

Tree Feature Evaluation Software

User Manual

MSpace

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1. Introduction

1.1 Purpose of Preparation

This manual has been prepared to facilitate the use of tree feature evaluation software by the user. The manual spells out in detail how the software works and explains to the user how to use each function in the software.

The intended users are researchers and technicians in the field of forest land investigations as well as developers and testers of the software.

1.2 Background

Software name: Feature Evaluation.

Project proponent: MSpace member.

Software developer: MSpace member.

Product user: The software's task proponents, software developers,
and MSpace member-authorized entities and
individuals.

1.3 Reference

[1] Liang X, Hyypä J, Kaartinen H, et al. International benchmarking of terrestrial laser scanning approaches for forest inventories[J]. ISPRS Journal of Photogrammetry and Remote Sensing, 2018, 144.

2. Software Overview

2.1 Purpose

The software is designed to evaluate the predicted results of tree features

(e.g., tree height, diameter at breast height (DBH), and stem curve) using reference data from the plots.

2.2 Functions

- (1) A function to calculate tree matching relationships based on predicted results and reference data.
- (2) A function to evaluate the predicted results of tree features using relevant formulas, including but not limited to coordinates, tree height, diameter at breast height (DBH) and stem curve.
- (3) A function to translate the global language. Currently, only two languages, Chinese and English, are supported.

3. Runtime Environment

3.1 Hardware

Hardware devices that can run the Windows 10 operating system.

3.2 Software

The following lists the supporting software systems required to run this system:

- (1) Operating System: Windows 10.

4. Function Introduction

4.1 Input

4.1.1 File

(1) Tree Basic Feature File

The format of the Tree Basic Feature Prediction File and the Tree Basic Feature Reference File is shown in Table 1. Each row represents the basic feature data of each tree. The first column is the unique ID number of each tree; the second to fourth columns represent the coordinates of each tree; and each subsequent column represents the one-dimensional features of each tree, such as tree height, diameter at breast height, etc. The file extension of the basic tree features is .txt. Please refer to Appendix I for detailed examples of the file format.

Note: The Tree Basic Feature Prediction File should have the same semantic information as each column of data in the Tree Basic Feature Reference File. If some coordinates or feature information are missing in the tree basic feature prediction file, please use "NaN" or "nan" as a filler to indicate the missing data. The data in each line are separated by tabs or spaces.

Table 1 Input file format for "Evaluation of Tree Parameter Prediction".

Data Name	ID	X(m)	Y(m)	Z(m)	Feature 1	Feature 2	...
Data Type	int64	double	double	double	double	double	...

(2) Stem Curve File

The format of the Stem Curve Prediction File and Stem Curve Reference File is shown in Table 2. Each four rows represent the stem curve data of a tree, where the diameter at breast height is in the first row, the X-coordinate in the second row, the Y-coordinate in the third row, and the height in the fourth row. For the stem curve data of each tree, the first column is unique to the tree with four identical ID; the subsequent columns represent the diameter at breast height, X-coordinate, and Y-coordinate of the tree at different heights, respectively. The extension of the stem curve file is .txt. Please refer to Appendix II for a detailed example of the file format.

Note: Some coordinates or feature information is missing in Stem Curve Prediction Files, please use "NaN" or "nan" as filler to represent the Missing data. The data in each line are separated by tabs or spaces.

Table 2 Input file format for "Evaluation of Stem Curve Prediction".

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

(3) Matching Relationship File

The format of the matching relationship file is shown in Table 3. Each row represents a pair of matching relationships, where the first column represents the IDs of the trees in the prediction file and the second column represents the IDs of the trees in the reference file. The extension of the matching relationship file is .txt.

Note: The matching relationship file is optional. The data in each line is separated by a tab or space.

Table 3 The format of the Matching Relationship File.

Data Name	Extracted Tree ID	Reference Tree ID
Data Type	int64	int64
Example Data	6	1
	8	2
	⋮	⋮

4.1.2 Parameter

- (1) **Search Radius (m):** The input data for this parameter is positive and it is used to determine the range of each tree in the prediction file when performing a neighborhood search.
- (2) **Column of Matching Feature:** This parameter is the input data for the function "Evaluation of Basic Features Prediction". The parameter is a positive integer less than the number of columns in the tree basic feature file. The function of this parameter is to specify the columns of the Tree Basic Feature File to be used as matching features.
- (3) **Extraction Height of Diameter at Breast Height and Coordinates:** This parameter is the input data for the function "Evaluation of Stem Curve Prediction". The parameter is a positive number. After inputting the parameter by the user, the program extracts the diameter and center coordinates nearest to the specified height as the diameter at breast height (DBH) and coordinates of the tree from the stem curve data of each tree.

