

Label3D Maize User Manual

Beijing Research Center for Information Technology in Agriculture

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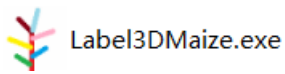
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1. Open the toolkit

Double clicking the “Label3DMAize.exe” file to open the toolkit, and the main interface will popup.



Label3DMAize.exe

Visualization
window

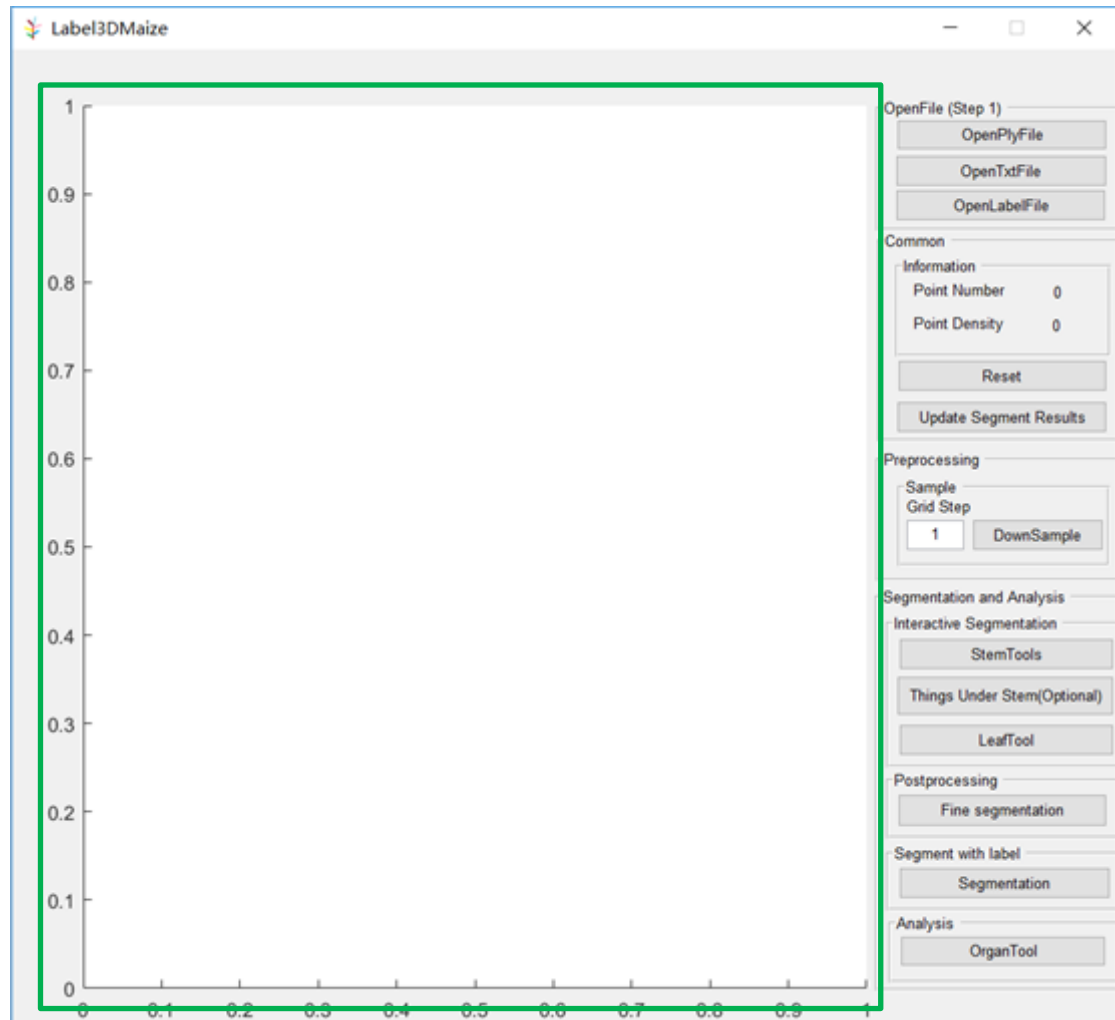


Figure 1. Main Interface of the toolkit.

The function of the main interface.

- Calling sub-interfaces.
- Displaying point cloud information.
- Visualization segmentation results of point clouds.

* Please do not close the main interface while the toolkit is running.

2. Interactive operations in the visualization window

Each sub interface of this toolkit contains a visualization window. In these visualization windows, there are two states: 3DView state and interactive points picking state.

3DView State

“3DView” state is the default state of a visualization window. In this state, users can rotate or zoom the camera by operating the mouse or keyboard.

Rotating mode: When the user presses the "R" key on the keyboard, the camera switches from zooming to rotating mode. Under this mode, pressing and holding the left mouse button will rotate over the x or y-axis, while pressing and holding the middle mouse button to rotate over the z-axis.

Zooming mode: When the user presses the "Z" key on the keyboard, the camera switches from rotating to zooming mode. Pressing and holding the left mouse button will zoom in or out. Pressing and holding the middle mouse button will move the plot.

Interactive points picking state

In some sub interfaces, interactive points picking can be realized in visualization window. Under this state, left mouse button can be used to select points.

On the embedded dialog of these sub-interfaces, there are radio buttons for switching between the 3DView and interactive points picking state.

3. Relationship between organ instance color and the order of organ instance label

In label3DMAize toolkit, each segmented organ instance corresponds to a label value. The label values are integers greater than 0. In order to visually represent the segmentation results, organ instances are represented via different colors. In practice, the color assigned to each organ is coincident to its order of organ label (See Figure 2). For example, suppose that the current window displays three organs: A, B, and C, with label values of 10, 5, and 12, respectively. According to the ascending order of their label value, the re-ordered organ sequence is B, A, C. Thus, the label orders of B, A, and C are 1, 2, and 3. Their corresponding colors are red, green, and blue.



Figure 2. Corresponding colors for organ instance with different labels.

4. Main operation steps

- 1) Importing point cloud file.
- 2) Point cloud down sampling. (Optional)
- 3) Stem segmentation using “Interactive Segmentation—Stem Tools”.
- 4) Pot removal. (Optional)
- 5) Coarse segmentation using “Interactive Segmentation—Leaf Tool”.
- 6) Fine segmentation using “Post processing—Fine Segmentation”.
- 7) Saving segmentation files by “Analysis—Organ Tool”.
- 8) Sample-based segmentation using “Segment with label—Segmentation”.

5. Importing point cloud file

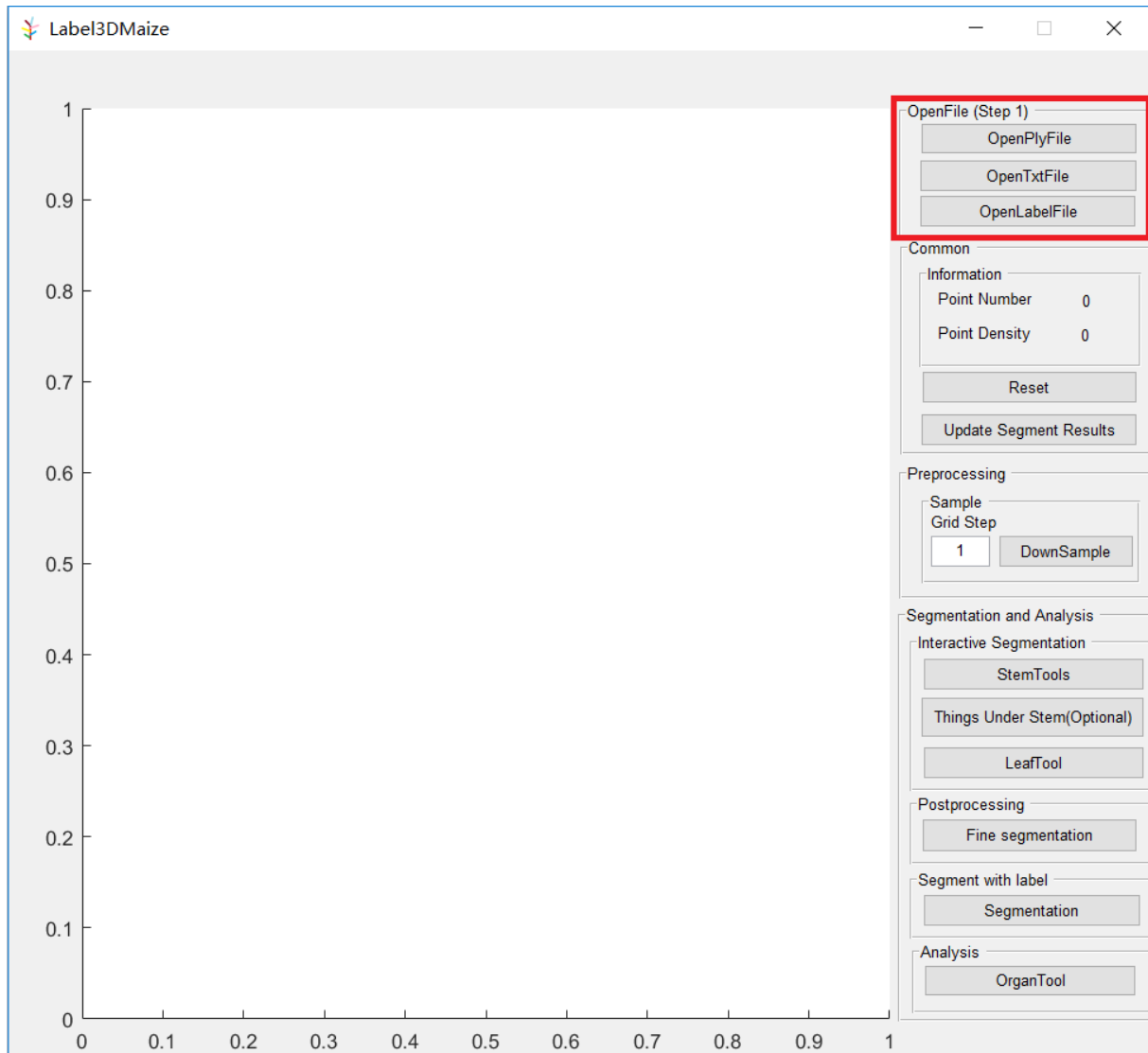


Figure 3. File importing buttons on the main interface.

OpenPlyFile button: This button is used to load the "ply" format point cloud files.

