0.15	0.15	0.15	0.15	0.15	

# Appendix I

## Examples of the Data Format for Individual Parameter Evaluation

### (1) The format of the reference file

Table 5. The example of reference file for individual parameter evaluation

ID	X	Y	Z	Parameter 1	Parameter 2	Parameter 3	Parameter 4	...
1	4.9	8.3	1.6	9.8	4.3	6.2	7.1	...
2	5.1	5.3	6.2	8.5	4.8	3.6	4.9	...
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	...

### (2) The format of the Prediction File

The prediction file with X, Y coordinates and Parameter 1.

Table 6. The example I of the prediction file for the individual parameter evaluation

ID	X	Y	Z	Parameter 1
1	5.3	6.2	NaN	10.6
2	8.3	1.6	NaN	6.2
⋮	⋮	⋮	⋮	⋮

In this example:

- Evaluate the Parameter 1. Keep it in the Prediction File and Reference File stay in the same column (i.e., column 5).
- The Z coordinate is missing., the Z coordinate in the column 4 of Prediction File are filled with NaN.
- The following parameters (i.e., parameter 2, parameter 3, parameter 4) are not compulsory to be included in the Prediction File.
- The prediction file with X, Y, Z coordinates and Parameter 1 and Parameter 4.

Table 7. The example II of the prediction file for the individual parameter evaluation

ID	X	Y	Z	Parameter 1	Parameter 2	Parameter 3	Parameter 4
1	9.8	4.3	6.2	8.3	NaN	NaN	10.6

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2	4.8	3.6	4.9	5.3	NaN	NaN	6.2
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮

---

In this example:

- Evaluate the Parameter 1 and Parameter 4. Keep them in the Prediction File and Reference File stay in the same column, i.e., column 5 and column 8, respectively.
- Fill the data in columns 6 and 7 of the Prediction with NaN.

## AppendixII

### Example of Data Format for Stem Curve Evaluation

#### (1) The format of Reference File

Table 8. The example of reference file for stem curve evaluation

Name	ID	Height					
		0.6m	1.3m	1.8m	2.2m	2.7m	...
Stem Diameter	1	3.2	3.1	3.0	2.9	2.8	...
X	1	5.2	5.1	5.2	5.1	5.0	...
Y	1	4.3	4.2	4.2	4.1	4.1	...
Height	1	0.6	1.3	1.8	2.2	2.7	...
Stem Diameter	2	2.2	2.1	2.0	2.0	1.9	...
X	2	1.2	1.1	1.2	1.1	1.0	...
Y	2	2.3	2.2	2.2	2.1	2.1	...
Height	2	0.6	1.3	1.8	2.2	2.7	...
⋮	⋮	⋮	⋮	⋮	⋮	⋮	

In this example:

- The Reference File contains the stem curve parameters of two trees.
- Rows 1 to 4 represent the stem curve parameters of the first tree, which include the stem diameter and plane coordinates of the tree at different heights, e.g., 0.6m, 1.3m, 1.8m, 2.2m, 2.7m, etc.
- Rows 5 to 8 represent the stem curve parameters of the second tree, same with the first tree.

#### (2) The format of the Prediction File

The parameters of stem curve data of two trees.

Table 9. The example of prediction file for stem curve evaluation

ID	Height			
	0.6m	1.3m	1.8m	...
1	3.2	NaN	3.0	...
1	5.2	5.1	5.2	...
1	4.3	4.2	4.2	...
1	0.6	1.3	1.8	...
2	2.2	2.1	NaN	...
2	1.2	1.1	1.0	...
2	2.3	2.2	2.1	...
2	0.6	1.4	1.7	...
⋮	⋮	⋮	⋮	⋮

In this example:

- The Prediction File contains the stem curve parameters of two trees.
- Rows 1 to 4 represent the stem curve parameters of the first tree, which include the stem diameter and plane coordinates of the tree at different heights, e.g., 0.6m, 1.3m, 1.8m, 2.2m, 2.7m, etc.
- Rows 5 to 8 represent the stem curve parameters of the second tree, with the same items as the first tree.
- Keep the parameters at the same height in Prediction and Reference Files in the same column.
- In the example, the stem diameter at 1.3m of the first tree is missing, and the stem diameter of the second tree at 1.8m is missing. They are filled with NaN.