4.2 Processing

4.2.1 Evaluation of Basic Feature Prediction

This function can be used to calculate the matching relationship between the prediction results and reference data of tree basic features. After that,

the prediction results of tree basic features are evaluated according to the matching relationship, and the flow chart of this function is shown in Figure 1.

Note: Predicted results and reference data should be in the same coordinate system.

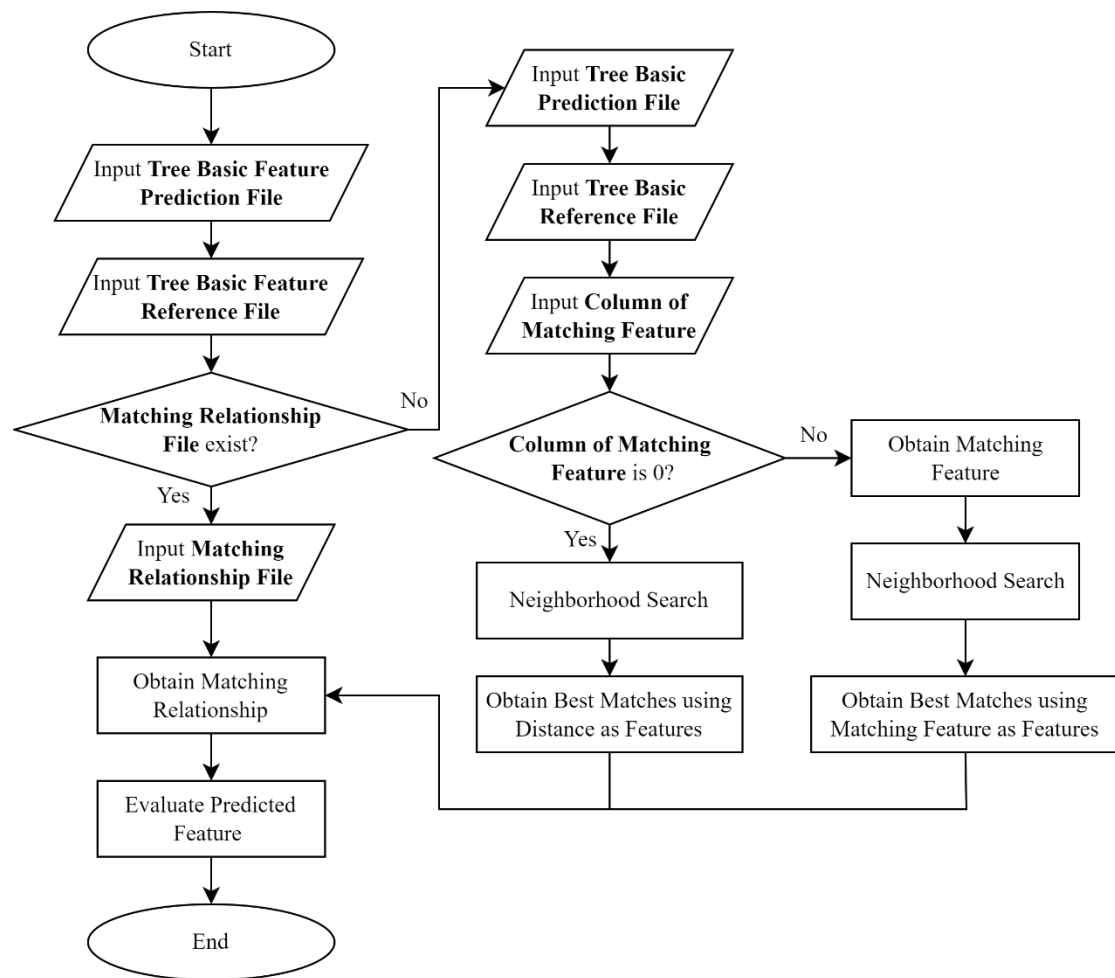


Figure 1 Flowchart of Evaluation of Basic Feature Prediction.

4.2.2 Evaluation of Stem Curve Prediction

This function can be used to calculate the matching relationship between the prediction result and reference data of the tree stem curve. After that,

the prediction result of tree stem curve is evaluated according to the matching relationship, and the flow chart of this function is shown in Figure 2.

Note: Predicted results and reference data should be in the same coordinate system.