OpenTxtFile button: This button is used to load the "txt" format point cloud files. Each row of the data in 'txt' format is [X Y Z R G B] (Figure 4), or [X Y Z]. Here, X, Y, and Z are the 3D coordinates of the points, and R, G, and B are the r, g, and b colors of the points.

```
0.0173940 -12.6753226 -289.7677124 0.255 0.192 0.192
0.0573940 -11.7953233 -289.7776961 0.204 0.165 0.156
```

Figure 4. Example of 'txt' format points.

OpenLabelFile button: This button is used to load the label file. "Label file" is a user defined file format, which is stored in 'txt' text format. Each row in this file format is [X Y Z L]. Here, L is the instances label, which is an integer greater than 0.

```

10.087797 13.680694 -548.917174 11
13.307796 14.985694 -548.937202 11
15.237796 15.950695 -549.237192 11
17.031129 16.857360 -549.280504 11

```

Figure 5. Example of the label file.

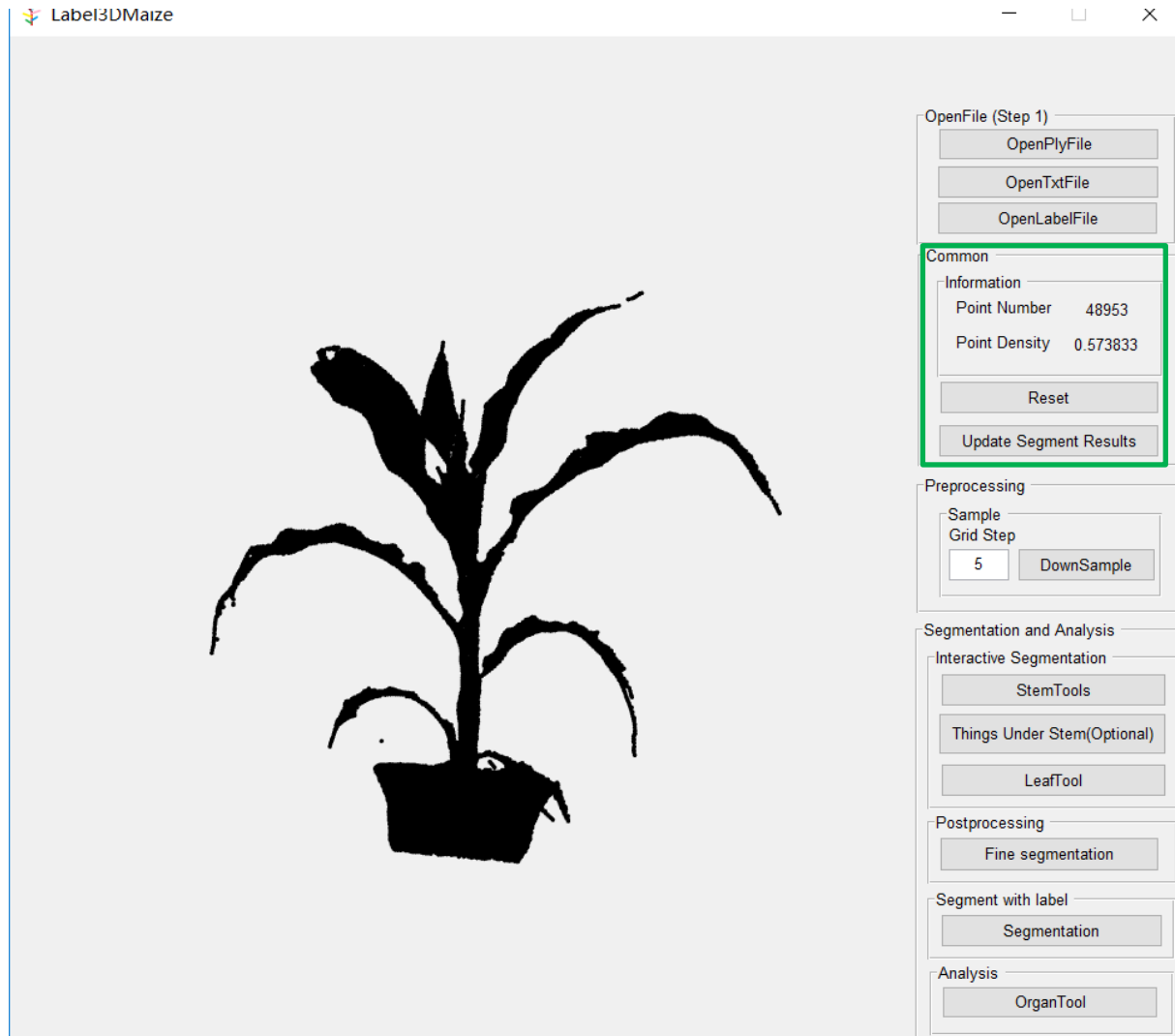


Figure 6. Basic information and operations of the imported point cloud.

After a point cloud file has been imported, the point cloud is shown in the visualization window. In addition, the basic information of the imported point cloud will be shown in the “Common” area on the embedded dialog of the main interface, including “Point number” and “point density”.

Functions of the two button in “Common” area.

Reset button: This button resets the point cloud to its original imported state, regardless of the subsequent procedures.

Update Segment Results: In the visualization window, the segmentation results of the point cloud will be updated visually.

6. Point cloud down sampling

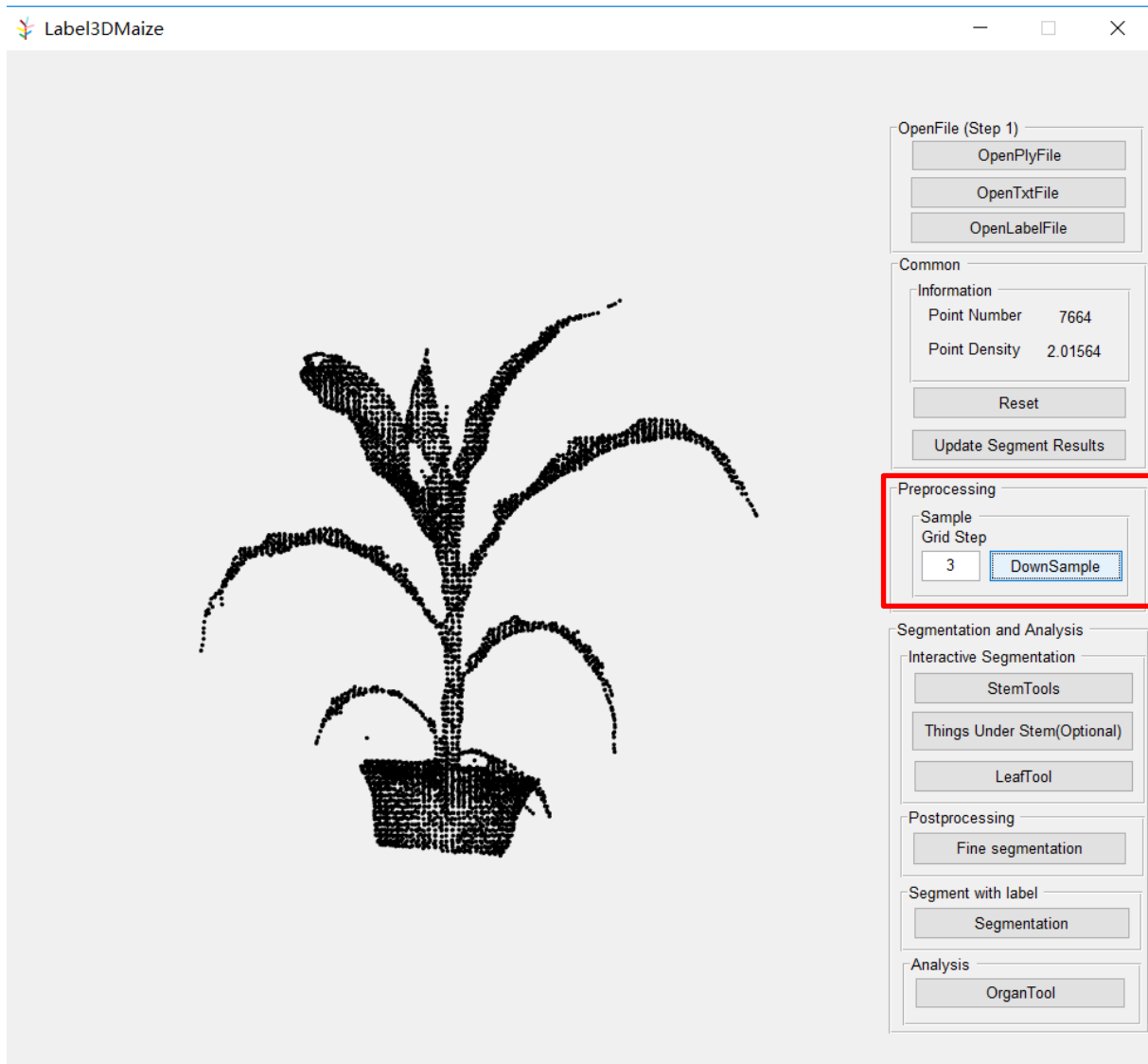


Figure 7. Point cloud down-sampling operation area.

DownSample button: It down-samples the current point cloud using a given grid filter.

Grid Step edit box: It specifies the size of a 3D box. Points within the same box are merged to a individual point.

*We strongly recommend to reduce the number of points less than 15000, otherwise the segmentation procedures will be rather slow.

7. Stem segmentation using “Stem Tools”

Pressing the “StemTools” button on the main interface to popup the stem tool sub-interface.

