Tomato Analyzer User Manual Version 4

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This document describes the functionality of the desktop version of Tomato Analyzer 4.0.

Tomato Analyzer is designed to provide analysis of slices of tomatoes, peppers, leaves and seeds. Version 4.0 of Tomato Analyzer has been modified to work better with asymmetric (curved) image slices (e.g., curvy tomatoes and peppers), hollow peppers as well as improving the distal and proximal end functions.

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Part 1: Basic Features

Image collection

Reliable analysis begins with the production of quality images. It is essential to use a clean, solid black background when scanning. Objects should be close to one another, but *not* touching. Shadows and other extraneous elements in the image will cause problems for the analysis.

The scanned image should be cropped to eliminate large empty space. This cropping is important because the software will find objects throughout the entire image and if most of the image is empty the software will not work properly. Conversely, if there is very little background area in the image, then the software may not detect darker objects. To detect these objects, use imaging software to extend the canvas size of the image and fill in the new canvas areas with black.

The image should be saved in a jpeg or tiff format. Tiff images have a larger file size, but preserve the image as it was originally scanned, so they work well with dark objects such as leaves. Jpeg images alter some of the colors in the image, reducing the accuracy of object boundary detection and color analysis.

The software is sensitive to image resolution and object size. It will not recognize objects that are small or large in terms of number of pixels. Table 1 provides recommendations for the scanning resolution depending on the object's size. Before embarking on collecting many images, it is prudent to test that the resolution of the images is sufficient for the analysis.

Object size	D	PI
Object size	JPEG	TIFF
< 0.5 cm	\geq 750	\geq 300
0.5 to 1 cm	600	200
1 to 8 cm	300	100
> 8 cm	100	72

Table 1 Object size and DPI setting recommendations

For accurate analysis, the DPI setting on Tomato Analyzer *must* be set to the same value as the images (see Part 2, "Settings: Scanner DPI"). If analyzing multiple images at once (see Part 1, "Export functions"), it is best that all images are saved at the same resolution.

Note!! Manual adjustments (described in Part 2) should be performed in the following order:

- 1. Boundary
- 2. Rotation
- 3. Distal End
- 4. Any other adjustments

Revising the boundary or rotation will make Tomato Analyzer recalculate all the measurements and thus reset other adjustments. Revising the distal end will reset the distal end protrusion.

Opening images

Start Tomato Analyzer and click on the "Open image" button. Select and open the image file from the pop-up dialog box. The selected image will be displayed in the left window and individual slices are displayed in the upper-right window by left-clicking on them with the mouse, as shown in *Figure 1*.

Note: The tmt files saved using older versions of Tomato Analyzer are not compatible with Tomato Analyzer 4.0. When an image associated with a pre-4.0 tmt file is opened, the software will pop up a dialog explaining why the tmt file won't be used. The analysis can proceed, but the data stored in the tmt file will be ignored. The user can select "Analyze" to reanalyze the image and click on the "Save Fruit" button to save the new results, which will overwrite the data in old tmt file.



Figure 1 Tomato Analyzer with loaded file and selected image

Automatic analysis

Prior to analysis, the user needs to set the DPI and measurement units to the appropriate settings by selecting "Select Scanner DPI and Units" from the "Settings" menu. The DPI setting needs to be the same as the image file to ensure that the size measurements (height, width, perimeter, area) are accurate. The "Units used" in the dialog box determines the units (cm, mm, in, or pixel) for the data output. Also, prior to performing analysis the user must select the attributes to be measured (see Part 2, "Settings: Scanning DPI and Units, and Attributes"). When blockiness, triangle, distal and proximal end angle are being measured, the user must choose settings for these attributes (see Part 2, "User-defined settings: Blockiness Position" and "User-defined settings: Proximal and Distal Angles"). In addition, settings for "Number of Morphometric Points" (for the morphometric or geometric analyses) and "Default Eccentricity Ellipse Size" (for the internal eccentricity) will need to be selected if these attributes are to be measured. By default, Tomato Analyzer always applies the last settings used.

To analyze the opened image, click the "Analyze" button. When finished, the perimeter of each fruit will be highlighted with a yellow line and the data corresponding to the user-selected settings will be displayed in the lower-right data window, as shown in *Figure 2*. The software will automatically *deselect* very large or small objects, such as a ruler or label. Additional objects can be deselected by right clicking on them. Only items outlined in yellow will be displayed in the data window or exported. Items outlined in blue will not be included in any analyses. TA does not recognize objects that are not outlined in blue or yellow.