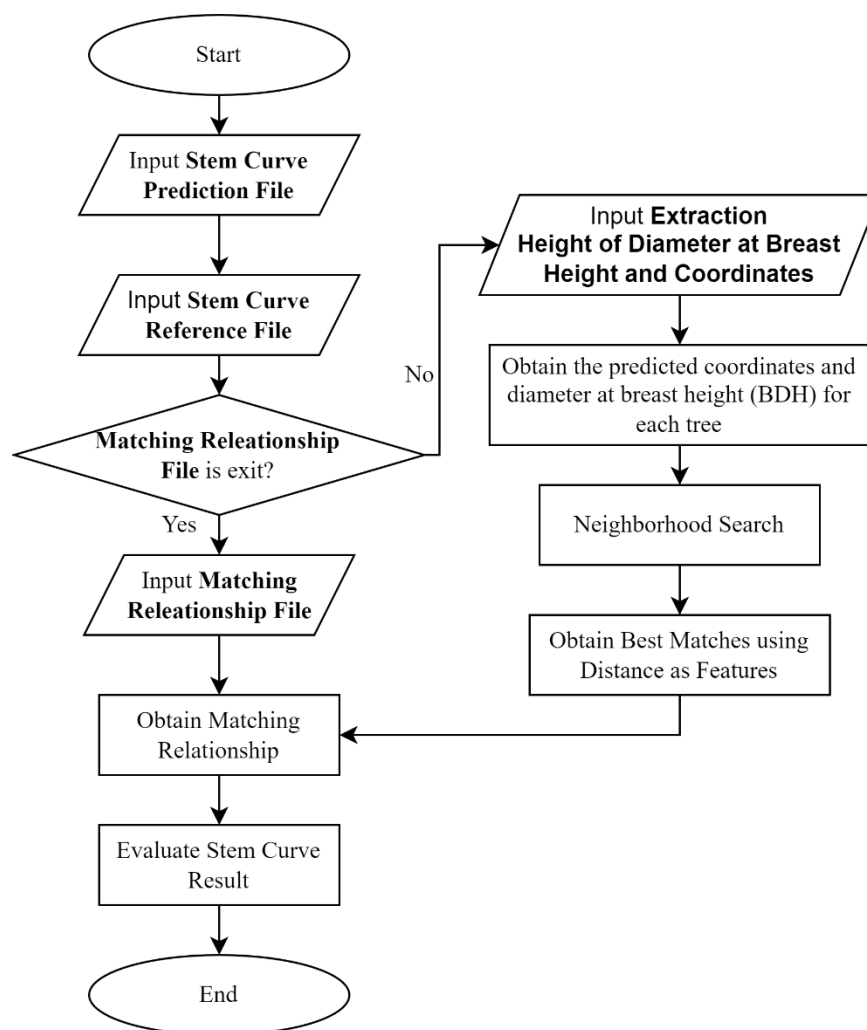


Figure 2 Flowchart of Evaluation of Stem Curve Prediction.

4.3 Output

4.3.1 Evaluation of Basic Feature Prediction

After obtaining the matching relationship between the prediction results and the reference data, the software uses equations (1)-(11) to evaluate the matching results, the location precision, and the prediction results of tree basic features, respectively. The results are shown in Fig. 3.

(1) Evaluation of Matching Relationship

$$TP = \hat{n}_T \quad (1)$$

where TP represents the True Positive and \hat{n}_T represents the number of trees in the prediction results that can match with the reference data.

$$FP = \hat{n}_F \quad (2)$$

where FP represents False Positive and \hat{n}_F represents the number of trees in the prediction that failed to match with the reference data.

$$FN = n_F \quad (3)$$

where FN represents False Negative and n_F represents the number of trees in the reference data that failed to match with the prediction results.

$$R = \frac{TP}{TP + FN} = \frac{\hat{n}_T}{\hat{n}_T + n_F} \quad (4)$$

where R represents Recall.

$$P = \frac{TP}{TP + FP} = \frac{\hat{n}_T}{\hat{n}_T + \hat{n}_F} \quad (5)$$

where P represents Precision.

$$MA = \frac{TP + TN}{TP + FN + FP + TN} = \frac{\hat{n}_T + n_T}{\hat{n} + n} \quad (6)$$

where MA represents Mean Accuracy. \hat{n}_T represents the number of trees in the prediction result that can match with the reference data. n_T represents the number of trees in the reference data that can match with the prediction result. \hat{n} represents the number of trees in the prediction result. n represents the number of trees in the reference data.

(2) Evaluation of Location Precision

$$RMSE_{loc} = ||\hat{L} - L||_2 = \sqrt{\frac{1}{n_{match}} \sum_{i=1}^{n_{match}} (\hat{L}_i - L_i)^2} \quad (7)$$

where $RMSE_{loc}$ represents the Root Mean Square Error of the location. \hat{L} represents the location of the tree in the prediction result. L represents the location of the tree in the reference data. n_{match} represents the number of trees that have matching relationship between the prediction result and the reference data.

