

---

# SegTrac User Manual

---

## Introduction

This document is used as a helpful guide for using the Breast Segmentation application. Any issues not covered here should be directed to Jacob Johnson.

## Contents

<b>1</b>	<b>Getting started</b>	<b>2</b>
1.1	Installation . . . . .	2
1.2	User Interface . . . . .	2
1.3	The Basics . . . . .	2
<b>2</b>	<b>Images</b>	<b>2</b>
2.1	Image Format . . . . .	2
2.2	Importing Images . . . . .	3
2.3	Loading Data . . . . .	4
2.4	Save Data . . . . .	4
<b>3</b>	<b>Processing</b>	<b>4</b>
3.1	Fix Image Orientation . . . . .	4
3.2	Top-Bottom Adjustment . . . . .	5
3.3	Autocorrect . . . . .	6
3.4	Manual Corrections . . . . .	6
3.5	PDWF Calculations . . . . .	8

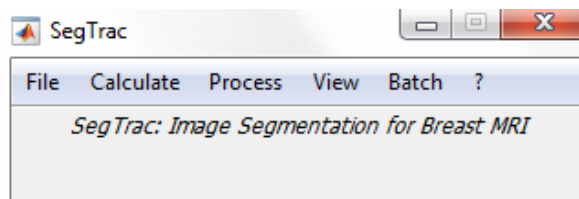
## 1 Getting started

### 1.1 Installation

Use the included instructions for installation of MATLAB Runtime version 9.0.1 or greater. Once installed, simply run the file 'SegTrac.exe' to begin the application.

### 1.2 User Interface

The SegTrac interface is shown below. The various utilities of the program can be access using the menubar across the top of the window. The upper half of the interface will display progress and status messages, while the bottom half of the display will display warning or error messages, should any occur.



### 1.3 The Basics

An example, simple use of the program to load DICOM images and segment them is as follows:

1. Run 'SegTrac.exe'
2. Select 'File→ Import Images...' or press 'Ctrl + I'. Other keyboard shortcuts are indicated next to menubar items.
3. Navigate to either the directory of your DICOM files for water images
4. Select the first DICOM file of the sequence and click 'Open'
5. You will be prompted again to navigate to the first DICOM file of the fat image sequence
6. Upon finishing import, select 'Calculate→Full'
7. After the segmentation has completed, you can select 'View→ Open Viewer' to visually examine all aspects of the segmentation.
8. To correct errors, select 'Process→Manually Correct'
9. When you are satisfied with the mask, select 'File→Save Data' which will prompt for a location to save the SegTrac output file as a MAT
10. Once the data is saved, it may be reloaded using 'File→Load' to review the aspects of the segmentation or make changes

## 2 Images

### 2.1 Image Format





SegTrac is currently designed to accept axial fat/water images in the form of a sequence of DICOMs. Additionally, preloaded DICOM sequences may be saved as .MAT files and imported that way as well.

For DICOM files, fat and water images should be stored alone in separate directories. All images in the sequence defined by the first image in the directory will be loaded as the image volume.

For MAT files, it is easiest to store each fat and water image volume in the same file as separate variables. SegTrac will load 3D arrays of doubles or uint8/16. If the values are complex, their magnitude will be taken. It is also possible to store the image volumes in separate files, or as fields of a structure.

A second set of images can be imported, i.e. complex images with phase information.

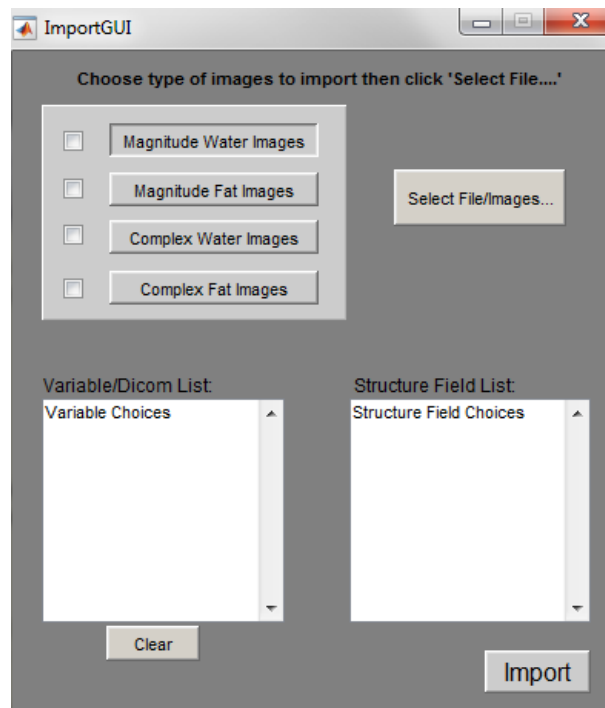
In order to conduct batch processing, images must be stored as separate variables in the same MAT file, with the series of MAT files stored in the same directory, like below.

