DENSEanalysis

Single slice DENSE analysis tool for MATLAB

Version 0.4
2009.07

User Manual

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NOTE FROM THE CREATOR…

Welcome to the DENSEanalysis software package!

This should make life easier for the DENSE user. With this software, you can:
- Easily navigate DICOM and DENSE images and cine sequences
- Define regions of interest for DENSE analysis
- View and export all sorts of DENSE derived physiological information

We're currently in the beta testing stage – we still want you to break it!

Be patient and let us know how it goes.

SYSTEM REQUIREMENTS

- Matlab r2009a
- Image Analysis Toolbox
- Spline Toolbox
- C-compiler

DENSEanalysis has been tested under MATLAB r2009a, and is not guaranteed to work with any other MATLAB releases.

Additionally, we assume you have knowledge of the DENSE MRI system, the look and feel of the acquired data, and the steps of the analysis process. This document is not a primer on the DENSE acquisition system!

TABLE OF CONTENTS

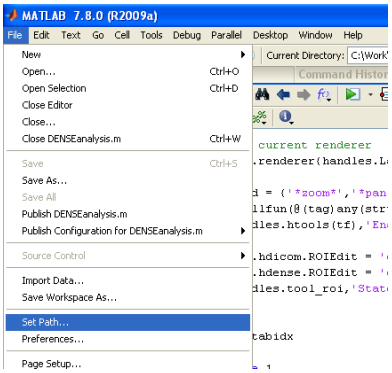
1. INSTALLATION & STARTUP

Installing the DENSEanalysis tool is simple - unzip the software and run the **`DENSEsetup`** script in MATLAB. This will add several search paths to your MATLAB installation, and compile necessary functions for use on your machine.

PRIOR TO INSTALLATION

- Ensure you meet the system requirements above
- If you have never compiled a mex-file in MATLAB before, run **`mex -setup`** in the MATLAB command window to select a compiler on your machine. On 32-bit Microsoft Windows platforms, MATLAB provides a C compiler. Alternatively, look here: http://www.mathworks.com/matlabcentral/fileexchange/22689
- If you have a previous installation of the DENSEanalysis program, remove any existing search paths pointing to that installation and restart MATLAB.

  From the MATLAB File Menu, choose "Set Path" (as illustrated on the right) and remove any folders referring to the existing installation



INSTALLATION

1. Unzip the **`DENSEanalysis.zip`** file to a location of your choice
2. Open MATLAB
3. Navigate MATLAB to the new DENSEanalysis folder
4. Run **`DENSEsetup`** in the MATLAB command window
   If you have previously installed the DENSEanalysis program, you may need to confirm the removal of some existing folders from the MATLAB search path.

Notes:

- If **`DENSEsetup`** failed for any reason, the DENSEanalysis program will not function as expected!

STARTUP

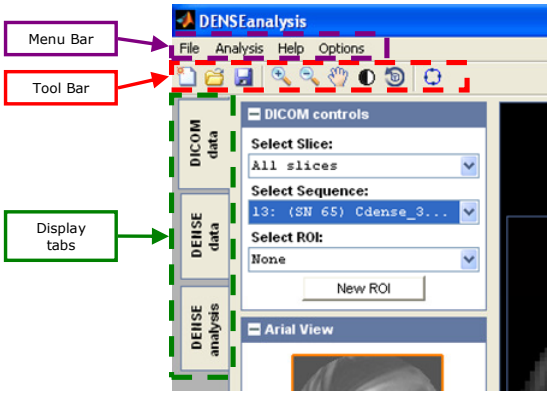
- Run **`DENSEanalysis`** from the MATLAB command window

2. OVERVIEW

The DENSEanalysis tool consists of three distinct visualization tools. The *DICOM tab* allows you to explore individual DICOM sequences and properties from a given study. The *DENSE tab* allows you to explore and edit DENSE sequences, which include multiple magnitude and phase DICOM sequences. Finally, the *analysis tab* allows you to explore tissue displacement, strain fields, and other physiological information derived from the DENSE acquisitions.

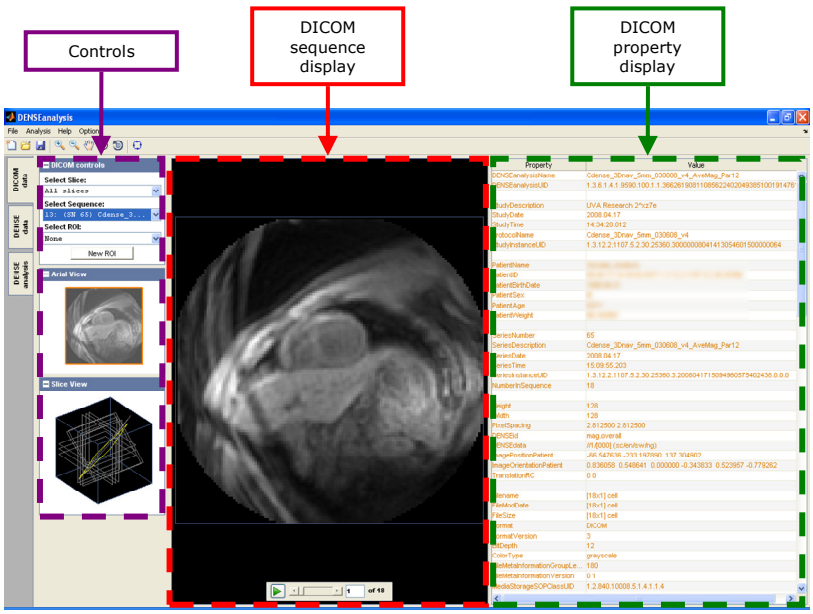
PRIMARY CONTROLS

The primary controls include a *menu bar* and *tool bar*, allowing you to load, explore, and save DENSE information. The *display tabs* allow you to switch between the three aforementioned display windows.



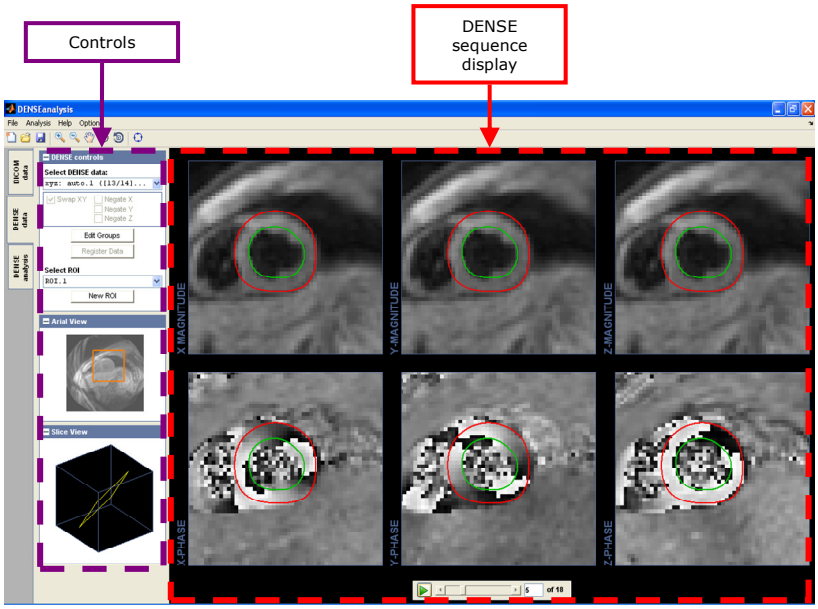
DICOM DISPLAY WINDOW

In the DICOM window, you can explore DICOM sequences as well as DICOM header information (Patient/Study properties, Image properties, Acquisition properties, etc.).