Figure 2 Tomato Analyzer following analysis of slices in an image

Save function

To save the changes made to the slices and the results of the analysis, click on the "Save Fruit" button. All current information, including manual adjustments and deselected objects, will be saved in a file with the same name as the image file, but with a "tmt" extension. Every time an image file is selected, the tmt file with the same name will automatically be opened and loaded. The tmt file should reside in the same folder as the jpg or tiff image file. If they don't appear together in the same folder, place the images in the folder where the Tomato Analyzer application is located on your computer. To revert to the original image file, without any of the adjustments, simply delete the associated tmt file. An alternative is to select "Analyze" to reanalyze the original image. However, beware that any tmt file with the same name as the image

will still be associated with the image the next time that the file is opened unless, of course, the new adjustments were saved.

Results and data window

Shape attributes are divided into ten groups: Basic Measurements, Fruit Shape Index, Blockiness, Homogeneity, Distal Fruit End Shape, Proximal Fruit End Shape, Asymmetry, Internal Eccentricity, Latitudinal Section, and Morphometrics. By default, the "Basic Measurement" group is always displayed. To view a different group, click on the tab of the corresponding group. If other tabs are not present use the settings menu and select attributes; when the window opens select all to view all group tabs. For detailed explanations of shape attributes, see Part 3 "Definitions of Measurements".

Each row of data in the window corresponds to a particular image slice. The data is displayed in the same order as the objects in the image, moving across each row of objects from left to right, then rows from top to bottom. Slice 1 in the data is in the upper left corner of the image, Slice 2 is the slice to the right of Slice 1, and so on; the last slice is in the lower right corner of the image. Click on a row in the data window to display the corresponding slice in the top window on the right. Alternatively, click on a slice in the left window and the corresponding data row will be highlighted.

By clicking on the attribute tab in the lower-right window it is possible to view how that attribute is being measured for each object. For example, by clicking on Distal End Angle, the angle measured by the software for all of the slices in the left window will be shown. This feature is very useful when identifying objects that require manual adjustments (see Part 2, "Manual Adjustments").

	roximal Fruit E Morphometrics		1	al Fruit End Shape lor Values L*	Asymmetry Distribution	Internal Eccentric Hue Distribution	ity Latitudinal Section Chroma Distribution
	Basic Mea	surement	s	Fruit Shape In	dex	Blockiness	Homogeneity
#	💛 Perimeter	🖊 Area		Mid-height 🛏 Maxim	um Width 🚺 He	ight Mid-width 🔲 Ma	ximum Height 🥒 Curved Heig
01	4.6752	1.5815	1.4000	1.4000	1.4200	1.4300	1.5394
02	4.6362	1.5561	1.3800	1.3900	1.3900	1.4000	1.4953
03	4.7459	1.6308	1.4300	1.4300	1.4600	1.4600	1.5138
04	4.6527	1.5580	1.3400	1.3500	1.4400	1.4400	1.5270
•							•

Figure 3 Data of measured attributes are stored in tabbed panes

Export functions

The user can export data for an individual image by selecting the Export Data button. The data will be exported to an Excel file (stored in a .csv format) and will display the values for each slice, the average, and the standard deviation.

The "Batch Analysis" function is used to export the values of the attribute from two or more images. Before performing batch analysis, each image should be analyzed individually, adjusted if necessary (e.g., proximal and distal points), and saved. To perform batch analysis, click on the "Open Image" button. Select the image files to be batch analyzed. Multiple files are selected

using the "Shift" or "Ctrl" key while selecting additional files. After the files are selected, click on the "Open" key. The user will be asked to select the type of batch analysis output: Average Only, Average and Standard Deviation, or Individual Measurements per image (see Figure 4).



Figure 4 Window to select the analysis batch type

Choose a name for the Excel (.csv) file that will be created and click on the "Save" button. The software will automatically open the files and begin the batch analysis.

If the image files have been previously analyzed and saved by Tomato Analyzer, the saved files (.tmt) will be opened for the batch analysis. If the image files have not been previously analyzed, the software will perform the analysis with the original images. The software may crash if too many images have been chosen for batch analysis. If this happens, select fewer files in subsequent analyses. If the software still crashes, check the date for the opened tmt file. If a tmt file was saved using an older version of Tomato Analyzer, delete the tmt file. Recall that Tomato Analyzer 4.0 cannot open tmt files saved using older versions of the application.