Name	Date modified	Type
 BatchExample_1	1/3/2017 4:57 PM	MATLAB Data
 BatchExample_2	1/3/2017 3:39 PM	MATLAB Data
 BatchExample_3	1/3/2017 3:39 PM	MATLAB Data
 BatchExample_4	1/3/2017 3:39 PM	MATLAB Data

In the example above, each BatchExample.mat file should have a water images variable and a fat images variable. Additionally, a complex version of each can be included in the import and final processing.

## 2.2 Importing Images

Once your images are ready for import, run SegTrac and select ‘File→Import Images...’. The following importing interface will appear.



For each set of images, select the type of image and then click ‘Select File/Images...’. Navigate to the directory that contains your water DICOM images, or contains a .MAT file that contains your water images. Select either the first image or the file and click ‘Open’.

If you are importing a .MAT file, the variables in the .MAT file will be displayed. Select the variable corresponding to the type of images. If your images are stored in a structure, the structure fields will also appear and you can select the field. You can select other variables from the same .MAT file for the other types of images, or you can select a new .MAT file.

If you are importing DICOM images, the list of images will be displayed. Repeat the selection for each other type of images.

The ‘Clear’ button erases the import selection for the type of images selected. A .MAT or DICOM file will have to be re-selected or that type of image will not be imported.

There is no need to import all types of images for every function of SegTrac. A full segmentation by SegTrac requires magnitude water and magnitude fat images only. The viewing functionality of SegTrac can be used after loading just one image type.

By default, SegTrac assumes the second set of images are complex images corresponding to the magnitude images that are already loaded, but there is no requirement for the images to be complex. They simply must have the same matrix size. The images are accessible in the viewer and will be saved in the SegTrac output file.

## 2.3 Loading Data

Once you have imported images and run any calculation (or none at all), you may save the images into a formatted SegTrac output .mat file. These files can then be loaded, rather than imported, using ‘File→Load Data File...’. All aspects of segmentation will be reloaded to SegTrac and will be accessible to view, redo, or correct.

### 2.3.1 Loading Next File

If you are working with several SegTrac output files in a directory, such as in batch processing, a shortcut command is included to load immediately the next available file in the directory (alphabetically). Select ‘File→Load Next...’ and the next file will be loaded without the need to select it. If you had already loaded the last file in the directory, SegTrac will loop back and load the first file.

### 2.3.2 Loading Fields

## 2.4 Save Data

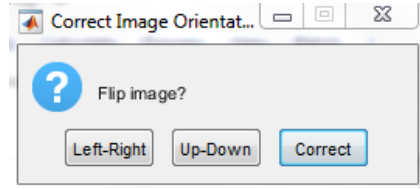
At any point after images are imported, you can generate a SegTrac data file by selecting ‘File→Save Data...’. You will be prompted to choose a location and filename for the data file. All pertinent aspects of the segmentation will be saved in a specifically formatted .mat file. This allows you to use the ‘Load Data File’ option rather than importing images.

## 3 Processing

### 3.1 Fix Image Orientation

While images acquired from a scanner are generally oriented such that the anterior direction is down and the posterior is up, radiologist are

accustomed to viewers which automatically flip these images to be the opposite. SegTrac also automatically detects and flips the orientation of imported images as necessary. However, in the event that a mistake is made or the user has preference for the other orientation, the Fix Image Orientation interface can be used.



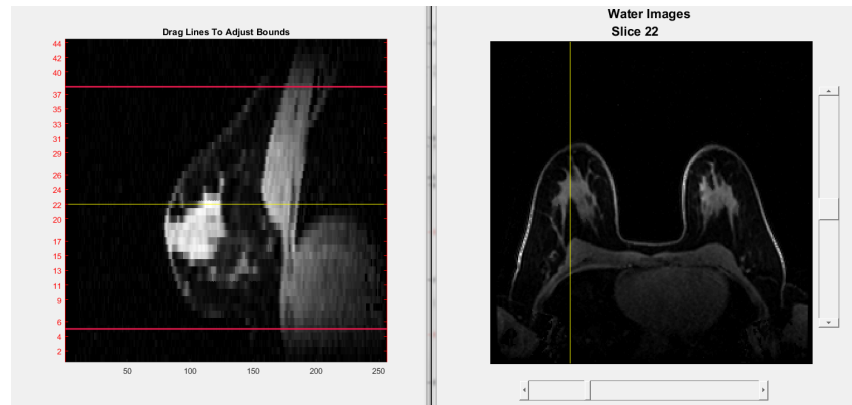
Upon selecting 'Process→Fix Image Orientation', you will be prompted by the center slice of the water images and asked for which orientation to flip. Note that while R/L orientation is less obvious, generally the R/L orientation and the A/P orientation are linked- if one needs to be flipped then the other should be too.