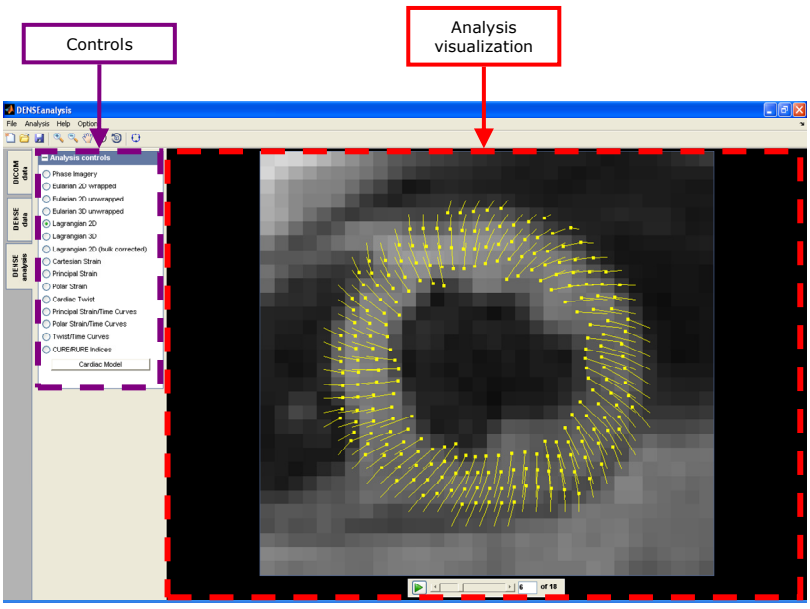
DENSE DISPLAY WINDOW

In the DENSE window you can explore and edit DENSE sequences, which include multiple magnitude and phase DICOM sequences.



ANALYSIS DISPLAY WINDOW

Finally, in the analysis window you can visualize tissue displacement, strain fields, and other physiological information derived from the DENSE acquisitions.



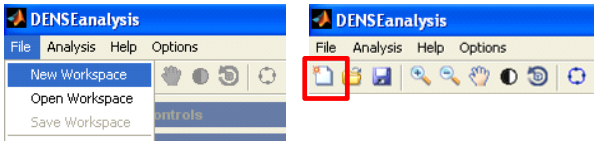
3. LOADING/SAVING PATIENT DATA

The visualization and storage of DICOM data is a simple process; select any DICOM directory containing DENSE information and the software will automatically locate, organize, and load DICOM files. After loading and manipulating the image sequences of interest, you can save their progress to a unique **`.dns`** file.

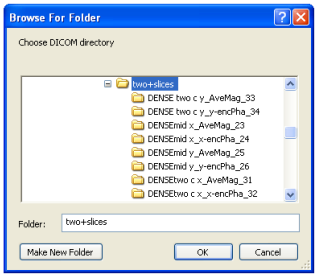
NEW PATIENT WORKSPACE

You must first create a new patient workspace and populate the workspace with DICOM imagery. The software will only load DICOM files from a single patient within a single base directory. Make sure you have ALL the images you require within this directory, and that ALL cine sequences are complete.

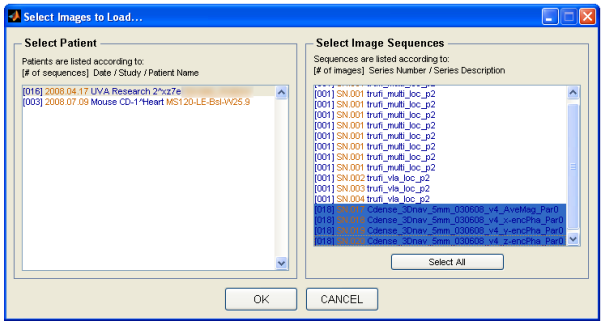
- Select the **`New Workspace`** option from the menu or tool bar



- Navigate to the directory holding the DICOM and DENSE files of interest and select.
- Select **OK**.



- After the software has organized the DICOM files within the directory, select the (single) patient and (multiple) image sequences you wish to load.
- Select **OK**.



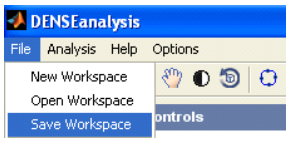
Notes:

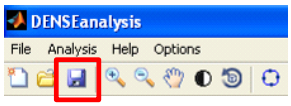
- Due to the complex organization of DICOM and DENSE imagery, the creation of a patient workspace is a ONE TIME process.
- Creating a new workspace can be time consuming, as the software must evaluate every DICOM file within the selected directory. Consider saving your workspace immediately after creation!
- Creating a new workspace will erase the currently loaded workspace. Don't forget to save your work!

SAVE PATIENT WORKSPACE

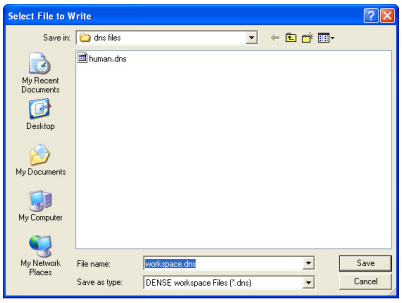
The patient workspace can be stored in a **`.dns`** file, saving your progress, allowing for a faster reload, and simplifying data transfer between computers. This workspace will contain all the DICOM imagery, DICOM properties, DENSE organization, and user-defined regions of interest.

- Select the **`Save Workspace`** option from the menu or tool bar





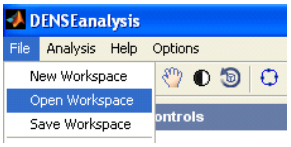
- Navigate to the required directory, enter a file name for the new **`.dns`** workspace file.
- Select **`Save`**.

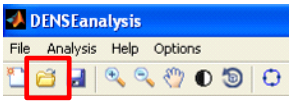


OPEN PATIENT WORKSPACE

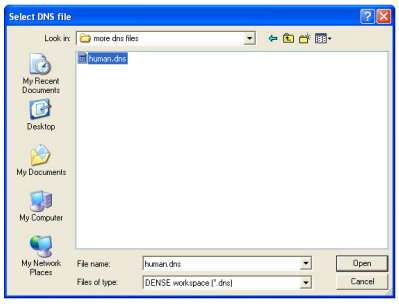
You can continue work within an existing patient workspace by opening a previously daved **`.dns`** file.

- Select the **`Open Workspace`** option from the menu or tool bar





- Navigate to the required **`.dns`** workspace file and select.
- Select **`Open`**.