User Settings

This feature allows the user to apply exactly the same settings for all items in the Settings menu (e.g., Blockiness Position, Number of Morphometric Points) and for Color Test to a population previously analyzed. To save the settings for later use select "Load/Save settings: Save Settings" from the "Settings" menu. A file dialog will pop up, prompting the user for a name for the user settings file (*.ctmt). The saved settings can be loaded by choosing "Load/Save settings: Load Settings" from the "Settings" menu and locating the settings file.

Part 2: Advanced Options

Additional manipulations

Whereas most features of Tomato Analyzer are measured using the external boundary of the objects, shape attributes of internal features can be measured as well. Tomato Analyzer allows the user to draw an ellipse on the object around the feature of interest. Several measurements can be taken using the dimensions of the ellipse and the outer boundary.

Internal Eccentricity

This feature was developed to measure the degree of fruit eccentricity of longitudinally cut fruit. The user can set the "Default Eccentricity Ellipse Size" in the "Settings" menu to approximate the features to be measured (see Figure 5). After the default size, the user can adjust each ellipse manually using the "Adjust Eccentricity Ellipse" function in the "Revise" menu (See "Adjust eccentricity ellipse" in the "Manual adjustments" section, and "Default eccentricity ellipse size" in Part 2: "User Defined Settings"). Tomato Analyzer will measure various eccentricity features from the ellipse and the boundary of the object.



Figure 5 Ellipse settings

Latitudinal Section

The "Latitudinal Section" tab houses features that are measured in cross sections of tomato fruits and peppers. The attributes are: "Lobedness Degree", "Tomato Pericarp Area", "Tomato Pericarp Area Ratio", "Tomato Pericarp Thickness", "Tomato Pericarp Thickness Ratio", "Pepper Pericarp Boundary, "Pepper Pericarp Area", and "Pepper Pericarp Thickness".

The tomato pericarp attributes measure the thickness of the walls of the tomato fruit (see "Latitudinal Section: Tomatoes" in Part 3). To set the tomato pericarp boundary, select a fruit to appear in the upper right corner and use the "Tomato Pericarp Boundary" feature in the "Revise"

menu. The pericarp thickness varies per fruit therefore the user can select a default value for each object in the image. The default setting will result in a boundary that is a fraction of the outer boundary. The tomato pericarp boundary can be further adjusted via the "Adjust Tomato Pericarp Boundary" feature (see "Manual Adjustments" in Part 2). The "Tomato Pericarp Area" and "Tomato Pericarp Thickness" features can also be used to measure placenta and columella area. "Lobedness Degree" does not require manual manipulations and is measured automatically.

The pepper pericarp attributes measure the thickness of the walls of peppers (see "Latitudinal Section: Peppers" in Part 3). The pepper pericarp boundary can be adjusted via the "Adjust Pepper Pericarp Boundary" feature (see "Manual Adjustments" in Part 2).

Manual adjustments

Sometimes Tomato Analyzer does not perfectly find the slice outline or the proximal and distal ends correctly, leading to incorrect results for many measurements. Usually this can be corrected through manual adjustment of the image and objects. The available adjustments appear under the "Revise" menu (see

Figure 6) and include: Rotate, Boundary, Proximal End, Distal End, Flat Proximal/Distal Angle Micro/Macro, Auto-rotate, Adjust Eccentricity Ellipse, Adjust Distal Protrusion, Adjust Tomato Pericarp Boundary, Default Tomato Pericarp Boundary, and Adjust Pepper Pericarp Boundary.

Note: An adjustment selected under the Revise menu remains selected until a different adjustment is chosen, allowing the user to perform the same adjustment on a sequence of slices by clicking on the slice image and clicking the Revise button.