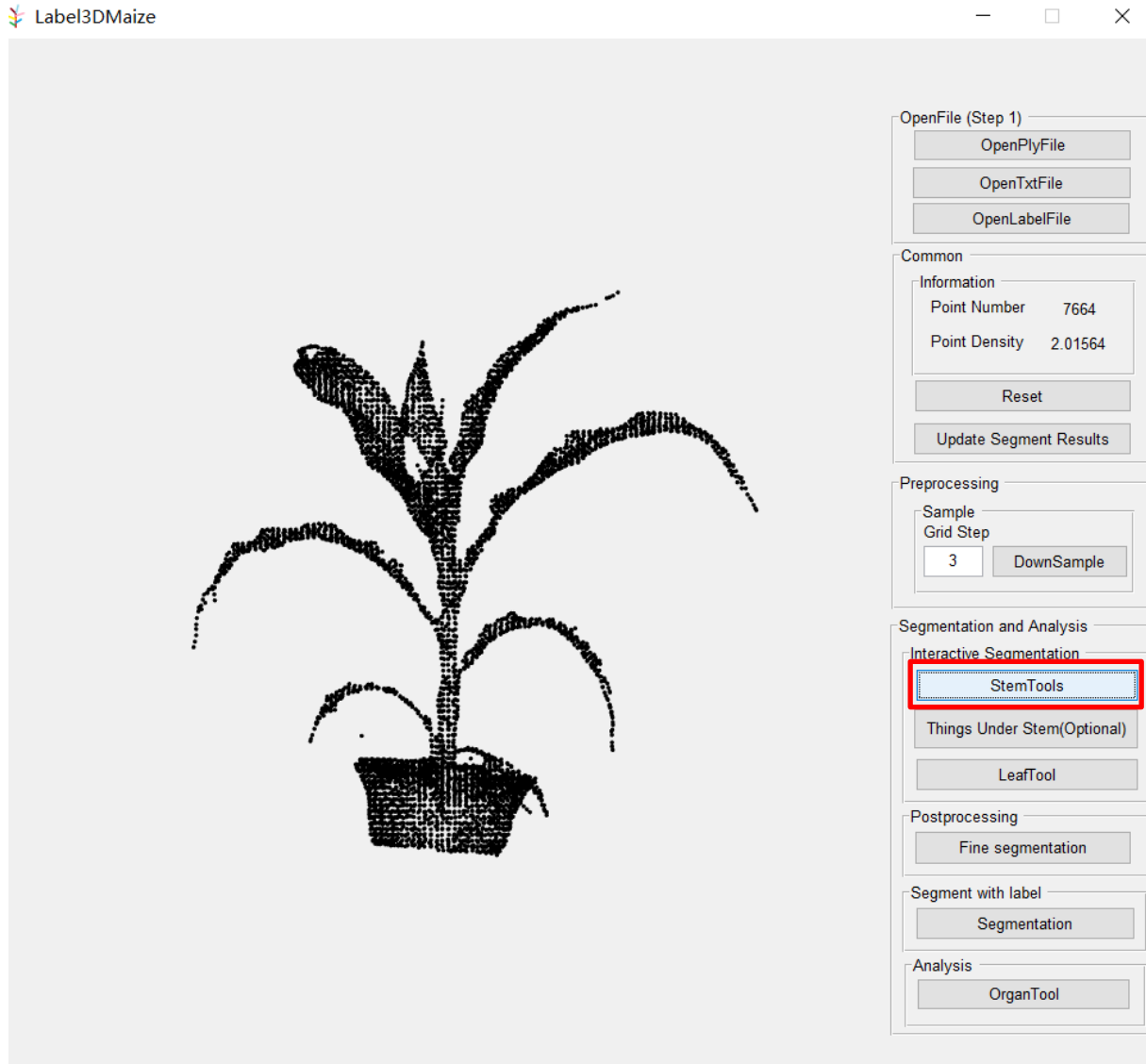


Figure 8. The “StemTools” button on the main interface.

Operation steps

1) Seed points selection at the bottom of stem.

- Pressing the “SelectBottomStem” radio button (Figure 9-2), then the visualization window will switch to the interactive points picking state. Users could pick up points using the left mouse button.
- After selecting a point, click the “Add” button (Figure 9-4) to add the selected point to the seed point sets, and the color of the selected point will turn red.
- Users can select multiple points, and the final seed point s_0 at the bottom of stem is the median point of all the

selected points.

- Points with dark-red color are used to visually indicate the stem radius parameters r_1 in the manuscript. The distance between the dark-red points and s_0 is less than r_1 .
- Clicking the “Clear” button (Figure 9-5) clears all the selected points from the seed point set. All red and dark-red points turn to black.

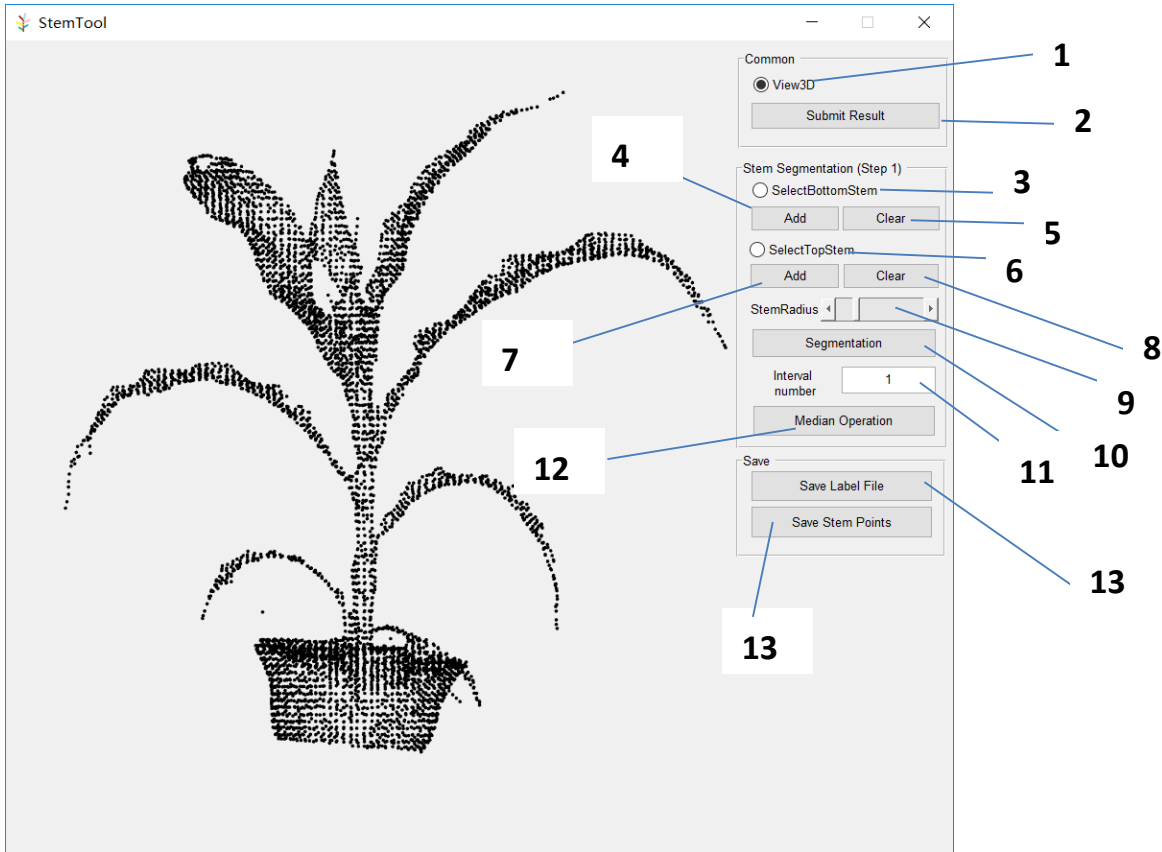


Figure 9. The stem tool sub-interface.



Figure 10. Illustration of bottom seed point selection.

2) Seed points selection at the top of stem

- Pressing the “SelectTopStem” radio button (Figure 9-6), then the visualization window will switch to the interactive points picking state. Users could pick up points using the left mouse button.

- After selecting a point, click the “**Add**” button (Figure 9-7) to add the selected point to the seed point set, and the color of the selected point will turn into blue.
- Users can select multiple points, and the final seed point s_n (see the manuscript) at the top of stem is the median point of all the selected points.
- Points colored with dark-blue visually indicates the stem radius parameters r_1 . The distance between the dark-blue points and s_n is less than r_1 .
- Clicking the “**Clear**” button (Figure 9-8) clears all the selected points from the seed point set. And all blue and dark-blue points turn to black.



Figure 11. Illustration of top seed point selection.

3) Stem radius adjustment

The **StemRadius slider**(Figure 9-9) can be used to adjust the radius parameter r_1 in the manuscript. Larger r_1 corresponds to a thicker stem. Dark-blue and dark-red points offers a visual way for the users to adjust this parameter (Figure 12).

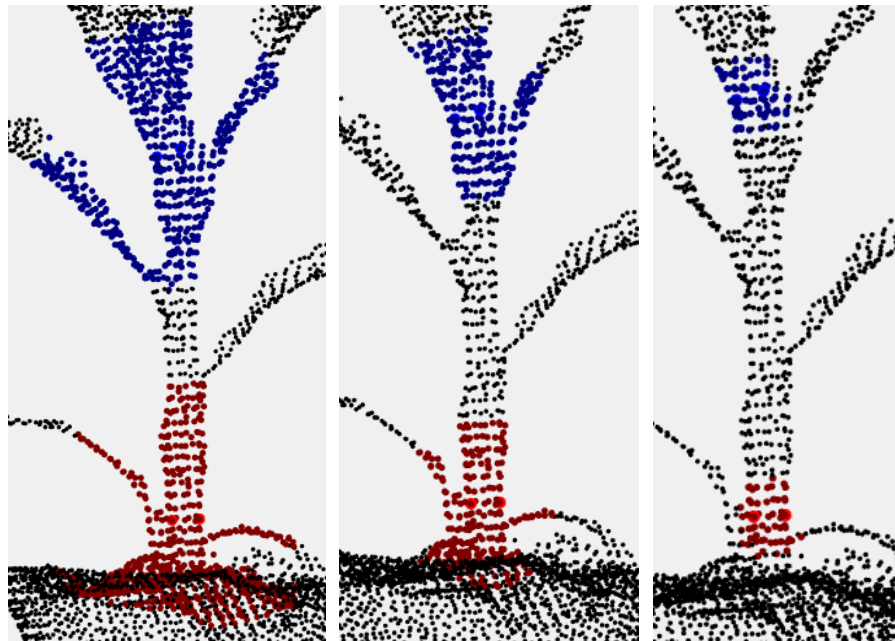


Figure 12. Seed points selection results with different r_1 .

4) Segmentation

The stem points can be segmented by clicking the **Segmentation button** (Figure 9-10) after the seed points were selected. The segmented stem point cloud is visualized in green in the toolkit.



Figure 13. An example of segmented stem.

5) Median operation (optional)

Because the maize stem gradually thins from the bottom to top, a uniform radius r_1 may generate over segmentation, i.e., classifying the points of other organs into the stem. Besides, the region growing algorithm in our paper also over segments points in some regions at the bending of the stem. Therefore, a simple median operation is integrated in the toolkit to eliminate the over segmented points.

User could enter the number of segments of the stem in the **edit box “interval number”** (Figure 9-11). After that, clicking the **“Median Operation button”** (Figure 9-12) and median operations is performed once. Users can perform median operations multiple times.