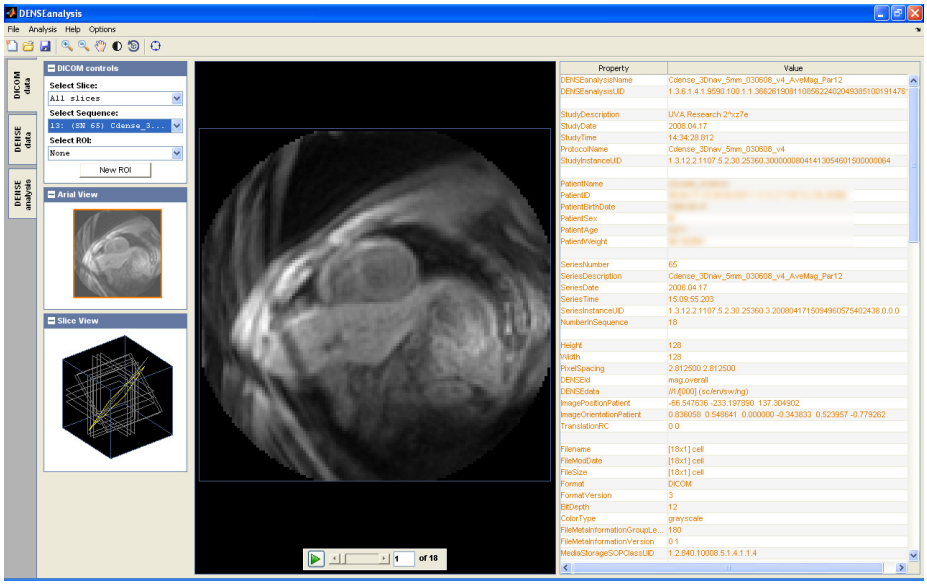


Notes:

- Opening an existing workspace will erase the currently loaded workspace. Don't forget to save your work!

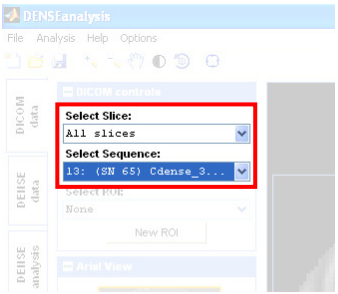
4. THE DICOM DISPLAY TAB

In the DICOM display tab, you may explore DICOM sequences as well as DICOM header information. On the right of the DICOM display tab are the DICOM file properties, including patient & study information, series and sequence information, acquisition information, etc. Scroll through the properties table at the right of the DICOM display panel. In the center of the DICOM display tab are the image sequences themselves, and on the left are display controls.



SELECTING A SEQUENCE

You may select and view any DICOM sequence in the patient workspace using the DICOM controls. Simply select a sequence from the **`Select Sequence`** dropdown box. Additionally, you may limit the visible sequences to a single slice plane using the **`Select Slice`** dropdown box.



EXPLORING THE SEQUENCE

The software offers a number of options for the exploration of DICOM image sequences.

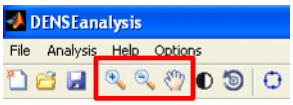
Playback

Navigate through a video sequence using the playback device.

- Scroll through the video, enter a specific frame of interest in the white box, or play the video in a continuous loop.

Zoom & Pan

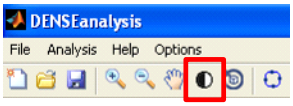
Zoom in or out of the scene using the zoom and pan options. The **`Arial View`** on the left displays the current display box (Note the **`Arial View`** is not interactive).



- Select the zoom or pan tools
- For zoom, left click within the image scene. For pan, left click and hold within the image scene to drag the image to a new location.
- Right click within the scene for more options.

Contrast adjustment

Adjust the contrast of the scene for better visualization. Note that each video frame is initially normalized to the available image intensities (i.e. black represents the lowest intensity value within the frame; white represents the largest intensity value within the frame).

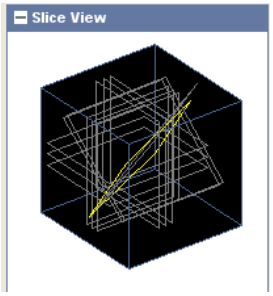


- Select the contrast tool.
- Left click and hold within the image scene. Vertical movement of the cursor adjusts brightness; horizontal movement of the cursor adjusts contrast.
- Right click within the scene for more options.

Slice viewer

Explore the acquisition slice plane of the current sequence relative to other sequences within the patient workspace.

The yellow slice highlights the current sequence. Left click and hold within the slice view to rotate the display.

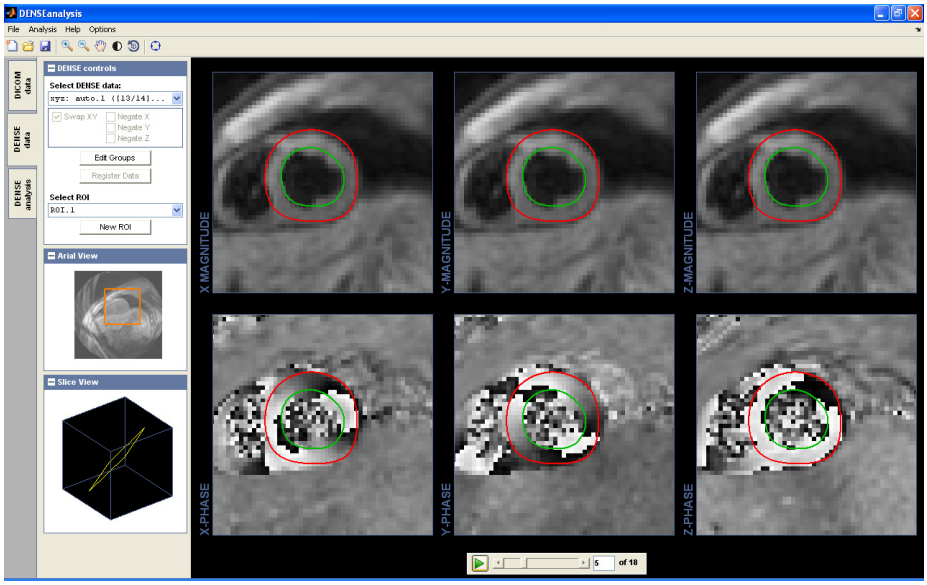


REGIONS OF INTEREST

Users can define a number of different regions of interest within any DICOM sequence. See Section 6 for more information.

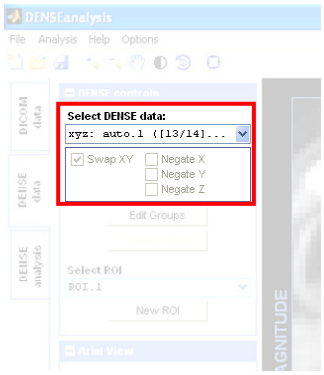
5. THE DENSE DISPLAY TAB

In the DENSE window you can explore and edit DENSE groups, each group consisting of up magnitude and phase DICOM sequences in up to three distinct displacement encoding directions. Within the DENSE display window, the top row of images displays the magnitude information while the bottom row displays the phase information. On the left of the DENSE tab are the various control options.