(3) Evaluation of Basic Feature Prediction

$$RMSE_f = ||\hat{F} - F||_2 = \sqrt{\frac{1}{n_{match}} \sum_{i=1}^{n_{match}} (\hat{F}_i - F_i)^2} \quad (8)$$

where $RMSE_f$ represents the Root Mean Square Error (RMSE) of the prediction results of tree basic features. \hat{F} represents the tree features in the prediction results. F represents the tree features in the reference data.

n_{match} represents the number of trees that have matching relationship between the prediction results and the reference data and do not lack the feature information.

$$Bias_f = \frac{\sum_{i=1}^{n_{match}} (\hat{F} - F)}{n_{match}} \quad (9)$$

where $Bias_f$ represents the bias of the prediction result of tree basic features. \hat{F} represents the tree features in the prediction results. F represents the tree features in the reference data. n_{match} represents the number of trees that have matching relationship between the prediction

results and the reference data and do not lack the feature information.

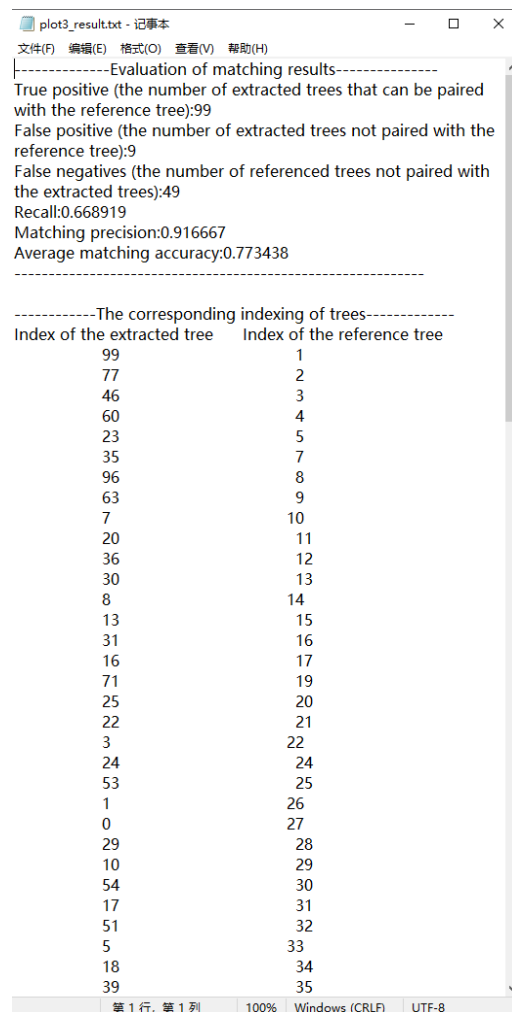
$$RMSE_f\% = \frac{RMSE_f}{\bar{F}} \times 100\% = \frac{\sqrt{\frac{1}{n_{match}} \sum_{i=1}^{n_{match}} (\hat{F}_i - F_i)^2}}{\frac{1}{n_{match}} \sum_{i=1}^{n_{match}} F_i} \times 100\% \quad (10)$$

where $RMSE_f\%$ represents the Relative Root Mean Square Error (RMSE) of the prediction results of tree basic characteristics. \hat{F} represents the tree features in the prediction results. F represents the tree features in the reference data. n_{match} represents the number of trees that have matching relationship between the prediction results and the reference data and do not lack the feature information.

$$Bias_f\% = \frac{Bias_f}{\bar{F}} \times 100\% = \frac{\sum_{i=1}^N (\hat{F} - F)}{\frac{1}{n_{match}} \sum_{i=1}^{n_{match}} F_i} \times 100\% \quad (11)$$

where $Bias_f\%$ represents the Relative Bias of the prediction result of tree

basic features. \hat{F} represents the tree features in the prediction results. F represents the tree features in the reference data. n_{match} represents the number of trees that have matching relationship between the prediction results and the reference data and do not lack the feature information.



```

-----Evaluation of matching results-----
True positive (the number of extracted trees that can be paired
with the reference tree):99
False positive (the number of extracted trees not paired with the
reference tree):9
False negatives (the number of referenced trees not paired with
the extracted trees):49
Recall:0.668919
Matching precision:0.916667
Average matching accuracy:0.773438
-----

-----The corresponding indexing of trees-----
Index of the extracted tree   Index of the reference tree
99                           1
77                           2
46                           3
60                           4
23                           5
35                           7
96                           8
63                           9
7                            10
20                           11
36                           12
30                           13
8                            14
13                           15
31                           16
16                           17
71                           19
25                           20
22                           21
3                            22
24                           24
53                           25
1                            26
0                            27
29                           28
10                           29
54                           30
17                           31
51                           32
5                            33
18                           34
39                           35

```

Figure 3 Output result of "Evaluation of Tree Parameter Prediction".