6) Stem segmentation result submission

*After the segmentation of the stem point cloud, users have to click the **“Submit Result” button** (Figure 9-2) , so that the operation results in this sub-interface can be synchronized to the main interface.

7) Segmentation result saving (optional).

Users can save the result of stem segmentation. The first way is to save as a label file by clicking the **“Save Label File” button**. In the label file, the label of the stem points is 1, and the label of other points is 2. The second way is to save the stem points into a “ply” file by clicking the **“Save stem points” button** (Figure 9-14).

8) 3DView State

During the process of stem segmentation, users can switch the visualization window to “3DView mode” by clicking on the **radio button “View3D”** (Figure 9-1), to facilitate interactive point picking operations.

8. Pot removal (Optional)

After stem segmentation, if the input point cloud of maize shoot contains a pot, users can click the **“Things Under Stem”** button in the main interface to remove the pot point cloud.

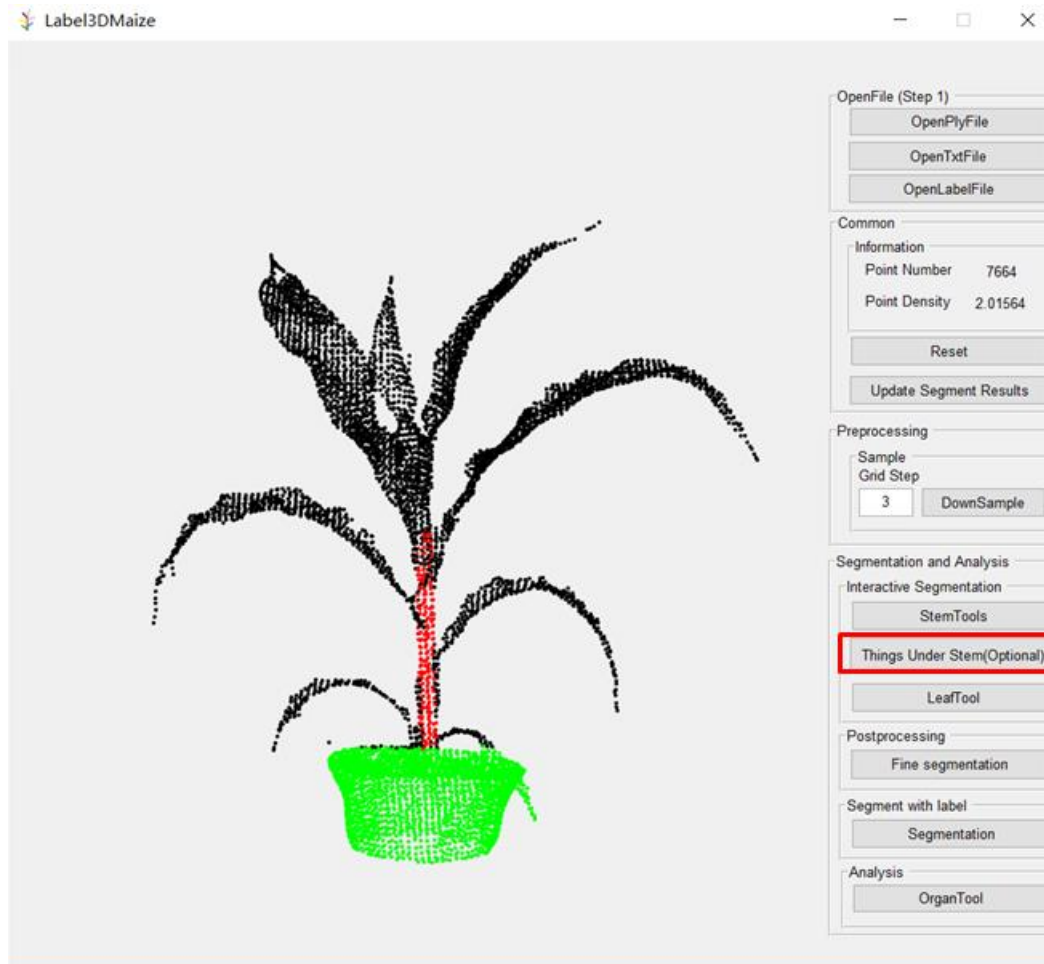


Figure 14. Pot removal interface.

9. Coarse segmentation using “Interactive Segmentation—Leaf Tool”

The coarse segmentation sub-interface could be popup by clicking the “**LeafTool**” button in main interface.

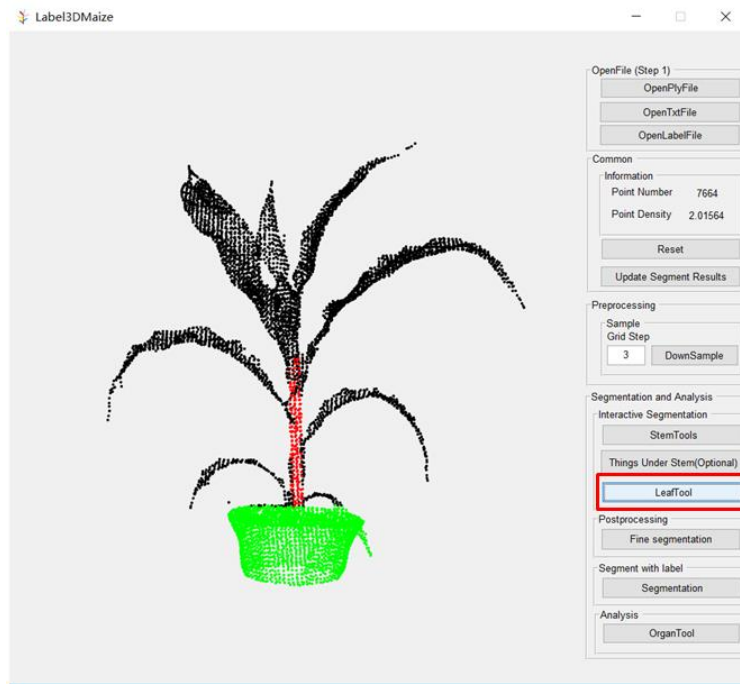


Figure 15. Coarse segmentation sub-interface triggered illustration.

Operation steps

1) Select the organ seed points

After stem segmentation, the point cloud of maize shoots was spatially divided into several relatively discrete organs (excluding the stem). The highest point of each organ was regarded as the seed point. There are two methods to select the seed points. The first is manual interactive selection, the other is automatic selection. We suggest that users use manual interaction to select seed points.

The process of manual interactive selection

- When clicking the **radio button “Select peak”** (Figure 16-5), the visualization window will switch to the Interactive state. The users pick up points using left mouse button.
- After selecting a point, click the **“Yes” button** (Figure 16-6) to add the point as the seed point for a organ, and the selected point will turn red .
- If there is a wrong point to delete, the user can click **radio button “Select peak”** (Figure 16-5). After that, the user

selects a red point (the selected seed point) and then clicks the **“Yes” button** (Figure 16-7), which is no longer a seed point. If the point selected by the user is not a seed point, the toolkit will automatically find the seed point closest to the point and delete it. The deleted point changes from red to black.

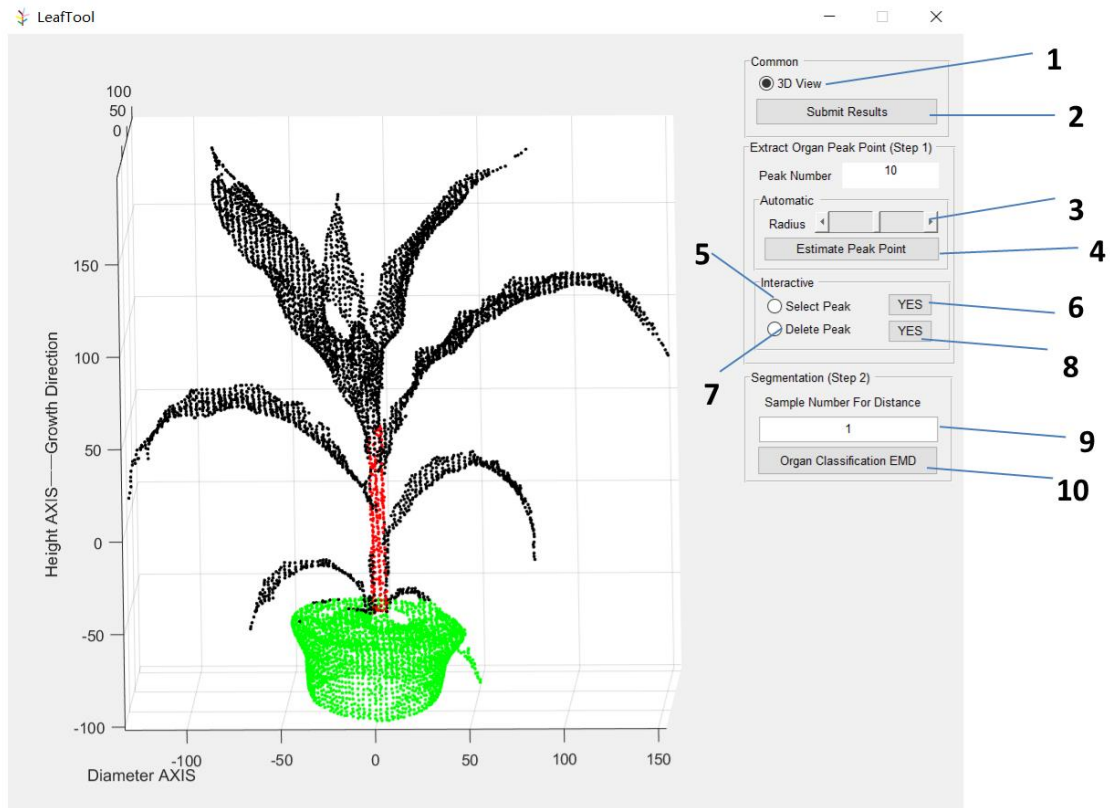


Figure 16. The LeafTool sub-interface for coarse segmentation.

*** The seed point of each organ is the highest point of this organ. Of course, users only need to select points in the highest region as much as possible.

*** *In this toolkit, the label of stem point cloud is 1 by default, while the labels of other organs are determined by the order of selecting seed points by default. For example, in this step, if the seed point of the lowest leaf is selected first, then the label of this leaf is 2 by default.