The center slice of the fat images will be prompted next and the orientation adjustments, if any, will be applied.

The same adjustments will also be applied to the corresponding complex images. If segmentationw was already performed, it will need to be rerun.

### 3.2 Top-Bottom Adjustment

Changes can be retroactively made to the top and bottom limits of the segmentation using the Top-Bottom Adjustment interface. Access the interface by selecting 'Process→Top-Bottom Adjustment'.



On the left is a sagittal reformat of the image volume. On the right is an axial view. You can scroll through the image volume axially while the right window is highlighted, and through the volume sagittally while the left window is highlighted. The yellow lines on each plot indicate the location of the slice of the other window. The bounds are indicated on the sagittal view with red lines. Clicking and dragging on these lines will adjust the bounds, once the interface is closed.

If the bounds are adjusted such that slices only need to be removed, not added to the segmentation (i.e. Top moved down or bottom moved up) then upon closing either window, SegTrac will remove those slices from the segmentation. The corrected mask will be updated accordingly.

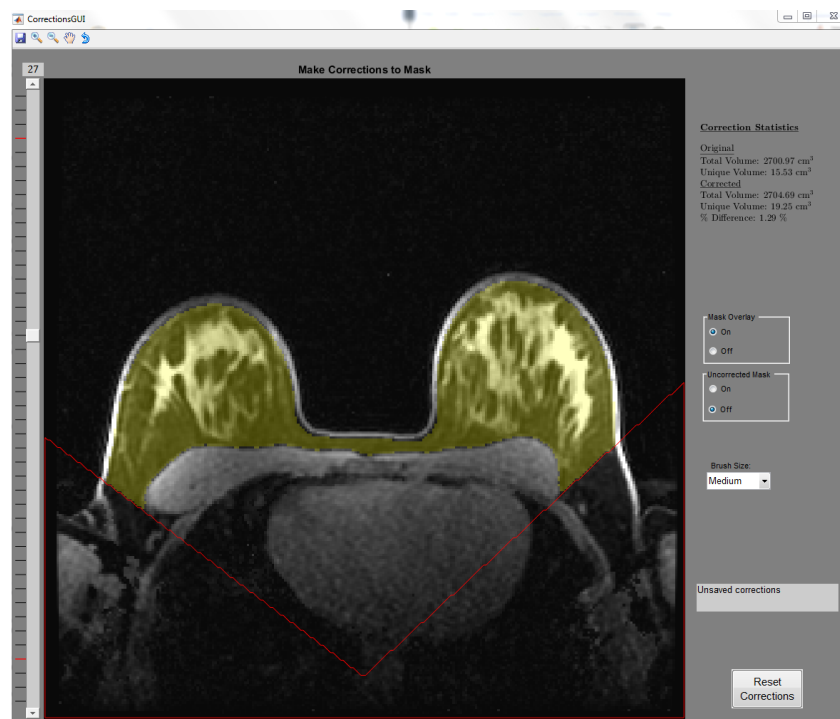
If the bounds are adjusted to *add* slices to the segmentation, then the segmentation will need to be rerun. Upon closing either window, the segmentation will run using the newly set bounds. The corrected mask will be preserved, and the additional slices will be added to it. You will need to use the corrections interface to correct the newly added slices.

### 3.3 Autocorrect

SegTrac comes equipped with a trained Neural Network function that uses data from over 100 subjects to help identify errors made in the automated segmentation of the chest wall. It works by comparing each slice of the segmentation to the slices above and below it, as well as to an atlas made from previous subjects. In the preferences interface, you may indicate whether you wish to have the autocorrections performed automatically after the segmentation is calculated. If not, then autocorrections can be performed by selecting ‘Process→Autocorrect’.

### 3.4 Manual Corrections

Selecting ‘Process → Manually Correct’ will open the corrections interface which will appear like below.



#### 3.4.1 User Interface

Each aspect of the corrections interface is described below

**Slice Slider** Slices can be scrolled through using the slider on the left, by moving the scroll wheel on your mouse, or by pressing the up/down arrows on your keyboard. The current slice number is indicated at the top of the slider. The top and bottom bounds are indicated on the left with red markers.