Rotate	Shift+R
Reset Rotation	Alt+R
Boundary	Shift+B
Reset Boundary	Alt+B
Proximal End	Shift+P
Distal End	Shift+D
Flat Proximal Angle Micro	
Flat Proximal Angle Macro	
Flat Distal Angle Micro	
Flat Distal Angle Macro	
Reset Proximal Angle Micro	
Reset Proximal Angle Macro	
Reset Distal Angle Micro	
Reset Distal Angle Macro	
Auto-Rotate	Shift+A
Reset Auto-Rotate	Alt+A
Adjust Eccentricity Ellipse	Shift+E
Reset Eccentricity Ellipse	Alt+E
Adjust Distal Protrusion	Shift+T
Reset Distal Protrusion	Alt+T
Eliminate Distal Protrusion	Alt+L
Adjust Tomato Pericarp Boundary	Shift+I
Reset Tomato Pericarp Boundary	Alt+1
Default Tomato Pericarp Boundary	Shift+U
Adjust Pepper Pericarp Boundary	Shift+Z
Reset Pepper Pericarp Boundary	Alt+Z

Figure 6 The Revise menu

Boundary

To adjust the boundary:

- a. Click on the fruit in the left window. It will appear in the upper right window.
- b. Click the arrow next to the "Revise" button and select "Boundary" from the drop down list.
- c. In the upper-right window, select the boundary location that needs to be adjusted. This is accomplished by left clicking on the start point and end point of the incorrect boundary. As a result, the delimited boundary will be removed (see Figure 7).
- d. To add a new boundary, left click from the start point toward the end point. Continue clicking to follow the desired contour. Right clicking will undo a previous modification. Multiple modifications can be undone by consecutive right clicks (see Figure 7).
- e. To confirm the new boundary, press the "Enter" key. Press the "Esc" key to cancel the operation.
- f. Click on "Reset Boundary" to return to the original boundary setting.





 Original boundary
 Select the segment of the boundary that needs to be modified

 Image: Comparison of the boundary of the boundary of the boundary
 Image: Comparison of the boundary of the bound

Figure 7 Adjusting the slice boundary

Rotate

This feature is used when an object is not completely vertical. Note: this feature cannot be used for latitudinal cuts of peppers.

- a. Click on the appropriate fruit in the left window. It will appear in the upper-right window.
- b. Click the arrow next to the "Revise" menu button and select "Rotate" from the drop down list.
- c. An axis will be displayed in the upper-right window. Drag the green square at the end of the axis and the fruit will rotate accordingly (see Figure 8).
- d. Press the "Enter" key to finish.
- e. Click on "Reset Rotation" to return to the original alignment.



Original image

After rotation

Figure 8 Slice rotation

Proximal end

If there is an error with the position of the proximal end, the measurements derived from this feature will be incorrect. To efficiently find the fruit in an image that requires adjustments, select one fruit so that it appears in the window on the right. Select the "Proximal Fruit End Shape" tab and the "Proximal Angle Micro or Micro" in the data output section below the selected fruit. The proximal angles will now be shown for each fruit in the image on the left and angles that seem unusual can be found. To change the position of the proximal end:

- a. Click on the desired fruit in the left window. It will appear in the upper right window.
- b. Click the arrow next to the "Revise" menu button and select "Proximal End" from the drop down list.
- c. In the upper-right window, click and drag the vertex indicator to the correct position (see Figure 9).
- d. Press the "Enter" key to finish.



Figure 9 Adjusting the proximal endpoint

Distal end

The position of the distal end of the object can also be changed manually. To efficiently find fruit that need distal end adjustments, follow the directions for the proximal end. To change the position of the distal end:

- a. Click on the desired fruit in the left window. It will appear in the upper-right corner.
- b. Click the arrow next to the "Revise" menu button and select "Distal End" from the drop down list.
- c. In the upper-right window, click and drag the vertex indicator to the correct position (see Figure 10).
- d. Press the "Enter" key to finish.



Original image



After adjusting Distal End

Figure 10 Adjusting the distal endpoint

Distal end protrusion

Adjust right endpoint

This function allows the user to define the endpoints of the distal end protrusion or indentation.

- a. Under the "Distal Fruit End Shape" tab, select the column labeled "Distal End Protrusion" and select a slice to adjust.
- b. Click the arrow next to the "Revise" menu button and select "Adjust Distal Protrusion" from the drop down menu.
- c. Drag the points that appear to the desired positions along the boundary (see Figure 11).
- d. Press the "Enter" key to finish. A line will appear showing the cutoff of the tip area and the tip area will be recalculated. The results will appear in the Distal End Protrusion column.
- e. If the tip area is not in the desired position, selecting "Reset Distal Protrusion" under the "Revise" menu button will reset the points to their initial positions.
- f. If a tip area is found but should not exist, selecting "Eliminate Distal Protrusion" from the "Revise" button will move the points to the bottom of the fruit, resulting in 0.0 for the "Distal End Protrusion" column.