4.2.2 Evaluation of Stem Curve Prediction

After obtaining the matching relationship between the prediction results and the reference data, the software uses equations (12)-(17) to evaluate the matching results, the location precision, and the tree stem curve

prediction results, respectively. The results are shown in Fig. 4.

(1) Evaluation of Matching Relationship

The evaluation method is the same as that used in the function "Evaluation of Tree Basic Features Prediction".

(2) Evaluation of Location Precision

The evaluation method is the same as that used in the function "Evaluation of Tree Basic Features Prediction".

(3) Evaluation of Stem Curve Prediction

For individual tree, stem curve prediction precision was evaluated using equations (12) and (14):

$$RMSE_i = \sqrt{\frac{1}{m_i} \sum_{j=1}^{m_i} (\hat{d}_i(\hat{z}_{i,j}) - d_i^{interp}(\hat{z}_{i,j}))^2} \quad (12)$$

where 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 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 reference diameter at height $\hat{z}_{i,j}$ obtained by linear interpolation based on the reference data.

$$MAE_i = \frac{1}{m_i} \sum_{j=1}^{m_i} |\hat{d}_i(\hat{z}_{i,j}) - d_i^{interp}(\hat{z}_{i,j})| \quad (13)$$

where i is the index of the tree and j is the index of the diameter in the i -th tree. MAE_i represents the Mean Absolute Error (MAE) of the 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 reference diameter at height $\hat{z}_{i,j}$ obtained by linear interpolation based on the reference data.

$$Bias_i = \frac{1}{m_i} \sum_{j=1}^{m_i} (\hat{d}_i(\hat{z}_{i,j}) - d_i^{interp}(\hat{z}_{i,j})) \quad (14)$$

where i is the index of the tree and j is the index of the diameter in the i -th tree. $Bias_i$ represents the Bias of the 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 reference diameter at height $\hat{z}_{i,j}$ obtained by linear interpolation based on the reference data.

For the plots, the stem curve prediction precision was evaluated using equations (15)-(17):

$$\overline{RMSE} = \frac{1}{n_{match}} \sum_{i=1}^{n_{match}} RMSE_i \quad (15)$$

Where \overline{RMSE} represents the Average Root Mean Square Error (RMSE) of all trees, and n_{match} represents the number of trees that have matching relationship between the prediction result and the reference data and do not lack the feature information. $RMSE_i$ represents the Root Mean Square Error of the stem curve of the i -th tree.

$$\overline{MAE} = \frac{1}{n_{match}} \sum_{i=1}^{n_{match}} MAE_i \quad (16)$$

where \overline{MAE} represents the Average Mean Average Error (MAE) of all trees, and n_{match} represents the number of trees that have matching relationship between the prediction result and the reference data and do not lack the feature information. MAE_i represents the Mean Average Error of the stem curve of the i -th tree.

$$\overline{Bias} = \frac{1}{n_{match}} \sum_{i=1}^{n_{match}} Bias_i \quad (17)$$

where \overline{Bias} represents the Average Bias of all trees, and n_{match} represents the number of trees that have matching relationship between the prediction result and the reference data and do not lack the feature information. $Bias_i$ represents Bias of the stem curve of the i -th tree.

```

stemCurve.txt - 记事本
文件(F) 编辑(E) 格式(O) 查看(V) 帮助(H)
|-----Evaluation of matching results-----|
True positive (the number of extracted trees that can be paired
with the reference tree):4
False positive (the number of extracted trees not paired with the
reference tree):1
False negatives (the number of referenced trees not paired with
the extracted trees):0
Recall:1
Matching precision:0.8
Average matching accuracy:0.888889
-----

-----The corresponding indexing of trees-----
Index of the extracted tree   Index of the reference tree
2                             0
3                             1
4                             2
0                             3
-----

-----Positional precision-----
Root Mean Square Error (RMSE) of distance:0.187083
-----

-----Evaluation of stem curve precision (all trees)-----
Root Mean Square Error of diameter for all trees:0.1
Mean Absolute Error of diameter for all trees: 0.1
Bias of diameter for all trees: -5.55112e-17
-----

-----Evaluation of stem curve precision(per tree)-----
---Root Mean Square Error of diameter per extracted tree---
Index of the extracted tree   Root Mean Square Error
2                             0.1
3                             0.1
4                             0.1
0                             0.1
Mean of Root Mean Square Error: 0.1
STandard Deviation of Root Mean Square Error: 1.8411e-16
Mean of Relative Root Mean Square Error(%): 1.77938
-----

-----Mean Absolute Error of diameter per extracted tree-----
Index of the extracted tree   Mean Absolute Error
2                             0.1
3                             0.1
-----
第 1 行, 第 1 列    100%  Windows (CRLF)  ANSI

```

Figure 4 Output result of "Evaluation results of Stem Curve Prediction".