SELECTING A DENSE GROUP

You may select and view any DENSE group in the patient workspace. Simply select a group from the **`Select DENSE data`** dropdown box.



The **`Swap XY`**, **`Negate X`**, **`Negate Y`**, and **`Negate Z`** indicate DENSE specific acquisition flags. These boxes are not interactive.

EXPLORING A DENSE GROUP

The software offers a number of options for the exploration of DENSE image sequences.

Playback

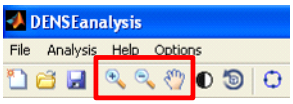
Navigate through the sequence using the playback device.

- Scroll through the video, enter a specific frame of interest in the white box, or play the video in a continuous loop.

Zoom & Pan

Zoom in or out of the scene using the zoom and pan options. The **`Arial View`** on the left displays the current display box (Note the **`Arial View`** is not interactive). All six DENSE axes are tied to the same limits.

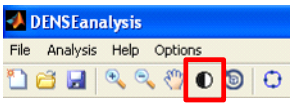
- Select the zoom or pan tools
- For zoom, left click within any image scene. For pan, left click and hold within any image scene to drag the image to a new location.
- Right click within any scene for more options.



Contrast adjustment

Adjust the contrast of the magnitude scene for better visualization. The magnitude data is initially normalized to the available image intensities and may be adjusted. The phase data contrast and brightness is fixed.

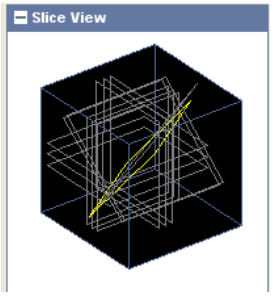
- Select the contrast tool.
- Left click and hold within any magnitude scene. Vertical movement of the cursor adjusts brightness; horizontal movement of the cursor adjusts contrast.
- Right click within any magnitude scene for more options.



Slice viewer

Explore the acquisition slice plane of the DENSE group relative to other groups within the patient workspace.

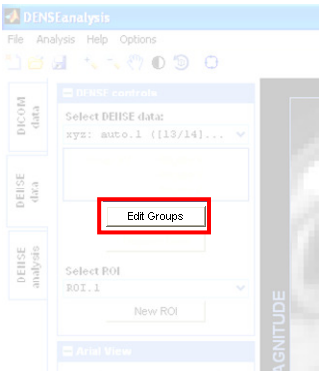
The yellow slice highlights the current group. Left click and hold within the slice view to rotate the display.



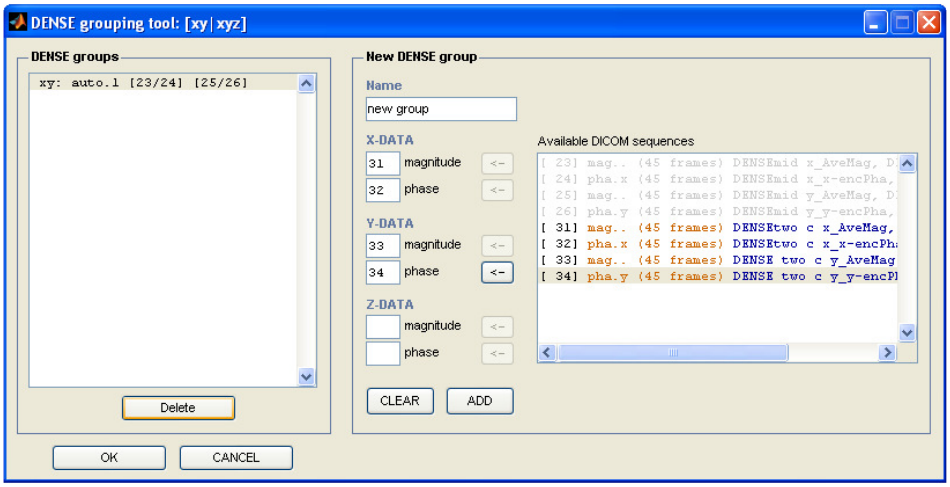
EDITING DENSE GROUPS

If the program fails to properly identify a DENSE group of interest, you may attempt to create your own group.

Select the **`Edit Groups`** button from the DENSE controls.



The DENSE grouping tool allows you to group magnitude and phase data into a single DENSE group, providing the DICOM sequences in question have consistent acquisition parameters. Each new DENSE group requires a name and paired magnitude/phase data.

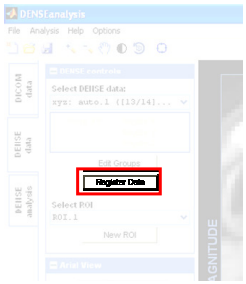


To create a new DENSE group:

- Enter a name in the **`Name`** field and press **`ENTER`**.
- Select a sequence from the **`Available DICOM sequences`**.
- Select the appropriate transfer arrow to add this DICOM sequence to the new DENSE group. After selection, some DICOM sequences will be disabled – these sequences are not compatible with the group under construction.
- Continue selecting from the enabled DICOM sequences, adding to the new DENSE group in the appropriate locations.
- After the DICOM sequence is complete and valid, select **`ADD`**.
- Select **`OK`** to return to the main software panel.

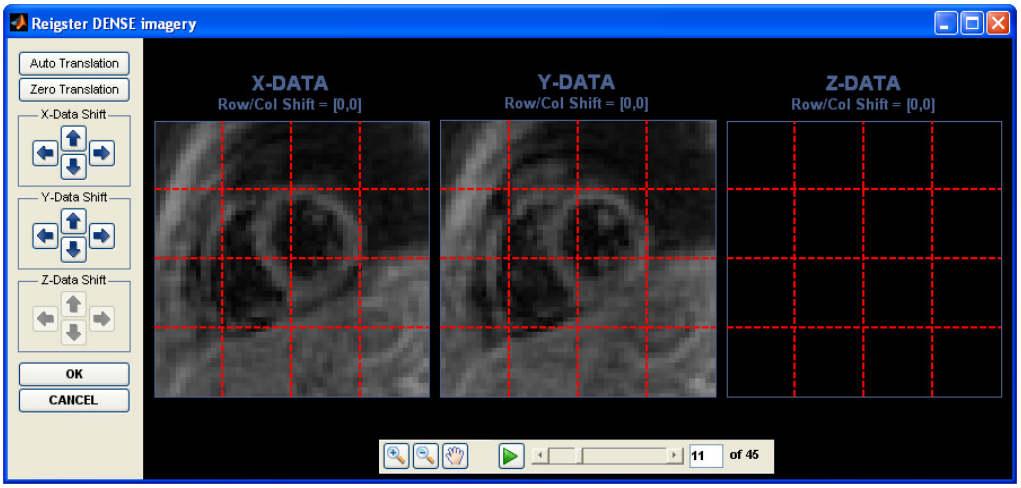
ALIGNING DENSE GROUPS

Some DENSE datasets consist of separate x, y, and z acquisitions, and these acquisitions may not be perfectly aligned. To correct this misalignment, you may access the alignment tool.