Figure 11 Revising distal end protrusion

Press the "Enter" key to finish

Flat proximal/distal angle

This function allows the user to change a proximal angle micro, proximal angle macro, distal angle micro, or distal angle macro value to 180° when the user decides an angle value is too small or too large for data collection. Selecting "Flat Proximal Angle Micro" under the Revise menu changes the proximal angle micro value for the selected slice to 180° and replaces the green lines showing the proximal angle micro with a blue line connecting the shoulder points of the slice (see Figure 12). Selecting "Reset Proximal Angle Micro" resets the proximal angle micro to its original value and replaces the blue line with the green lines showing the original angle. The same functionalities are available for proximal angle macro, distal angle micro, and distal angle macro.



Original angle



After "Flat Proximal Angle Micro"

Proximal Fruit End Sha	аре	Proximal Fruit End Sha	аре
Proximal Angle Micro 1.5	🏹 Proximal Angle Macro 🛛 151.2	Proximal Angle Micro 180.0	Y Proximal Angle Macro (151.2

Original angle value

After "Flat Proximal Angle Micro"

Figure 12 Selecting the flat angle option

Auto-rotate (for seeds only)

This function is specifically developed for tomato *seeds* in order to align them with the pointed end facing the same direction automatically. At this time, the auto-rotate function does not work on other objects such as fruits, leaves, or vegetables. To auto-rotate all seeds in an image, select "Auto-rotate" for any seed.

Adjust ellipse

This function allows the user to resize and/or move the internal ellipse to define internal fruit areas for tomatoes. This function is used to calculate the Internal Eccentricity attributes in Tomato Analyzer.

- a. Select the Internal Eccentricity tab, and then select any of the columns in the tab. Select a "Default Eccentricity ellipse size" from the "Settings" menu.
- b. Select a slice and click on the "Revise" button. Select "Adjust Eccentricity Ellipse" from the drop down menu.
- c. Two points will appear representing the top and left points of the ellipse. Moving them resizes and re-centers the ellipse with respect to the two new points.
- d. Once these points have been set to their desired positions, press the "Enter" key.
- e. The ellipse will be redrawn. If the position is acceptable, press "Enter" again and the values in the columns will be updated.
- f. If the internal ellipse needs to be moved without being reshaped, click on the center of the slice where the points were. Two lines appear and three green points. Move the point positioned approximately in the center of the fruit to a new location to move the ellipse without resizing it.
- g. Press "Enter" to finish.

Adjust tomato pericarp boundary

This function allows the user to define the tomato pericarp region and needs to be adjusted when 'Tomato Pericarp Area" and "Tomato Pericarp Thickness" are selected in the "Latitudinal Section" tab. Note: for fruits that are over-ripe, it may be difficult or impossible to distinguish the pericarp from the remainder of the fruit.

- a. Select a slice and click on the "Revise" drop down menu. Select "Default Tomato Pericarp Boundary" and set the default that best fits the pericarp. The default setting will result in a boundary that is a fraction of the outer boundary.
- b. For further adjustments, select "Adjust Tomato Pericarp Boundary" from the "Revise" drop down menu.
- c. In the upper-right window, select the pericarp boundary location that needs to be modified. This is accomplished by left clicking on the start point and end point of the incorrect boundary. As a result, the delimited boundary will be removed (see Figure 13). For the best outcome, the smallest possible section of boundary should be selected at any one time.
- d. To add a new boundary, left click from the second point back to the first point. Continue clicking to follow the desired contour. Right clicking will undo a previous modification. Multiple modifications can be undone by consecutive right clicks (see Figure 13).
- e. To confirm the new boundary, press the "Enter" key. Press the "Esc" key to cancel.

f. Select "Reset Tomato Pericarp Boundary" to return the boundary to its original position.





Original boundary

Select the segment of the boundary that needs to be modified



Add new boundary

Adjusted boundary

Figure 13 Revising the pericarp boundary

Adjust pepper pericarp boundary

This function allows the user to define the pepper pericarp region and needs to be adjusted when "Pepper Pericarp Area" and "Tomato Pericarp Thickness" are selected in the "Latitudinal Section" tab. Note: the pepper must be hollow and completely black in the middle for Tomato Analyzer to be able to calculate the pericarp boundary.