5. Operational Notes

5.1 Installation and Initialization

The software is green software. Just open the zip package and double-click

 **Feature Evaluation.exe** to enter the main window of the system, which is

shown in Figure 5:

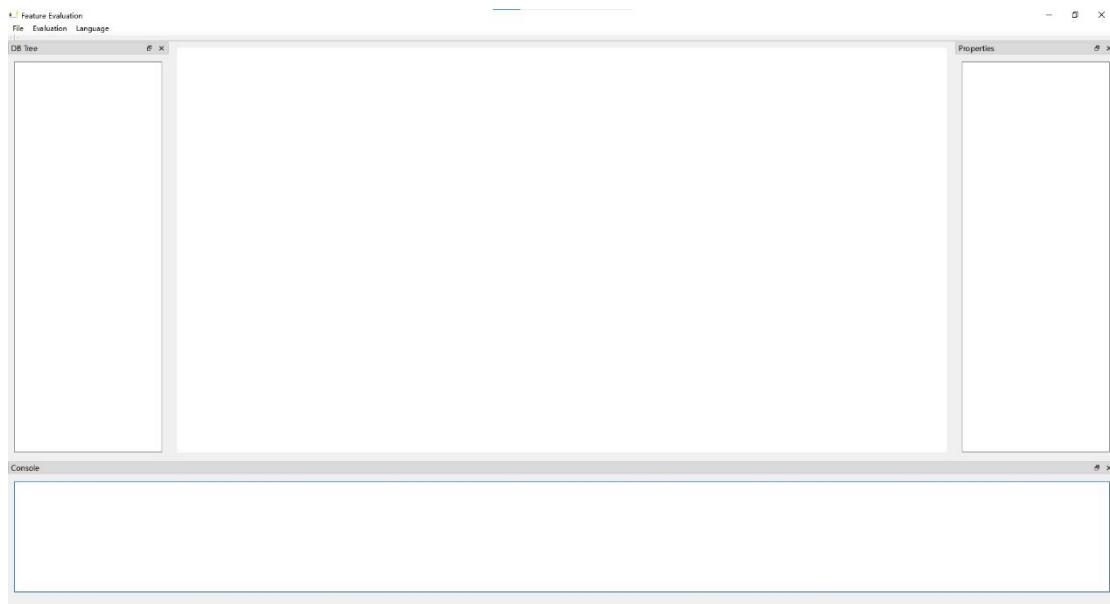

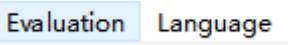
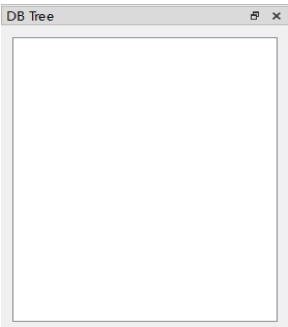
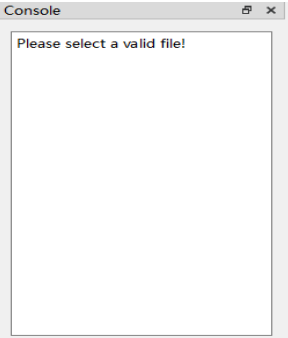
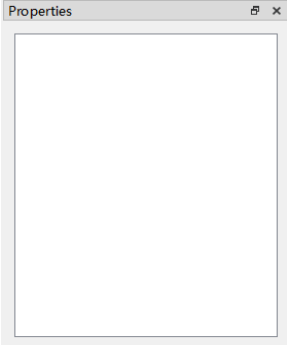


Figure 5 The main window of the tree evaluation software.

5.2 Software Widget Description

Widget	Name	Function Description
 Feature Evaluation	Software name	None
	Menu bar	None
	DB Tree	Display point cloud data and position data, including right-click menu.
	Console	Output Operation Information

	Properties	Display data properties information (This content is not developed yet)
---	------------	---

5.3 Usage Guide

5.3.1 Evaluation of Basic Feature Prediction

The Dialog of "Evaluation of Basic Feature Prediction" is displayed by clicking "Evaluation \ Evaluation of Basic Feature Prediction", as shown in Figure 6.