Select the **`Register Data`** button from the DENSE controls.

IMPORTANT NOTE:
TRANSLATION OF A DICOM SEQUENCE IS PERMANENT.
Any translation will be applied whenever the user views the DICOM sequence in question, e.g. in the DICOM display tab or in another DENSE group. We suggest aligning all DICOM sequences prior to the definition of any regions of interest.



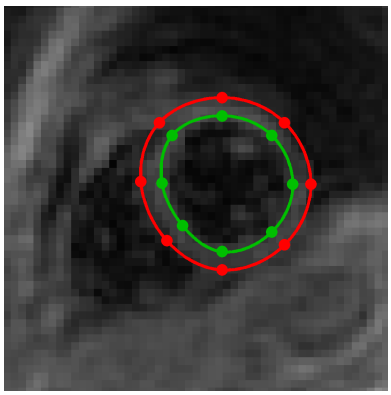
The DENSE alignment tool allows the user to translate each encoding direction separately. This translation will be applied to both the magnitude and phase imagery.

- You may zoom, pan, and playback the magnitude imagery at will to better determine alignment. Use the fixed red lines to align features within the imagery.
- The following alignment options are available:
  - Manual select the arrows to manually translate each sequence.
  - Automated select **`Auto Translation`**.
  - Reset select **`Zero Translation`**
- Select **`OK`** when complete.

REGIONS OF INTEREST

Users can define a number of different regions of interest within any DENSE group. See Section 6 for more information.

6. REGIONS OF INTEREST



To produce meaningful physiological measurements from the acquired data, you must outline a tissue *region of interest*. Each region of interest defines a single continuous piece of tissue over all time. There are a variety of closed regions you may consider, including two cardiac specific regions (short-axis and long-axis).

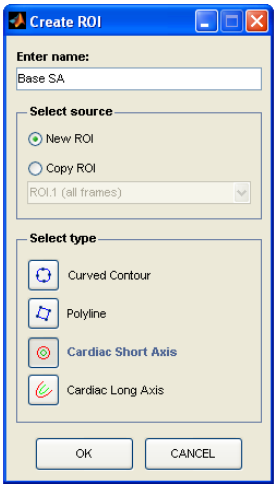
Regions of interest can be accessed from either the DICOM display tab or the DENSE display tab. You will first create an empty region of interest, and subsequently outline the tissue region on every frame of the sequence. Additionally, the software offers an automated technique to propagate a region from a single frame across time, termed *Motion Guided Segmentation*.

SELECTING A REGION OF INTEREST

You may select and view any region of interest in the patient workspace, in both the DICOM and DENSE display tabs. Simply select a region from the **`Select ROI`** dropdown box and the region will be overlaid on the sequence display.

CREATING AN EMPTY REGION OF INTEREST

- Select the **`New ROI`** from the DICOM or DENSE controls. This will access the **`Create ROI`** tool.

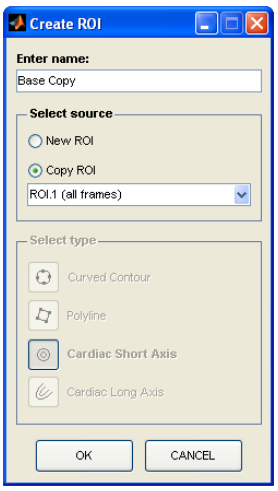


- Provide the region with a descriptive **`Name`**
- Select **`New ROI`**
- Select the type of ROI you wish to define from the available options. Note this type cannot be changed at a later time
- Select **`OK`**

COPYING AN EXISTING REGION OF INTEREST

- Select the **`New ROI`** from the DICOM or DENSE controls. This will access the **`Create ROI`** tool.

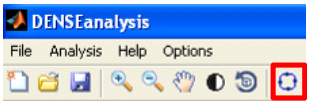
- Provide the region with a descriptive **`Name`**
- Select **`Copy ROI`**
- Select from the dropdown list of available regions
  - You may copy the first frame of an existing region provided that region is defined on the same slice plane as the current sequence
  - You may copy all frames of an existing region provided that region is completely compatible with the current sequence (same slice plane, same image extents, same number of images in the sequence, etc.)
- Select **`OK`**



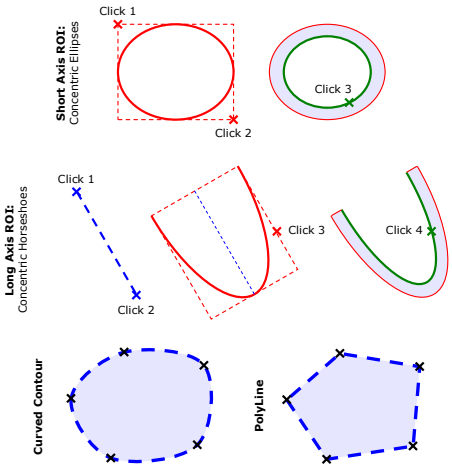
DRAWING THE REGION OF INTEREST

- Select the region you wish to edit from the **`Select ROI`** dropdown box

- Select the Edit ROI tool



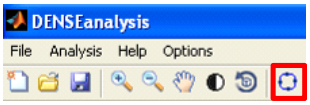
- Right click in any axes (DICOM or DENSE display tab) and select from the available options. These options may include:
  - **`Draw Contour`** or **`Redraw Contour`** See the diagram at right
  - **`Delete Contour`**
  - **`Copy Frame XX Contour`**
  - **`Motion Guided Segmentation`** (described later in this chapter, available in the DENSE tab only)



EDITING A REGION OF INTEREST

- Select the region you wish to edit from the **`Select ROI`** dropdown box

- Select the Edit ROI tool



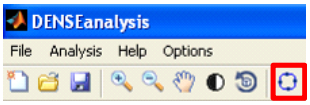
- The region of interest on any frame may be manipulated a number of different ways:
  - Drag any control point to a new location
    left click and hold any control point
  - Drag the entire contour to a new location
    left click and hold any segment
  - Add a point
    right click any segment and select **`Add Point`**
  - Delete a point
    right click any control point and select **`Delete Point`**
  - Smooth/Corner point
    right click any control point and select **`Smooth Point`** or **`Corner Point`**
  - Curved/Straight segment
    right click any segment and select **`Curved Segment`** or **`Straight Segment`**