- a. Select a slice and click on the "Revise" drop down menu. Select "Default Pepper Pericarp Boundary".
- b. In the upper-right window, select the pericarp boundary location that needs to be modified. This is accomplished by left clicking on the start point and end point of the incorrect boundary. As a result, the delimited boundary will be removed (see Figure

14). For the best outcome, the smallest possible section of boundary should be selected at any one time.

- c. To add a new boundary, left click from the second point back to the first point. Continue clicking to follow the desired contour. Right clicking will undo a previous modification. Multiple modifications can be undone by consecutive right clicks (see Figure 14).
- d. To confirm the new boundary, press the "Enter" key. Press the "Esc" key to cancel.
- e. Select "Reset Pepper Pericarp Boundary" to return the boundary to its original position.



Original boundary

Select the segment of the boundary that needs to be modified



Add new boundary

Adjusted boundary

Figure 14 Revising the pepper pericarp boundary

Settings

Settings can be changed by selecting "Settings" from the menu.

Scanner DPI and Units

The dpi value of the scanned image and the unit of measurement can be adjusted by entering a new DPI value or selecting a new unit. Units include pixels, centimeters, millimeters, and inches and refer to output data values that are size measurements, such as area, perimeter, length and width. The default settings are 300 dpi and pixels.

Scanner DPI and U	Inits	×
Scanner DPI	100	OK
Units Used	Centimeter 💌	Cancel

Figure 15 Setting scanner DPI and units

Attributes

The traits that are measured and displayed in the data window, saved in the data export file (csv), or saved in the batch analysis can be selected. Individual attributes or an entire measurement group can be selected by clicking on the group or attribute. All attributes of a measurement group can be shown by clicking on the "+". For some measurement groups (Custom Color Parameters), attributes are not shown until the user creates them.



Figure 16 Selecting attributes to measure

User-defined settings

User-defined settings can be changed by selecting "Settings" from the menu.

Blockiness Position

The upper and lower blockiness positions can be changed by entering a new value. The default settings are 0.1 and 0.9 for the upper and lower positions, respectively. See "Definitions of measurements: Blockiness" in Part 3 of this manual to learn how the blockiness positions are used in Blockiness attribute calculations.

Blockiness Position	×
Upper position	ОК
0.1	Cancel
Lower position	

Figure 17 Revising the blockiness position

Proximal and Distal Angles

These settings are used for calculating the Distal Angle Macro, Distal Angle Micro, Proximal Angle Macro, and Proximal Angle Micro. See "Definitions of measurements: Distal End Fruit Shape and Proximal End Fruit Shape" to understand how the Macro Distance and Micro Distance settings affect these calculations.

Proximal and Distal Angles
Macro Distance 10
<u> </u>
Micro Distance 5
OK Cancel

Figure 18 Revising the proximal and distal angles

Number of Morphometric Points

To measure shape without selecting individual attributes, TA offers a morphometric or geometric analysis of each object. This function finds points along the boundary of each tomato slice in the loaded image. Statistical tools such as Principal Component Analyses can be used to analyze the points in the exported data.

For this feature to work properly, the user needs to adjust the boundary and the Proximal and Distal Ends in the "Revise" menu, if necessary (see "Manual adjustments: Boundary, Proximal and Distal End"). The Distal and Proximal Ends are used as landmark points for every object. The number of points measured along the boundary can be selected by "Number of Morphometrics Points" under the "Settings" menu. The number of points that can be measured ranges from 4 to 200 (even numbers only). Setting the number of morphometric points automatically sets exactly that number of morphometric points to be displayed or exported, as if the user had selected them in the "Select Attributes" setting. See "Definitions of Measurements: Morphometrics" in this manual to understand how the number of morphometric points affects the calculation.

When setting the number of morphometric points, be aware that exported files may exceed the number of columns that can be opened by certain versions of Excel. Excel 2003 and older versions allow no more than 256 columns.

Number of Morphometric Points	×
Number of Morphometric Points 12	
OK Cancel	

Figure 19 Revising the number of morphometric points

Default Eccentricity Ellipse Size

To allow the user to set the default size of the "Internal Eccentricity" ellipse "Default Eccentricity Ellipse Size" can be selected from the "Settings" menu. The software will resize the ellipse based on the value chosen in the dialog box, which represents a percentage of the fruit size. The ellipses of all objects in the image will be resized to the selected default.