Additionally, when either the top or bottom slice is active, a large red ‘B’ or ‘T’ will appear next to the slice number.

**Mask Overlay** Toggle both the corrected and uncorrected segmentation mask overlays using the radio buttons on the right side of the interface. When both overlays are ‘On’, the different regions of the mask are color-coded. Regions that are only part of the corrected mask are yellow, regions that are only part of the uncorrected mask are blue, and regions that are part of both masks are light green.

The corrected mask overlay can also be toggled by pressing ‘o’ on your keyboard.

**Brush** Use the dropdown below the mask toggles to select brush size to be used for corrections. The medium brush is selected by default. Note that due to limitations with MATLAB software, the actual footprint of the large brush is a circle that circumscribes the square cursor. For this reason, precise corrections are best done by the small and medium brush sizes.

Brush size can also be increased by pressing ‘period’ (the ‘>’ key) and decreased by pressing ‘comma’ (the ‘<’ key).

**Message Box** The textbox below the brush dropdown menu indicates whether the corrections you have made since the interface was opened are saved or not. Any error messages will also appear here.

**Reset Corrections** The reset corrections button can be used to return the corrected mask to its original, uncorrected state. You will be asked for confirmation before the corrections are reset. Additionally, you will have to save the changes in the interface, and then save the data file in SegTrac in order to make the reset permanent. If corrections are reset inadvertently, simply close the corrections interface without saving changes.

**Correction Statistics** After making each correction to the mask, the data displayed in the upper right corner of the interface will be updated.

**Toolbar** The toolbar contains buttons for saving corrections, zooming and panning, and undo. Note that the undo button can only toggle undo/redo the last change that was made, and only applies to the slice that is currently active. For example, after making a correction and then shifting to the next slice, the undo button will not have any effect until a correction is made on the new slice.

The small and medium brushes will line up with the selection being made. The large brush is a circle, but due to limitations of MATLAB, the cursor will only appear as a large square. Note that the cursors will not change size when zoom mode is activated, while the effective footprint increases by a factor of two. This means the brush and the cursor will no longer line up and the edge of the brush will have to be estimated based on the response of the GUI.

### 3.4.2 Using the application

Here are some tips to on how to properly use this application.

**Drawing** Click and drag on the image to edit the displayed mask. Ctrl-click or right-click drag to erase. Drawing too quickly will result in a non-continuous line.

**Holes** The application does not allow holes in the mask. Any hole that would be made by either an addition or erasure from the mask will automatically be

filled in. The application does allow the mask to be broken into multiple regions, but does eliminate isolated regions smaller than 10 pixels.

### 3.4.3 Troubleshooting

Small bits of mask are disappearing	Part of the processing of the mask after each edit is to remove tiny, standalone parts of the mask. This is designed to prevent unintended residue from erasing part of the mask. The application does not currently support any workaround. If this creates a problem in your use of the application, please contact Jacob Johnson and request a change.
My selections are not doing anything	There are two places where any selection you make will be ignored. The Vcut which defines the lateral boundaries of the mask is shown in red on all slices. The application does not support any selections outside of that boundary. The mask processing also removes any holes from the mask. Thus, any selection while in erase mode that is completely within the current mask will be ignored, as it will create a hole that will be filled in. If this behavior causes problems or there is other erroneous behavior, please inform Jacob Johnson.
The undo button doesn't do anything	You only get 1 undo/redo! Additionally, the undo button only works on a per-slice basis. If you switch slices, the undo button will not do anything until you make a change to the current slice.

## 3.5 PDWF Calculations

The % FT (Fibroglandular Tissue- Breast density) can be calculated after segmentation, and additionally compared with the result after corrections are made. Select 'Process→PDWF Calculations' to generate the following table.

File	Edit	View	Insert	Tools	Desktop	Window	Help			
								Water volume (cm^3)	Total Volume (cm^3)	% FT
Uncorrected mask								176	1406	12.5200
Uncorrected mask (complex map)								179	1406	12.7100
Corrected Mask								161	1387	11.5800
Corrected Mask (complex map)								164	1387	11.7900

The PDWF for each voxel is calculated by

$$WF = \frac{SI_w}{SI_w + SI_f} \quad (1)$$

where  $SI_w$  and  $SI_f$  are the signal intensities of the corresponding water and fat voxels, respectively. The overall % FT is calculated by summing  $WF$  over the entire segmentation mask, divided by the total volume of the segmentation mask. Volumes are converted to cubic centimeters using the spatial resolution known by SegTrac.



## Index

Holes, 7

Troubleshooting- Disappear, 8

Troubleshooting- Small bits, 8

Troubleshooting-Undo, 8