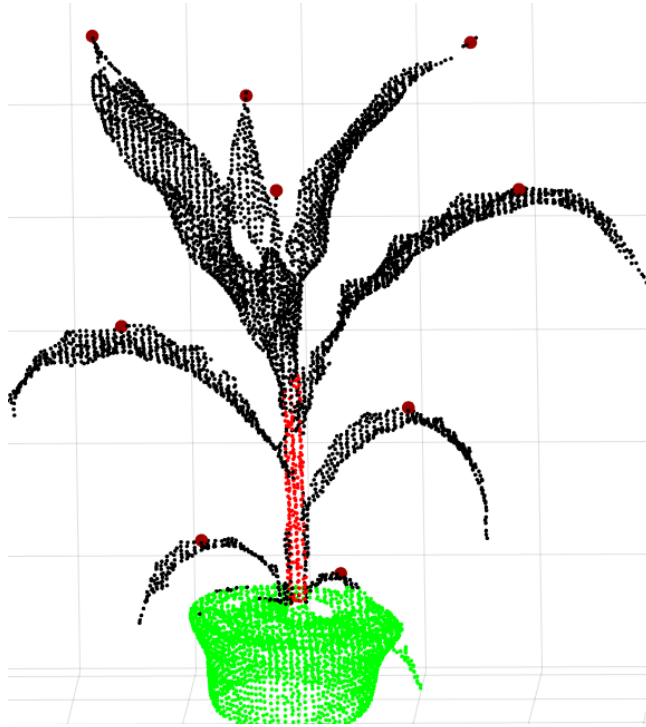


Figure 17. Seed points selection of organ instances

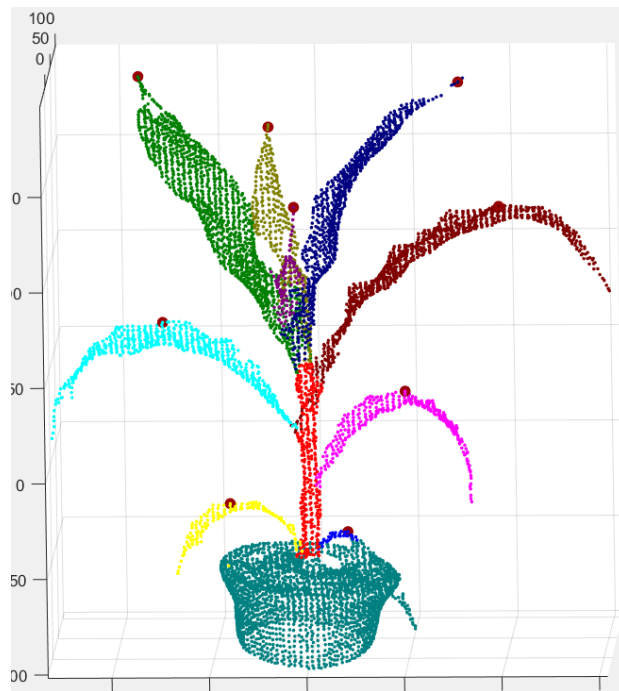


Figure 18. Visualization of a coarse segmentation result

The process of automatic selection

- Adjust radius parameter r_2 in our paper using the “**Radius slider** (Figure 16-3)”.
- Click the “**Estimate Peak Point button** (Figure 16-4)” to extract seed points.
- If the extracted seed points are incomplete or have errors, we can also use manual interaction to modify them.

2) Segmentation

- Click the **“Organ Classification EMD button (Figure 16-10) ”** to segment the organ points. Point clouds of different organ instances are represented by different colors.
- User can adjust the sample number parameter in **“Sample Number for Distance Edit box (Figure 16-9)”** . The parameter is an integer greater than 1. The default value of this parameter is 1.

3) **Submit Result**

*After the segmentation of coarse stem point cloud, the user must click the **“Submit Result” button (Figure 16-2)** , so that the operation results in this sub interface can be synchronized to the main interface.

4) **3DView State**

During the segmentation process, users can switch the visualization window to **“3DView mode”** by clicking the **radio button “View3D” (Figure 16-1)**, so that users can change the viewpoint interactively.

10. Fine segmentation using “Postprocessing—Fine Segmentation”

The user clicks the “**Fine segmentation**” button to start fine segmentation in main interface. A “RefineSegmentation” dialog box will pop up. We call this dialog box “**Main RefineSegmentation**” dialog box.

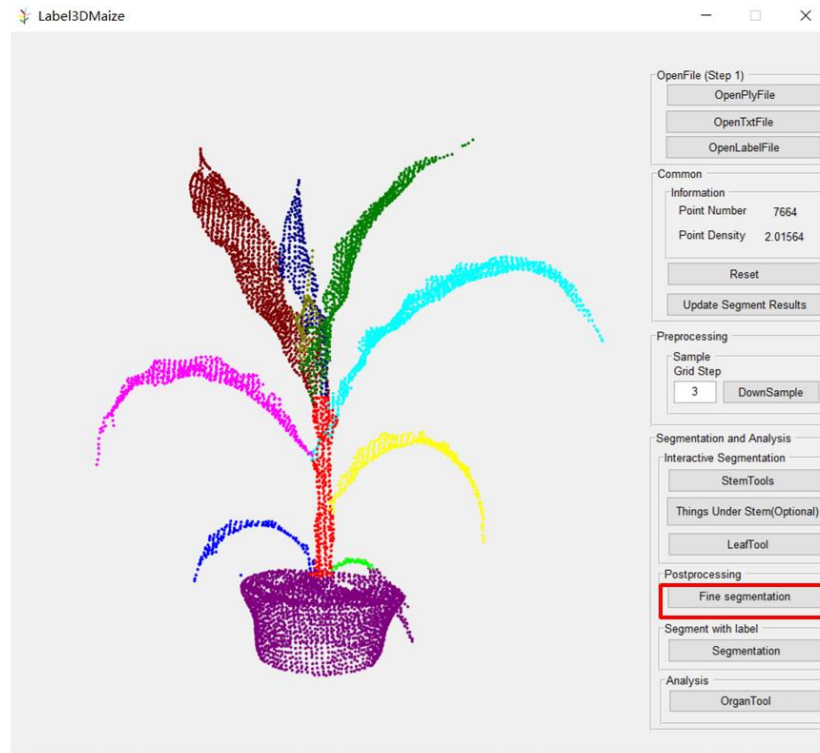


Figure 19. Fine segmentation sub-interface triggered illustration.

Operation steps

1) Organ instances selection

- When clicking the “**SelectOrgan**” radio button (Figure 20-3) , the Visualization Window will switch to the interactive state.
- After selecting a point, click the “**Yes**” button (Figure 20-6) to select the point of an organ, and the instance of the organ is selected. Then, the color of the organ will turn black.
- Users need to select two or more organ instances.
- If user need to reselect organ instance, click “**Reset**” button (Figure 20-5).

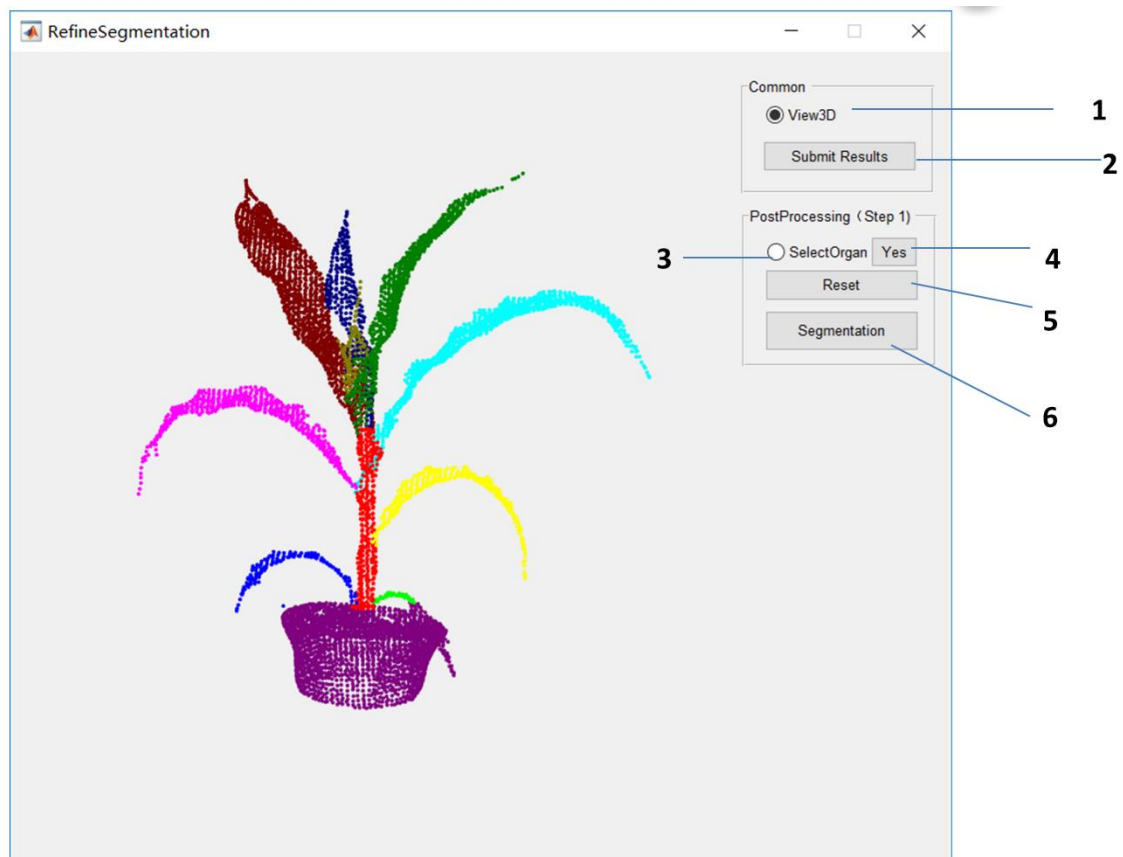


Figure 20. The sub-interface for fine-segmentation.



Figure 21. The color of selected organ instances turns into black.

2) Call Sub RefineSegmentation dialog box

Clicking the “**Segmentation button** (Figure 20-6)” to perform fine segmentation. A new “**Refinesegmentation**” dialog box as shown in the figure below will pop up. We call this dialog “**Sub RefineSegmentation dialog box**”. Users can interactively refine segmentation in this sub interface. In this sub interface, we only deal with the selected organ point cloud.