Default E	ccentricity Ellipse Size
	Set Ellipse Size
	90
<u></u>	<u></u>
	OK Cancel

Figure 20 Revising the eccentricity ellipse size

Default Tomato Pericarp Boundary

This feature is NOT listed under the "Settings" menu, but instead under the "Revise" menu. This allows the user to select a default setting for the tomato pericarp boundary on an object-by-object basis (see "Manual adjustments: Adjust Tomato Pericarp Boundary").





Basic Measurements

- **Perimeter** (P)
- Area (A)
- Width Mid-height (W_mid) The width measured at ½ of the fruit's height.
- Maximum Width (W) The maximum horizontal distance of the fruit.
- Height Mid-width (H_mid) The height measured at $\frac{1}{2}$ of the fruit's width.
- Maximum Height (H) The maximum vertical distance of the fruit.
- **Curved Height** (CH) The height measured along a curved line through the fruit (passing through the midpoints of opposing pairs of points on either side of the distal and proximal points).
- **Curved Width** (CW) The width of the fruit at mid-curved-height. This is measured by finding the distance between the two points of intersection of the line perpendicular to Curved Height and passing through the point at ½ of the curved height and the fruit boundary.

Fruit Shape Index



- Fruit Shape Index External I (H / W) The ratio of the Maximum Height to Maximum Width.
- Fruit Shape Index External II (H_mid / W_mid) The ratio of Height Mid-width to Width Mid-height
- **Curved Fruit Shape Index** (CH / CW) The ratio of Curved Height to the width of the fruit at mid-curved-height, as measured perpendicular to the curved height line.

Blockiness



- **Proximal Fruit Blockiness** (X / W_mid) The ratio of the width at the Upper Blockiness Position (U) to Width Mid-height
- **Distal Fruit Blockiness** (Y / W_mid) The ratio of the width at the Lower Blockiness Position (L) to Width Mid-height
- Fruit Shape Triangle (X / Y) The ratio of the width at the Upper Blockiness Position (U) to the width at the Lower Blockiness Position (L)

Homogeneity



- Ellipsoid The ratio of the error resulting from a best-fit ellipse to the area of the fruit. Error is the average magnitude of residuals (Res) along the fruit's perimeter, divided by the length of the major (longer) axis of the ellipse. <u>Smaller values indicate that the fruit is</u> <u>more ellipsoid.</u>
- **Circular** The ratio of the error resulting from a best-fit circle to the area of the fruit. Error is the average magnitude of residuals (Res) along the fruit's perimeter, divided by the radius of the circle. <u>Smaller values indicate that the fruit is more circular.</u>
- **Rectangular** (Sin / Sout) The ratio of the area of the rectangle bounding the fruit to the area of the rectangle bounded by the fruit.

Proximal Fruit End Shape



- Shoulder Height (Average(H_sl, H_sr) / H) The ratio of the average height of the shoulder points above the proximal end point (P) to Maximum Height (H). The shoulder points (P_sl, P_sr) are the two local y-axis maxima along the left and right halves of the perimeter (respectively). The height of the shoulder points (H_sl and H_sr) is measured against a line through the proximal point that is perpendicular to the line between the proximal point and the fruit's center of weight (assuming all pixels have equal mass).
- **Proximal Angle Micro** (∠EDF) The angle between best-fit lines drawn through the fruit perimeter on either side of the proximal end point. The Micro Distance setting determines the percentage of the perimeter from the proximal end point at which to center the linear regression points used to find the best-fit line. The points comprising 1% of the perimeter on either side of that center point are used in the regression.

- **Proximal Angle Macro** (∠EDF) The angle between best-fit lines drawn through the fruit perimeter on either side of the proximal end point. The Macro Distance setting determines the percentage of the perimeter from the proximal end point at which to center the linear regression points used to find the best-fit line. The points comprising 5% of the perimeter on either side of that center point are used in the regression.
- **Proximal Indentation Area** (K/S * 10) The ratio of the area of the proximal indentation (bounded by the proximal shoulder points, P_sl and P_sr) to the total area of the fruit, multiplied by 10.