MOTION GUIDED SEGMENTATION

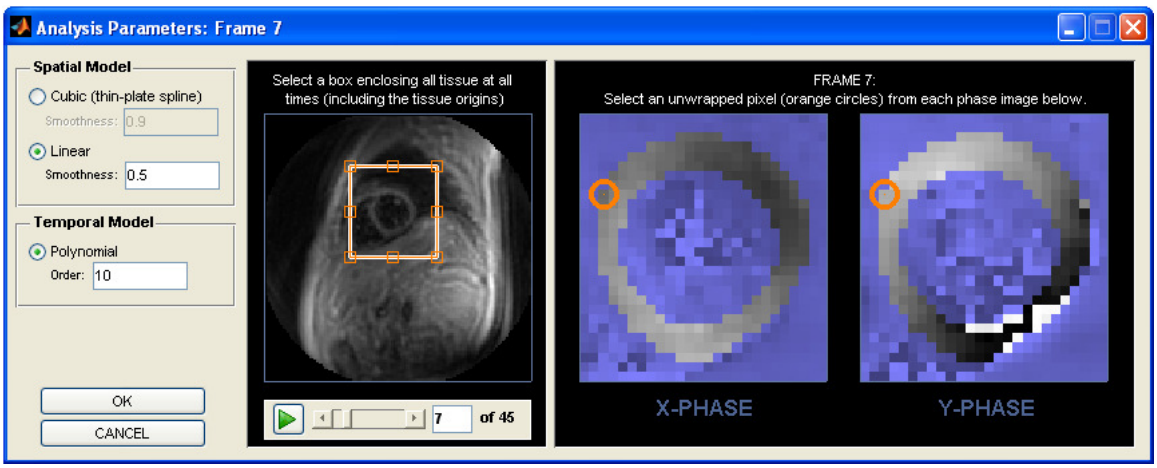
Rather than manually define the region of interest on every frame of a sequence, you can attempt Motion Guided Segmentation. This technique will propagate a tissue outline from a single frame across time using the DENSE displacement vectors. After automated segmentation, remember to closely examine the new contours for errors!

- Select the region you wish to edit from the **`Select ROI`** dropdown box (DENSE tab only)

- Select the **`Edit ROI`** tool



- Define a region of interest on a single frame of the DENSE sequence.
- Right click within any axes and select **`Motion Guided Segmentation`** to access the motion guided seg. tool



- Define the Spatial Model: we spatially smooth the displacement data using either a cubic (thin-plate spline) or linear model.
  - Select Cubic or Linear
  - Enter a smoothness parameter on the range (0,1], where 1 represents maximal spatial smoothing.
- Define the Temporal Model: we temporally smooth the displacement data using a polynomial of user specified order.
  - Enter an integer order for the temporal model. A lower order will produce a smoother solution.
- Define the tissue extents:
  - Manipulate the box to enclose all tissue of interest at all times.
- Define unwrapped pixels: to correct phase wrapping artifacts, we must identify some unwrapped pixels within each phase image.
  - Drag the Orange circles to identify pixels that are not wrapped.
  - Right click within the axes to add more unwrapping points if necessary
- Select **OK**

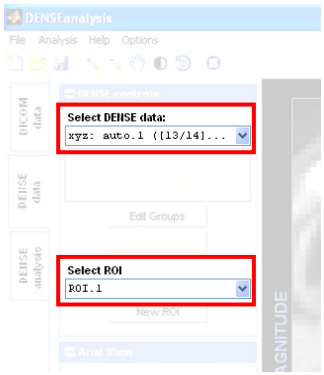
Notes:

- Thought the cubic model is more mathematically robust, it is also more computationally complex and may fail to execute on your machine. If you have a larger region of interest, we suggest using the linear model only.
- The smaller the tissue extents, the faster the process will execute.
- If the majority of pixels in the phase images suffer from wrapping artifacts, we suggest you **CANCEL** this operation and start again from a new frame.

7. RUNNING THE ANALYSIS

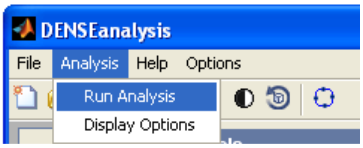
With a DENSE sequence and a completed region of interest in hand (with the tissue region outlined on every frame of the DENSE sequence), you're finally ready to analyze your data!

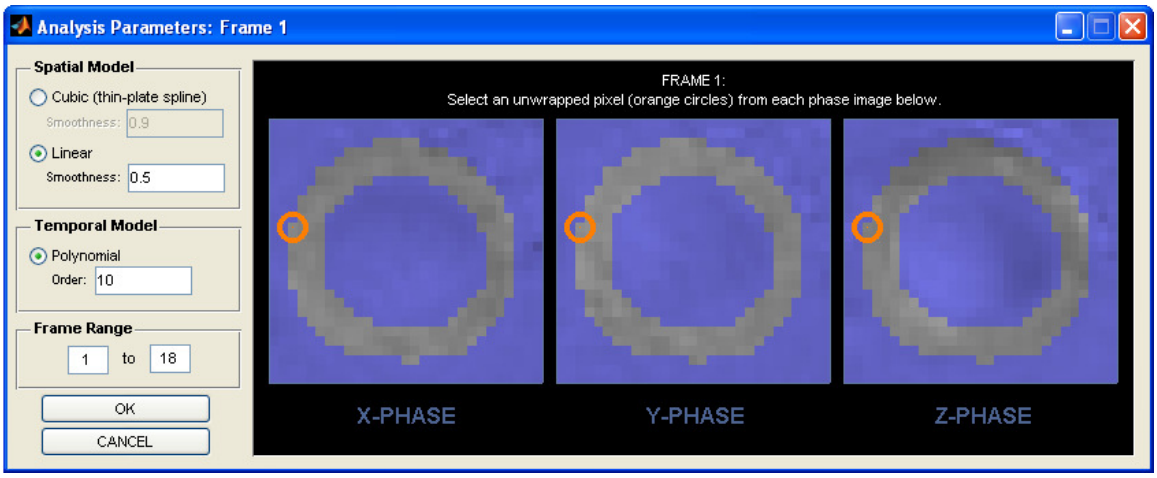
- Within the DENSE display tab, select a DENSE sequence and complete region of interest from the dropdown boxes



- Maneuver the DENSE display to a frame with good contrast and some pixels that do not suffer from wrapping artifacts.

- From the **`Analysis`** menu, select **`Run Analysis`** to access the analysis tool. If this option is disabled, your region of interest may not be complete.





- Define the Spatial Model: we spatially smooth the displacement data using either a cubic (thin-plate spline) or linear model.
  - Select Cubic or Linear
  - Enter a smoothness parameter on the range (0,1], where 1 represents maximal spatial smoothing.