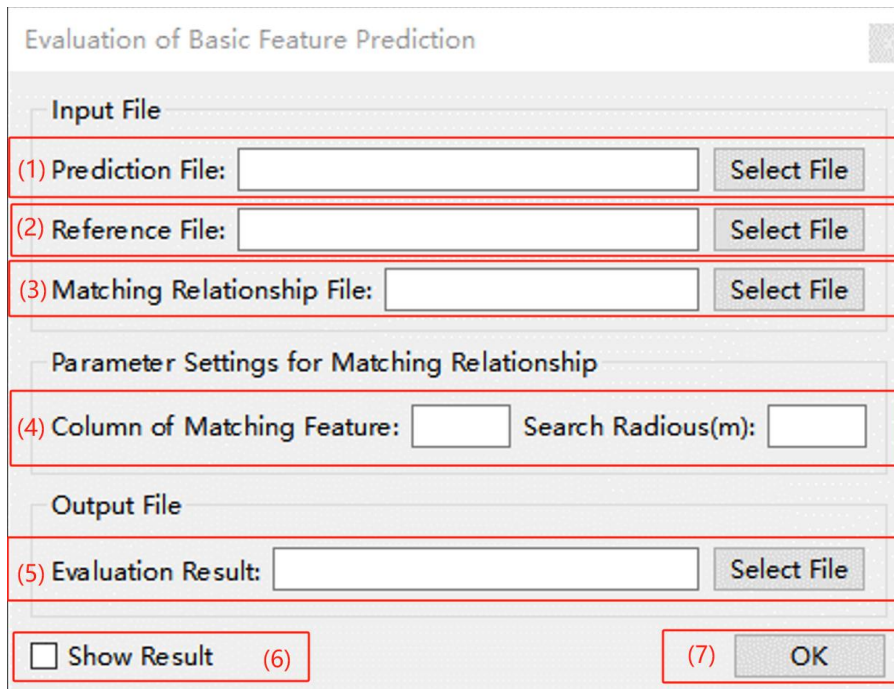


Figure 6 Dialog of " Evaluation of Stem Curve Prediction ".

(1) Click "Select File" to obtain the input path of the " Prediction File".

- (2) Click "Select File" to obtain the input path of the " Reference File".
- (3) If a matching relationship file exists, click "Select File" to obtain the input path of the "Matching Relationship File".
- (4) Input the " Column of Match Feature and "Search radius (m)".
- (5) Click "Select File" to obtain the input path of the " Evaluation Result".
- (6) Select "Show Result". If selected, after the function " Evaluation of Basic Feature Prediction" is completed, the matching results and graphs will be displayed, as shown in Figure 7. The matched and unmatched data will be displayed in the main window as a dock table, which can be dragged to different places by the user. At the same time, the 3D display window will use spheres to represent the coordinates of each tree, and the matched data will relate to line. The green sphere represents the coordinates of the predicted tree for the completed match, the yellow sphere represents the coordinates of the reference tree for the completed match, and the incomplete matched data is represented by the red sphere.
- (7) Click "OK" to evaluate the results of Tree Basic Feature Prediction.

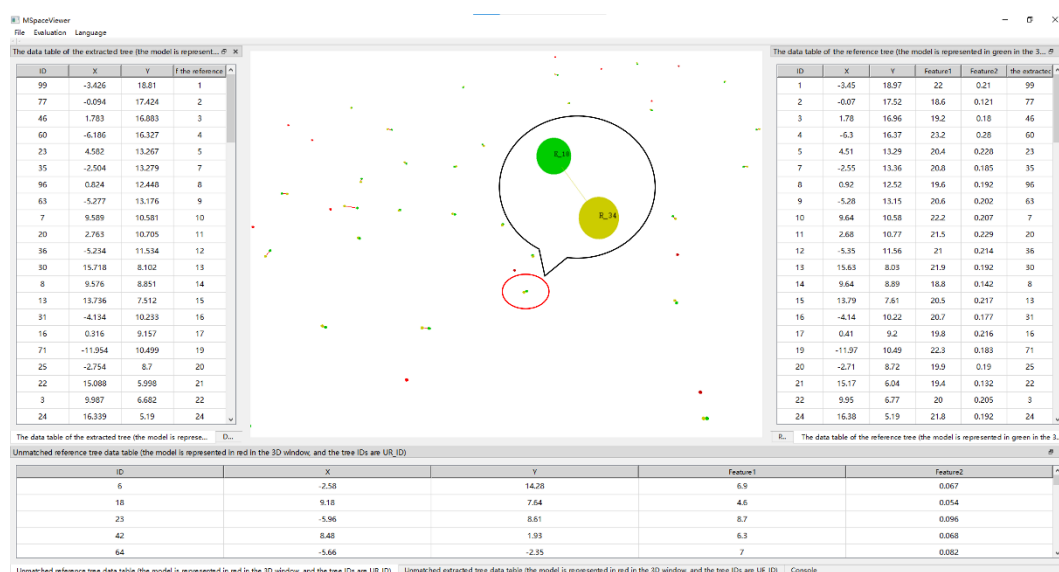


Figure 7 Matching results and graphs.