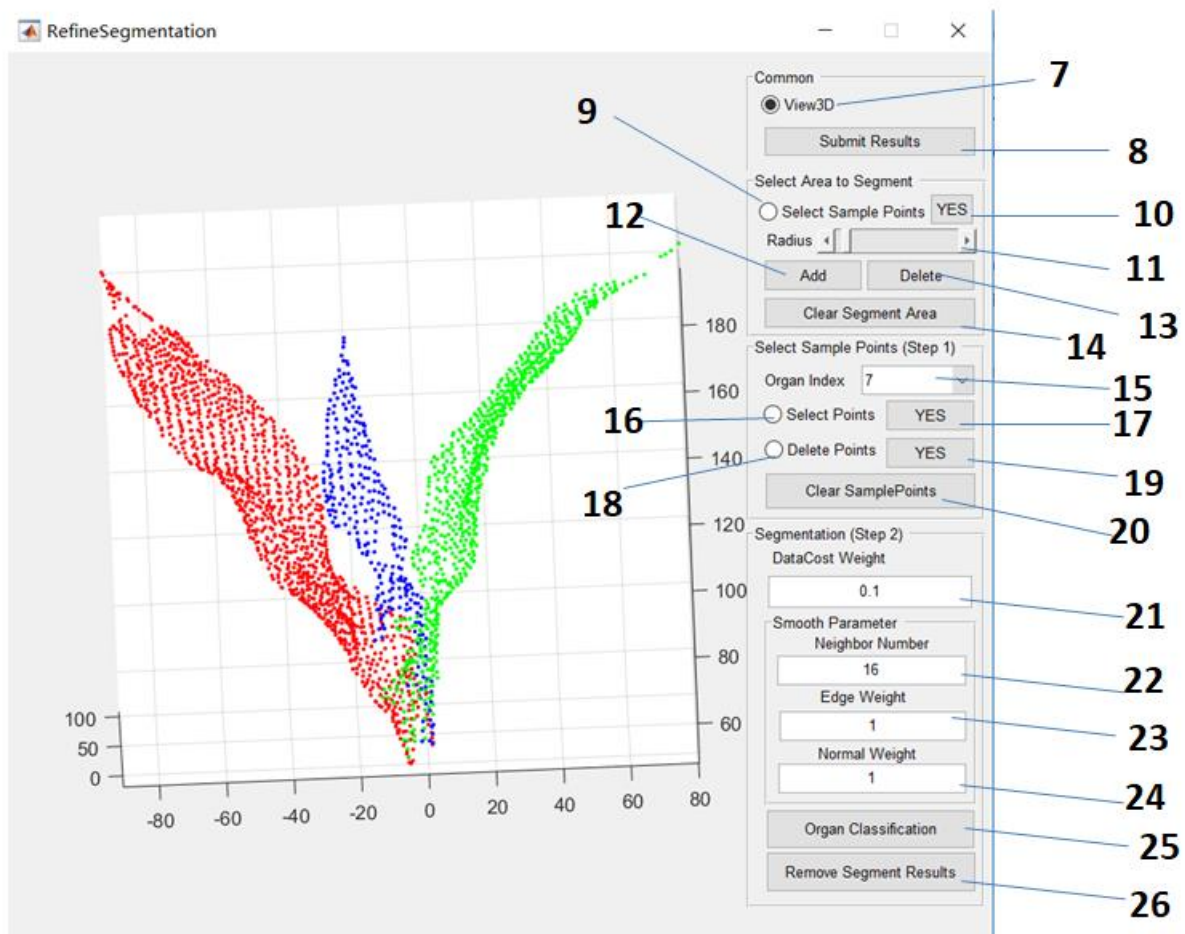


Figure 22. The Sub Refine-Segmentation dialog box.

3) Select the region of interest to segment

- Click the “**Select sample points**” radio button (Figure 22-9) , the Visualization Window will switch to the interactive state.
- Click the “**Yes button** (Figure 22-10)” to select a point P .
- Adjust the radius parameter using the “**Radius**” slider (Figure 22-11), all points whose distance point P is less than the radius value will turn grey, and these points are to be selected, we call these points “**candidate points**”

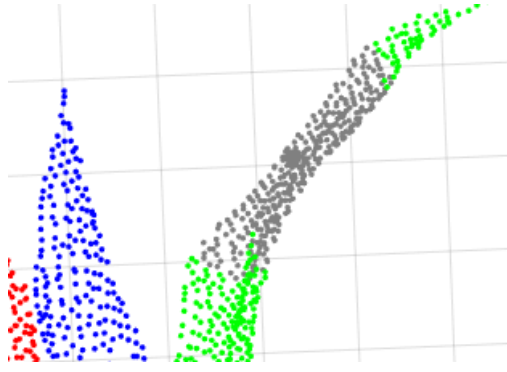


Figure 23. Candidate points selection.

- Click the “**Add**” button (Figure 22-12) to set all the “**candidate points**” to be “**interest points**” to be segment. In our paper, these **interest points** were represented by \emptyset_u . The **interest points** turn black.

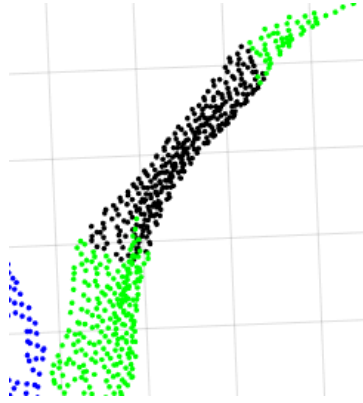


Figure 24. **Interest points**

- We can also remove points from interest points. After getting the **candidate points**, we can click the “**delete**” button(Figure 22-13) . If the candidate points contain interest points, these points will be removed from interest points \emptyset_u .
- We can also clear all the interest points by clicking the “**Clear Segment Area**” button (Figure 22-14).

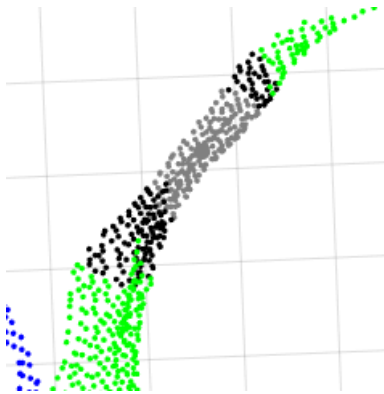


Figure 25. The candidate points(gray) contains the interest points.

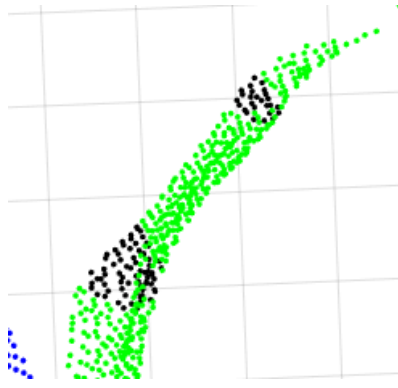


Figure 26. Remove these candidate points.

4) Select the seed points from interest points

- Select a specific organ instance L through the **“Organ Index” drop-down box**(Figure 22-15). The value in the drop-down box is the label value of the organ to be segmented.
- Click the **“Select Points” radio button** (Figure 22-16). The Visualization Window will switch to the interactive state.
- After select a point P using left mouse, click the **“Yes button**(Figure 22-17)” to set P as a seed point of organ instance L . The color of this seed point is the same with the color of the organ instance L .
- Users can select multiple seed points for each organ or not to select seed points for organs.

5) Delete the seed points.

- If the user wants to delete the selected seed points from organ L , the user needs to select this organ instance through the **“Organ Index” drop-down box**(Figure 22-15).
- Click the **“Delete radio button**(Figure 22-18)”, the Visualization Window will switch to the interactive state.
- After select a point P using left mouse , click the **“Yes button**(Figure 22-19)” to delete a point P from selected seed points of organ instance L . The color of this seed point turn black.
- All seed points of organ L can be cleared by clicking the button **“Clear SamplePoints button**(Figure 22-20)”

6) Classification

- Users adjust the parameters in **“DataCost Weight edit box** (Figure 22-21)” ,**“Neighbor Number edit box** (Figure 22-22)”, **“Edge Weight edit box** (Figure 22-23)” and **“Normal Weight edit box** (Figure 22-24)” respectively. The larger the value of dataCost weight, the greater the impact of user seed points on segmentation results.
- Click the **“Organ Classification button** (Figure 22-25)” to classify the interest points by α -expansion MRF.
- Click the **“Remove Segment Results**(Figure 22-26)” to remove the classification result.

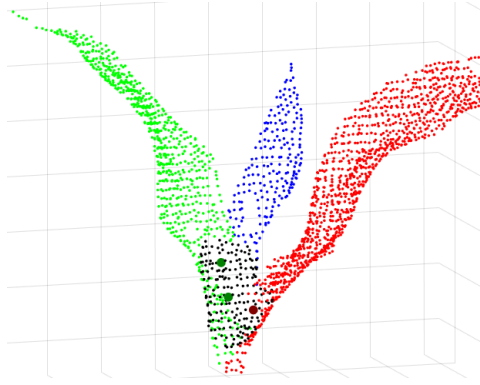


Figure 27. Select seed points

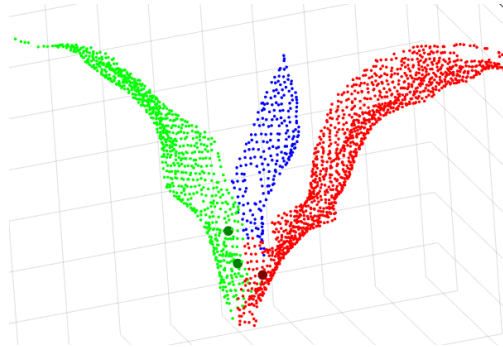


Figure 28. Classification result

7) **Submit the classification result**

Steps 3 to 6 can be performed several times until satisfactory classification results are obtained. Finally, click the “Submit Result (Figure 22-8) button” to submit the results obtained in the “sub refine segmentation dialog box” to the “Main refine segmentation dialog box”. After that, the user can close the “sub refine segmentation dialog box”.

8) **Submit the refine segmentation result**

Return to the “Main refine segmentation dialog box”. Steps 1 to 7 can be performed several times until satisfactory refine segmentation results are obtained. Finally, click the “**Submit Result button** (Figure 22-2)” to submit the results to the “main interface”. After that, the user can close the “Main refine segmentation dialog box”.

Additional instructions to Chapter 10 (Update)

Today is December 30, 2020, we have updated the fine segmentation function in the software. We find that compared with the MRF method used in our paper, it will save more time to provide users with more direct segmentation method in actual operation. We keep all the functions in the previous chapter 10, but add a new segmentation mode, which can be used to replace the operations in steps 3) to 6). Of course, the original operation functions from step 3 to step 6 are also retained. Here, we ignore the unchanged steps in Chapter 10, just add the introduction of new functions.