Distal Fruit End Shape



- Distal Angle Micro (∠EDF) The angle between best-fit lines drawn through the fruit perimeter on either side of the distal end point. The Micro Distance setting determines the percentage of the perimeter from the distal end point at which to center the linear regression points used to find the best-fit line. The points comprising 1% of the perimeter on either side of that center point are used in the regression.
- **Distal Angle Macro** (∠EDF) The angle between best-fit lines drawn through the fruit perimeter on either side of the distal end point. The Macro Distance setting determines the percentage of the perimeter from the distal end point at which to center the linear regression points used to find the best-fit line. The points comprising 5% of the perimeter on either side of that center point are used in the regression.
- **Distal Indentation Area** (K_i / S * 100) The ratio of the area of the distal indentation (bounded by the distal protrusion points, D_sl and D_sr) to the total area of the fruit, multiplied by 10.
- **Distal End Protrusion** (K_p / S * 100) The ratio of the area of the distal protrusion (bounded by the distal protrusion points, D_sl and D_sr) to the total area of the fruit, multiplied by 10.



• **Obovoid** – If the area of the fruit is greater below mid-height than above it, then Obovoid is calculated from the maximum width (W), the height at which the maximum width occurs (y), the average width above that height (w1), and the average width below that height (w2), and a scaling function *scale ob* as:

Obovoid = $1/2 * scale_ob(y) * (1 - w1/W + w2/W)$ If Obovoid > 0, subtract 0.4.

Otherwise, Obovoid is 0.

• **Ovoid** – If the area of the fruit is greater above mid-height than below it, then Ovoid is calculated from the maximum width (W), the height at which the maximum width occurs (y), the average width above that height (w1), and the average width below that height (w2), and a scaling function *scale_ov* as:

Ovoid = $1/2 * scale_ov(y) * (1 - w2/W + w1/W)$ If Ovoid > 0, subtract 0.4.

Otherwise, Ovoid is 0.

- **V.Asymmetry** The average distance (Res_w) between a vertical line through the fruit at mid-width and the midpoint of the fruit's width at each height.
- **H.Asymmetry.Ob** If the area of the fruit is greater below mid-height than above it, H.Asymmetry.Ob is the average distance (Res_h) between a horizontal line through the fruit at mid-height and the midpoint of the fruit's height at each width. Otherwise, it is 0.
- **H.Asymmetry.Ov** If the area of the fruit is greater above mid-height than below it, H.Asymmetry.Ov is the average distance (Res_h) between a horizontal line through the fruit at mid-height and the midpoint of the fruit's height at each width. Otherwise, it is 0.
- Width Widest Pos (y / H) The ratio of the height at which the maximum width occurs to the Maximum Height.

Internal Eccentricity



- Eccentricity ((yt yb) / H) The ratio of the height of the internal ellipse to the Maximum Height.
- **Proximal Eccentricity** ((yt yb) / (H yb)) The ratio of the height of the internal ellipse to the distance between the bottom of the ellipse and the top of the fruit.
- **Distal Eccentricity** ((yt yb) / yt)) The ratio of the height of the internal ellipse to the distance between the top of the ellipse and the bottom of the fruit.
- Fruit Shape Index Internal ((yt yb) / (yr yl)) The ratio of the internal ellipse's height to its width.
- Eccentricity Area Index The ratio of the area of the fruit outside the ellipse to the total area of the fruit.

Latitudinal Section

Tomatoes



- **Lobedness Degree** The standard deviation of distances (d) from the center of weight (assuming all pixels have equal mass) to the perimeter, multiplied by 100.
- **Pericarp Area** (**PA**) The area between the pericarp boundary (PB) and the perimeter (P).
- Pericarp Area Ratio The ratio of the pericarp area to the area of the whole fruit.
- **Pericarp Thickness** The pericarp area (PA) divided by the average of the length of the pericarp boundary (PB) and the perimeter (P).
- **Pericarp Thickness Ratio** The ratio of the Pericarp Thickness to the average of the Maximum Height and Maximum Width.

Peppers



- Pericarp Boundary (PB) The length of the (inner) pericarp boundary (PB).
- **Pericarp Area** (**PA**) The area between the pericarp boundary (PB) and the perimeter (P).
- **Pericarp Thickness** The pericarp area (PA) divided by the average of the length of the pericarp boundary (PB) and the perimeter.

Morphometrics



The morphometric points are a fixed number of points along the perimeter. If there are N morphometric points, N/2 - 1 are equally spaced between the proximal and distal ends on one side, N/2 - 1 are equally spaced between the proximal and distal ends on the other side, and the other 2 points are the distal and proximal end points themselves. The first morphometric point (1x, 1y) is always the proximal end point. The original coordinate point (0,0) is located in the upper left corner of the rectangle defined by the Maximum Width and the Maximum Height.