5.3.2 Evaluation of Stem Curve Prediction

The Dialog of "Evaluation of Stem Curve Prediction" is displayed by clicking "Evaluation \ Evaluation of Stem Curve Prediction", as shown in Figure 8.

Evaluation of Stem Curve Prediction

Input File

(1) Prediction File:

(2) Reference File:

(3) Matching relationship:

Parameter Settings for Matching Relationship

(4) Extraction Height of DBH and Coordinates(m): Search Radius(m):

Output File

(5) Evaluation Result:

(6)

Figure 8 Dialog of "Evaluation of Stem Curve Prediction".

(1) Click "Select File" to obtain the input path of the " Prediction File".

- (2) Click "Select File" to obtain the input path of the " Reference File".
- (3) If a matching relationship file exists, click "Select File" to obtain the input path of the "Matching Relationship File".
- (4) Input the "Extraction Height of DBH and Coordinates (m)" and "Search radius (m)".
- (5) Click "Select File" to obtain the input path of the " Evaluation Result".
- (7) Click "OK" to evaluate the results of Evaluation of Stem Curve Prediction.

● Appendix I

Example of Data Format for Evaluation of Tree Basic Feature

Prediction

1. Format of Reference File

ID	X	Y	Z	Feature 1	Feature 2	Feature 3	Feature 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. Format of Extracted File

(1) Extracted File with X, Y coordinates and Feature 1.

1		5.3		6.2	<i>NaN</i>	10.6
2		8.3		1.6	<i>NaN</i>	6.2
3		4.8		3.6	<i>NaN</i>	9.8
⋮		⋮		⋮	⋮	⋮

- **Example (1) is missing Z coordinate data. In order to keep Feature 1 in the Extracted File and the Reference File in the same column (i.e., column 5), so the data in column 4 of the Extracted File are set to *NaN* as fillers.**

(2) Extracted File with X, Y, Z coordinates and Feature 1, Feature 4.

1	9.8	4.3	6.2	8.3	<i>NaN</i>	<i>NaN</i>	10.6
2	4.8	3.6	4.9	5.3	<i>NaN</i>	<i>NaN</i>	6.2

3	6.2	8.5	4.8	8.3	<i>NaN</i>	<i>NaN</i>	9.8
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮

- **Example (2) is missing Feature 2 and Feature 3. In order to keep Feature 4 in the same column (i.e., column 8) in Extracted File and Reference File, the data in columns 6 and 7 of the Extracted File are set to NaN as fillers.**

● Appendix II

Example of Data Format for Evaluation of Stem Curve Prediction

1. Format of Reference File

	ID	Data 1	Data 2	Data 3	
Diameter	1	3.2	3.1	3.0	...
X	1	5.2	5.1	5.2	...
Y	1	4.3	4.2	4.2	...
Height	1	0.6	1.3	1.8	...
Diameter	2	2.2	2.1	2.0	...
X	2	1.2	1.1	1.2	...
Y	2	2.3	2.2	2.2	...
Height	2	0.6	1.3	1.8	...
⋮	⋮	⋮	⋮		

- The above example of Reference File is the stem curve of two trees.

Rows 1 to 4 represent the stem curve data of the 1st tree, which measures the diameter and horizontal coordinates of the tree at 0.6m, 1.3m and 1.8m, respectively. Rows 5 through 8 represent stem curve data for 2nd tree, which measures tree diameter and horizontal coordinates at 0.6m, 1.3m, and 1.8m, respectively.

2. Format of Extracted File

(1) The stem curve data for two trees (where the first tree is missing the diameter at 1.3m. The second tree is missing coordinate at 1.7m).

1	3.2	<i>N</i>	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	2.0	...
2	1.2	1.1	<i>N</i>	...
2	2.3	2.2	<i>N</i>	...
2	0.6	1.4	1.7	...
⋮	⋮	⋮		

- The above example of extracted file is the stem curve data of two trees. Rows 1 to 4 represent the stem curve data of the 1st tree, which measures the diameter and horizontal coordinates of the tree at 0.6m, 1.3m, and 1.8m, respectively, but missing the diameter at 1.3m. Rows 5 through 8 represent stem curve data for 2nd tree, which measures tree diameter and horizontal coordinates at 0.6m, 1.4m, and 1.7m, respectively, but missing coordinate data at 1.7m.