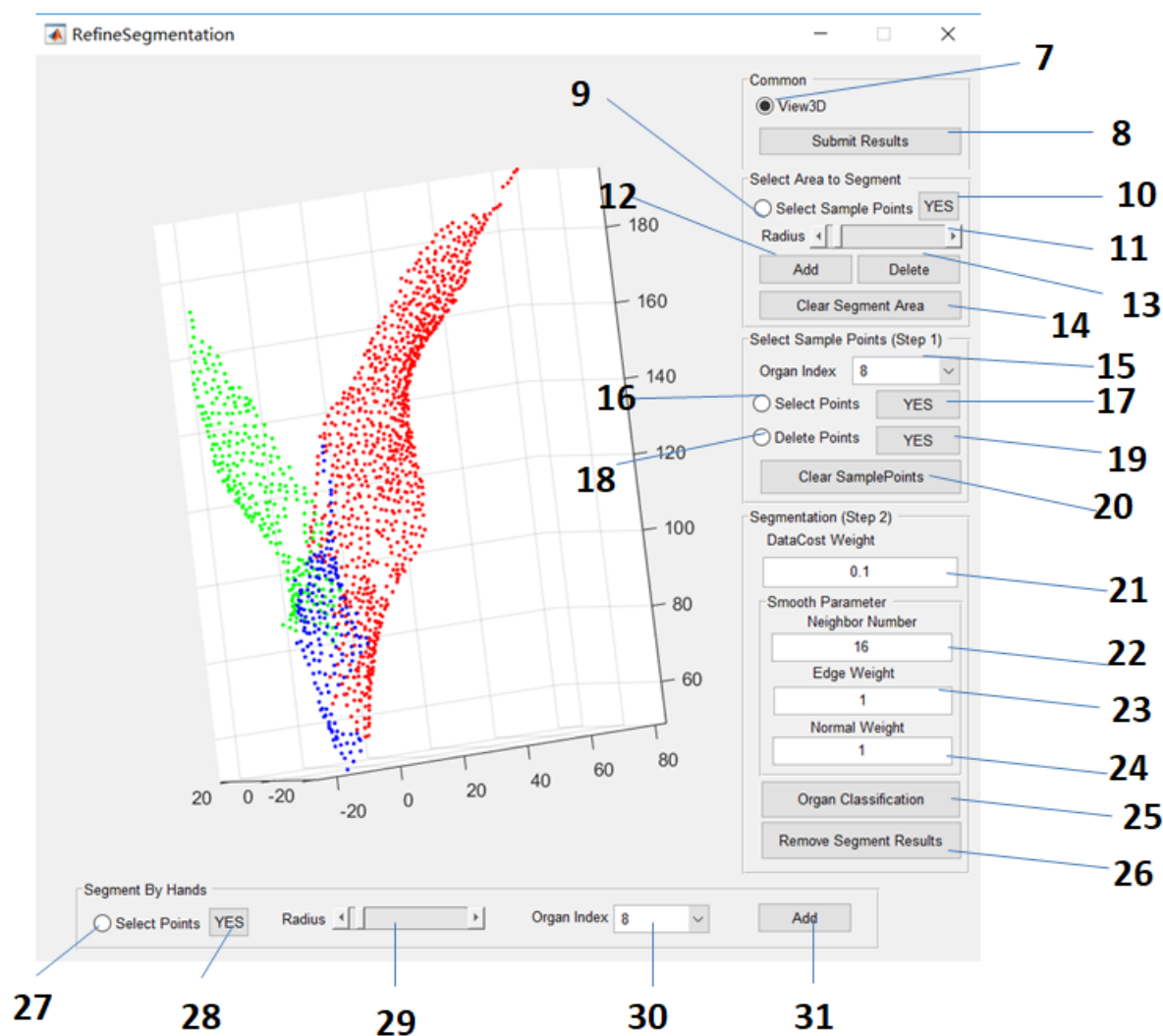


Figure 22*. The new Sub Refine-Segmentation dialog box.

New Operation steps (Replace the operations from steps 3 to 6)

1) Select the region of interest to segment

- Click the “Select Points” radio button (Figure22*-27) , the Visualization Window will switch to the interactive state.
- Click the “Yes button (Figure22*-28)” to select a point P .
- Adjust the radius parameter using the “Radius” slider (Figure22*-29), all points whose distance point P is less

than the radius value will turn grey, and these points are to be selected, we call these points “**candidate points**”

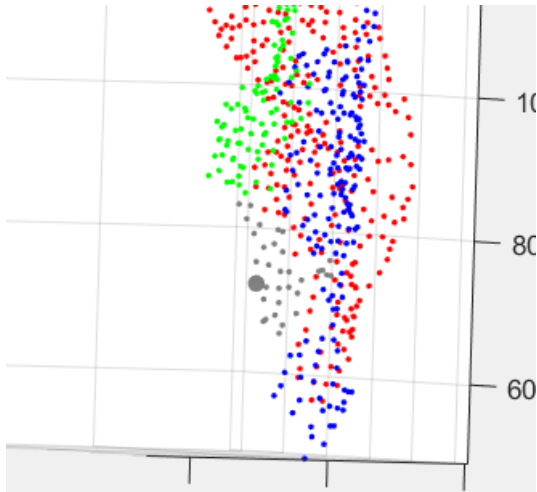


Figure . Candidate points selection.

2) Select the organ label

Select a specific organ instance L through the “**Organ Index**” drop-down box(Figure 22*-30). The value in the drop-down box is the label value of the candidate points selection to be segmented.

3) Segmentation

Click the “**Add button** (Figure 22*-31)” to add the candidate points into this organ.

11. Saving segmentation files by “Analysis—Organ Tool”

The user clicks the “**OrganTool button**” to start to save segmentation files in main interface. A “OrganTool” dialog box will pop up.

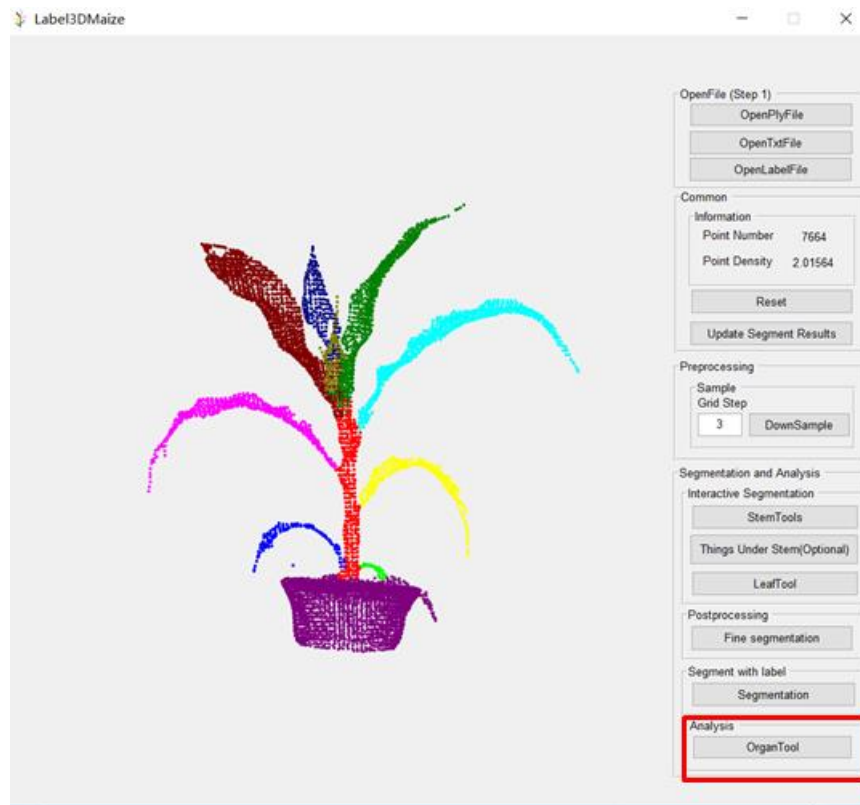


Figure 29. Segmentation result saving sub-interface triggered illustration.

Operation steps

1) Change label values (optional)

- Click the “**SelectOrgan radio button** (Figure 30-2)” , the Visualization Window will switch to the interactive state. User can select organ by left mouse button.
- Click the “**Select This Organ button** (Figure 30-3)” to select an organ instance to change the label value.
- Edit the new label value in the “**Organ Label edit box** (Figure 30-4)”.
- Click the “**Change Organ Label button** (Figure 30-5)” to give this organ instance a new label value.

2) Save the label file.

- Click the “**Save Point Label button** (Figure 30-6)” to save a label file.

3) Save ply file.

- If the user wants to store an organ point cloud file, first select the organ, and then click the “**Save Single Organ button** (Figure 30-7)” to save a organ ply file.
- If the user wants to save all the organs as different ply files at one time, just click the “**Save all Organ points button** (Figure 30-8)”. The ply file name of an organ with a label value of i is “ i .ply”, where i is an integer greater than or equal to 1.