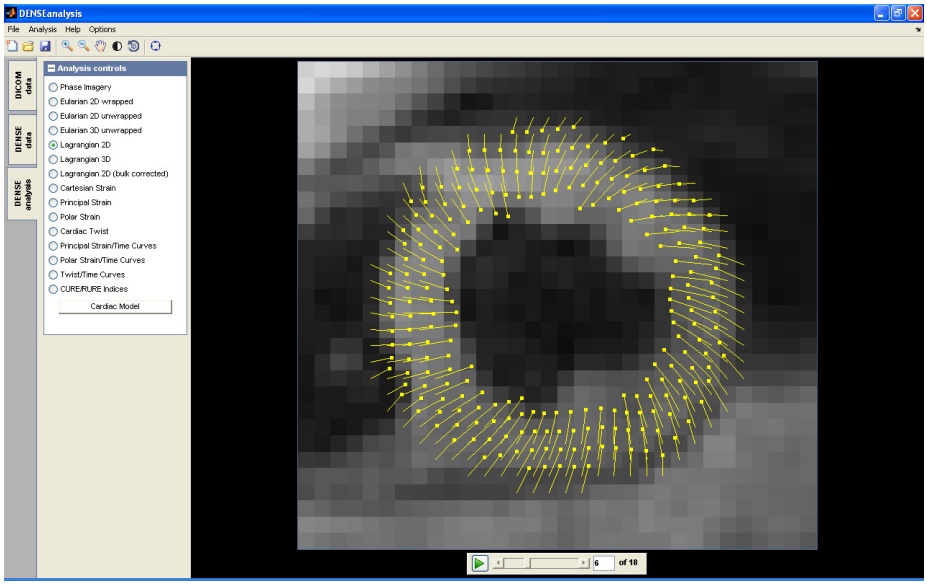
- Define the Temporal Model: we temporally smooth the displacement data using a polynomial of user specified order.
  - Enter an integer order for the temporal model. A lower order will produce a smoother solution.
- Define the frame range: rather than analyze the entire DENSE sequence, you can analyze just a portion of frame range if so desired.
  - Enter the beginning frame, from 1 to the displayed frame
  - Enter the ending frame, from the displayed frame to the end of the sequence
- Define unwrapped pixels: to correct phase wrapping artifacts, we must identify some unwrapped pixels within each phase image.
  - Drag the orange circles to identify pixels that are not wrapped.
  - Right click within any axes to add more unwrapping points if necessary
- Select **OK**

Notes:

- Thought the cubic model is more mathematically robust, it is also more computationally complex and may fail to execute on your machine. If you have a larger region of interest, we suggest using the linear model only.
- If the majority of pixels in the phase images suffer from wrapping artifacts, we suggest you **CANCEL** this operation and start again from a new frame.
- If the regions of interest on all frames do not overlap, analysis will likely cause an error. Please make sure that the region of interest on all frames overlaps!
- If you notice significant unwrapping errors in the Analysis tab, attempt this analysis again with different or additional unwrapped pixel markers, or from another frame.

8. THE ANALYSIS TAB

After successful analysis, you can visualize the unwrapped phase, tissue displacement, strain fields, and other physiological information derived from the DENSE acquisitions. The control panel on the left is used to switch between different analysis visualization tools.



EXPLORING ANALYSIS

The software offers a number of options for the exploration of the various analysis visualization options.

Playback

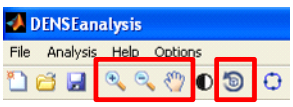
Navigate through video sequences using the playback device.

- Scroll through the video, enter a specific frame of interest in the white box, or play the video in a continuous loop.

Zoom, Pan, Rotate

Change the scene display using the zoom, pan, and rotate options when available.

- Select the zoom, pan, or rotate tools
- For zoom, left click within any image scene. For pan or rotate, left click and hold within any image scene to change the display.
- Right click within any scene for more options.



AVAILABLE VISUALIZATION TOOLS

- Phase Imagery: displays the original phase imagery in the top three axes, and the unwrapped phase imagery in the bottom three axes.

Important Note: Examine the phase imagery for unwrapping errors!
If unwrapping errors are present, please re-run the analysis!

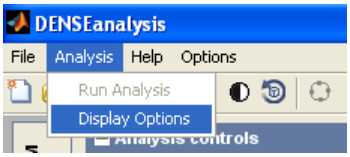
- Displacement Imagery: display displacement vectors in two and three dimensions, with square markers at the current location of a point within the tissue and lines pointing to the origin of that point.
  - Eularian 2D wrapped
  - Eularian 2D unwrapped
  - Eularian 3D unwrapped
  - Lagrangian 2D
  - Lagrangian 3D
  - Lagrangian 2D bulk corrected

- Strain Imagery: display color strain map sequences.
  - Cartesian strain
  - Principle strain
  - Polar strain (cardiac regions only)
  - Cardiac Twist (short-axis regions only)

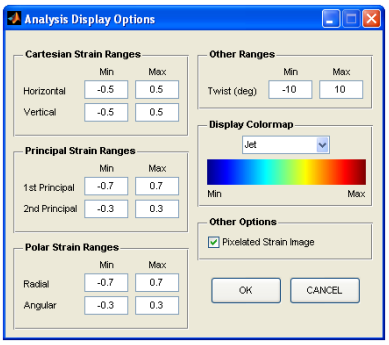
- Strain/Time Curves: for cardiac imagery, display average strain/time curves as a function of cardiac sector.
  - Principle strain/time curves
  - Polar strain/time curves
  - Cardiac Twist/time curves (short-axis regions only)
  - CURE/RURE indices (short-axis regions only)

VISUALIZATION DISPLAY OPTIONS

- From the **`Analysis`** menu, select **`Display Options`** to access the analysis display options tool.

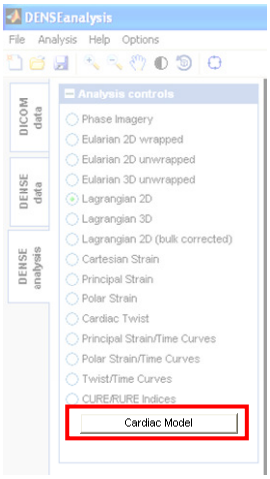


- You may change the strain display ranges, the strain colormap, and switch between a pixilated and non-pixilated strain image.
- Select **OK**

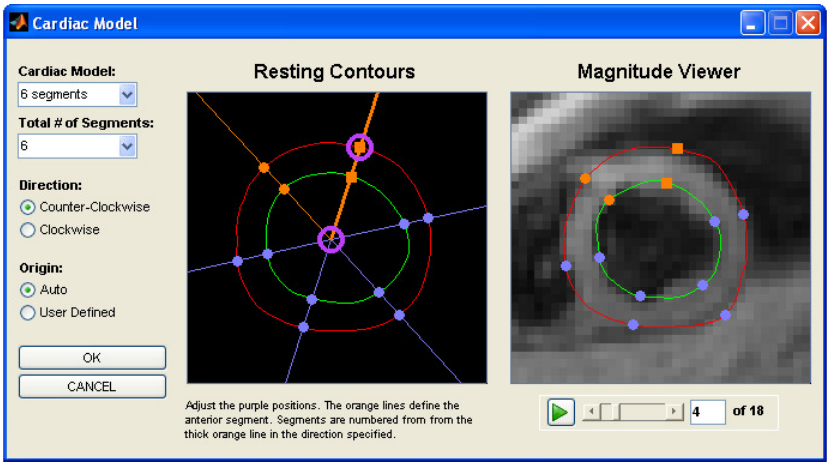


CARDIAC MODEL

- Additional visualization tools and export options are available for cardiac regions of interest, but these tools require additional input from the user.
- Access the cardiac model tool from the Analysis tab by entering any strain visualization option, or by selecting **`Cardiac Model`**.