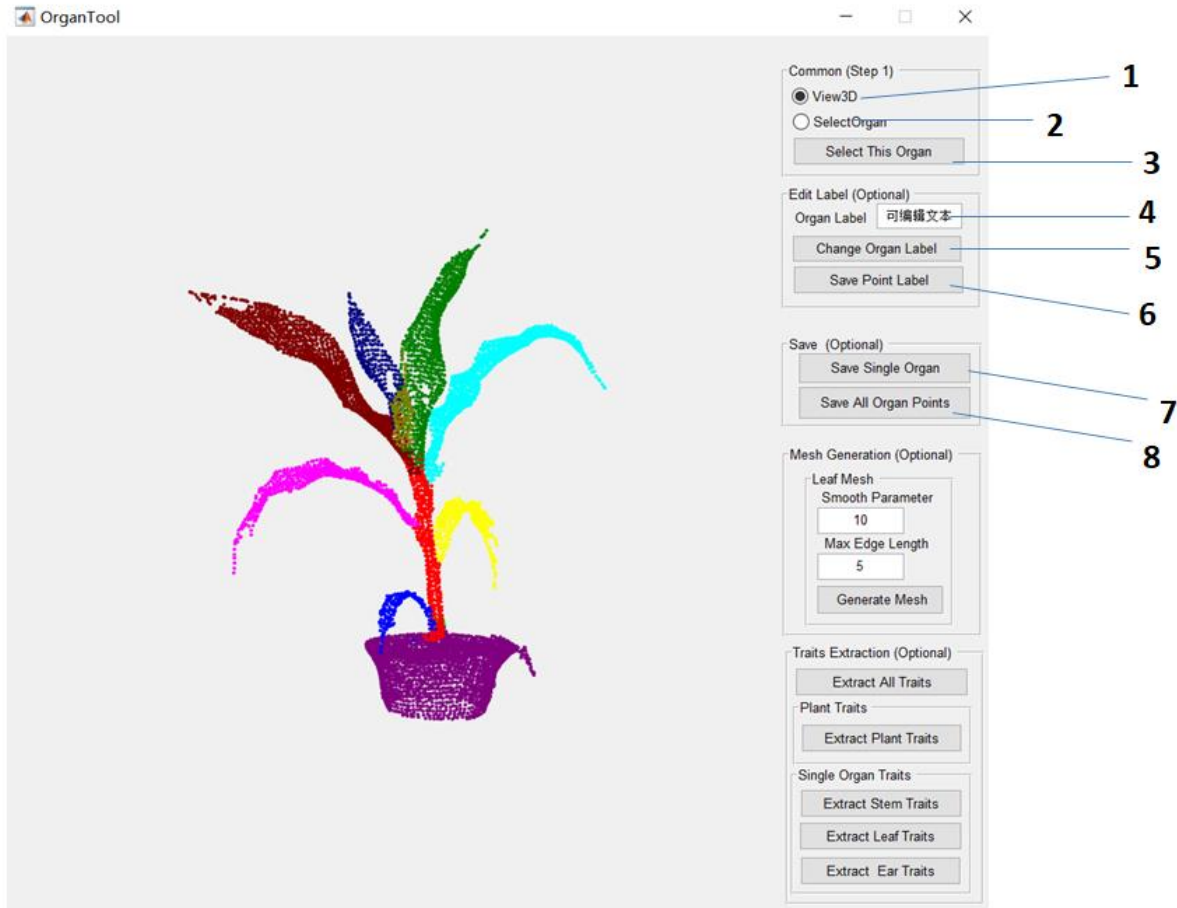


Figure 30. The OrganTool dialog box

12. Sample-based segmentation using “Segment with label—Segmentation”.

For a point cloud file with a large number of points, we first down-sample it, then perform interactive segmentation and save it as a label file. Then we use the label file to segment the original point cloud or other sparse point cloud.

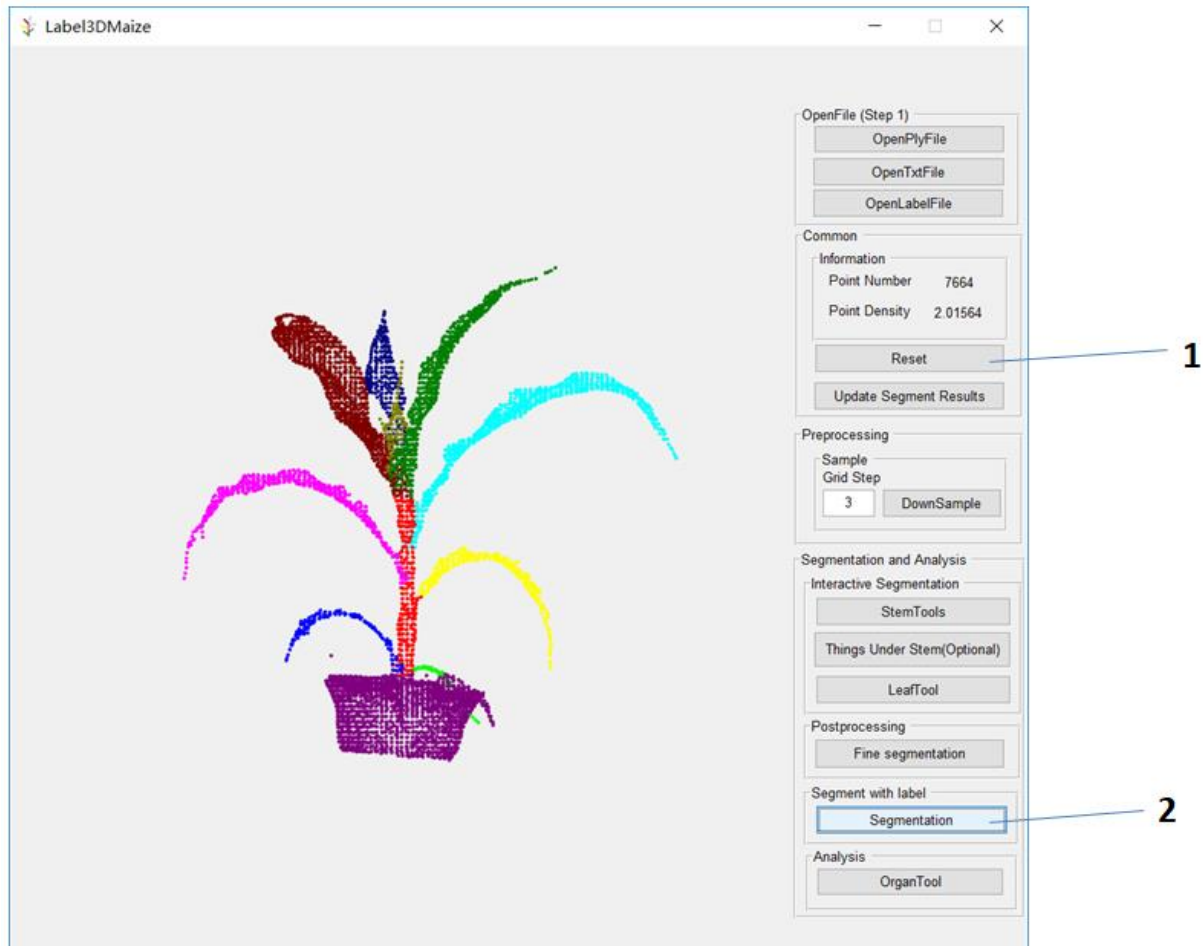


Figure 31. Main Interface

Operation steps

1) Resample the plant points.

- Click the “**Rest button** (Figure 31-1)” to recover the down-sampled point cloud to the original point cloud.
- If the user wants to segment a point cloud with different point number, just down-sample the point cloud shown as the section “Down sample point cloud”.

2) Load the “SegmentByLabel” dialog box.

Click the “**Segmentation button** (Figure 31-2)”, and the SegmentByLabel dialog box will pop up.

3) Load labeling File

Click the **“Load labeling File button (Figure 32-5)”** to load a label file. A new dialog box called ”Label file” will pop up, which shows the visualization of the segmentation result of the label file.

4) Segmentation

Click the **“Segment button (Figure 32-7)”** to segment the point cloud.

5) Submit result

Click the **“Submit Results (Figure 32-4)”** to submit the segmentation results.

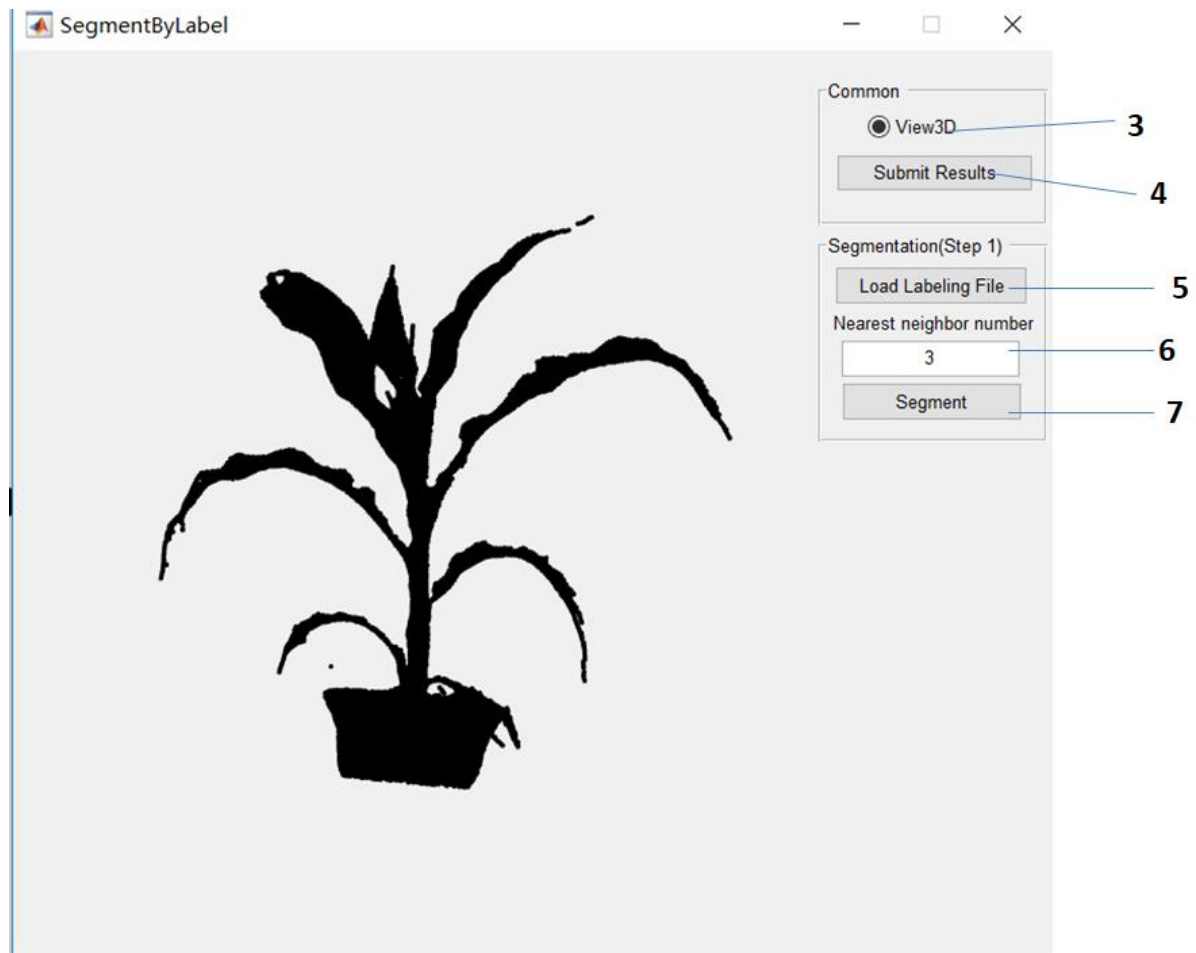


Figure 32. SegmentByLabel dialog box.