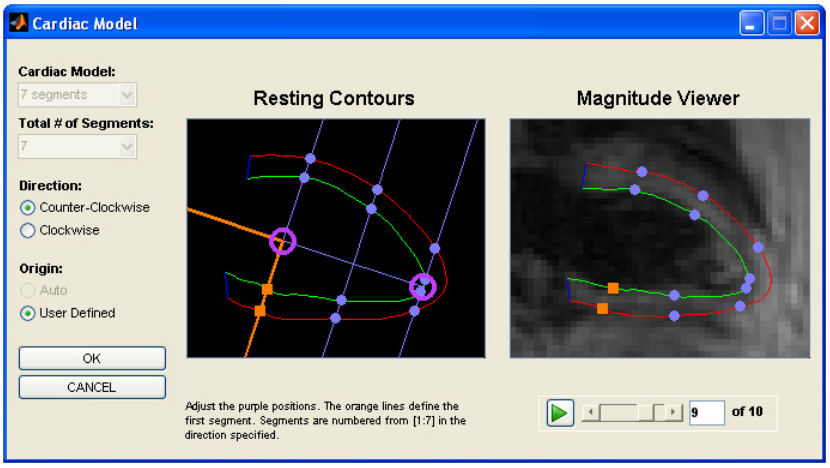


Short axis cardiac model



- Select the cardiac model options:
  - Model type: 4 (apex) or 6 (mid/base) segment model
  - Total number of segments
  - Direction: number the cardiac segments clockwise or counterclockwise
  - Origin: automated (center of the epicardium) or manually defined cardiac origin
- Drag the purple circles on the **`Resting Contours`** to define the anterior cardiac segment. Use the **`Magnitude Viewer`** to check your points throughout the image sequence.
- Select **`OK`**

Long axis cardiac model



- Select the cardiac model options:
  - Direction: number the cardiac segments clockwise or counterclockwise
  - All other model options are fixed.
- Drag the purple circles on the **`Resting Contours`** to define the first cardiac segment. Use the **`Magnitude Viewer`** to check your points throughout the image sequence.
- Select **`OK`**

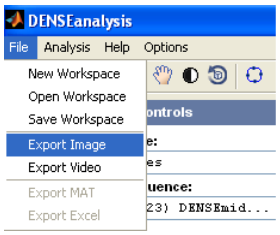
9. EXPORTING IMAGES & VIDEOS

You may export high-resolution images and videos, suitable for inclusion in your presentations and publications. Image and video export is accessible from any tab, exporting whatever is currently displayed.

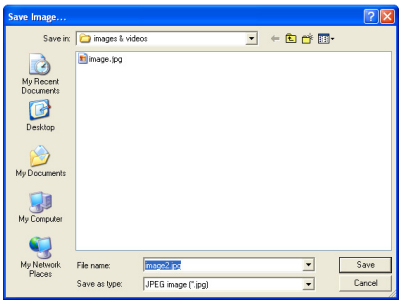
The exported imagery will be the same size as you see on screen, but at a resolution that you define. Note the software does not limit your image or video resolution; you may therefore make some very large files!

EXPORT IMAGE

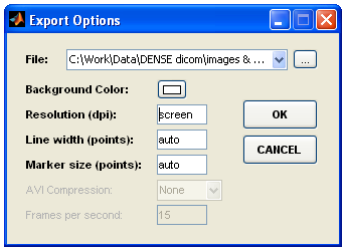
- From the **`File`** menu, select **`Export Image`** to access the image export tool.



- Navigate to the required directory, enter a file name, and select a file type. Available file types include BMP, EMF, EPS, JPG, PDF, and TIFF.
- Select **`Save`**.

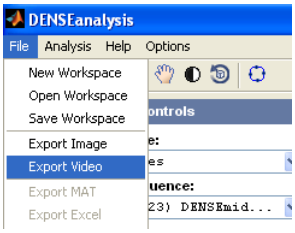


- Select from the available export options:
  - Background color
  - Resolution in dots per inch (positive integer or **`screen`**)
  - Line Width (positive integer, **`auto`**, or **`none`**)
  - Marker size (positive integer, **`auto`**, **`none`**)
- Select **`OK`**

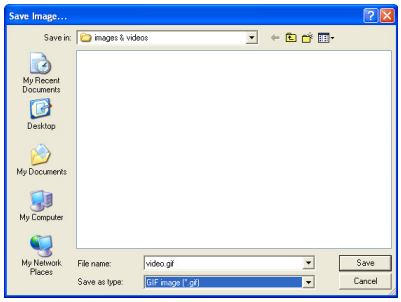


EXPORT VIDEO

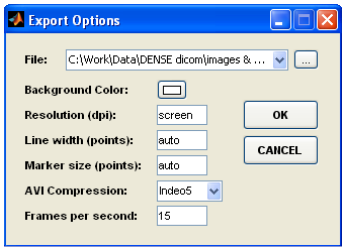
- From the **`File`** menu, select **`Export Video`** to access the video export tool.



- Navigate to the required directory, enter a file name, and select a file type. Available file types include AVI and GIF.
- Select **`Save`**.



- Select from the available export options:
  - Background color
  - Resolution in dots per inch (positive integer or **`screen`**)
  - Line Width (positive integer, **`auto`**, or **`none`**)
  - Marker size (positive integer, **`auto`**, **`none`**)
  - AVI compression codec (for AVI files only)
  - Frames per second



- Select **`OK`**

Notes:

Some AVI compression codecs may not be available on your machine, or the video may look strange after export. Try other AVI codecs (specifed by a 4-letter code) by right-clicking on the AVI compression bar and entering a new code. However, if this codec is not correctly installed and accessible by MATLAB, this function will end in error.

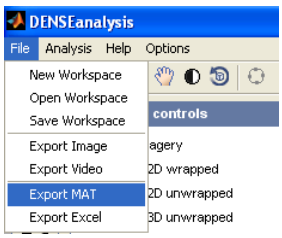
10. EXPORTING MAT AND EXCEL FILES

For further analysis, you may export matlab data files and Microsoft Excel files.

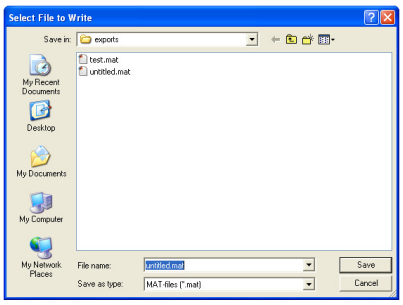
EXPORT MAT

The MAT file will contain wrapped and unwrapped phase imagery, acqusition parameters, and pixilated displacement information.

- Run analysis and select the Analysis tab.
- From the **`File`** menu, select **`Export MAT`** to access the MAT-file export tool.



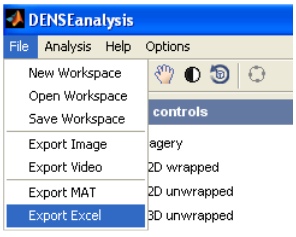
- Navigate to the required directory and enter a file name.
- Select **`Save`**.



EXPORT EXCEL

Excel file export is only enabled for cardiac regions of interest. This function will export strain and twist values for various cardiac sectors and layers.

- Run analysis of a cardiac region of interest, and select the Analysis tab.
- From the **`File`** menu, select **`Export EXCEL`** to access the EXCEL-file export tool.



- Navigate to the required directory and enter a file name.
- Select **`Save`**.
- If you have not previously defined the cardiac model, you will have to do so (see Section 8)