DENSEms

Multi-slice module for the DENSEanalysis software

Software release 2011a
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User Manual

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NOTE FROM THE CREATOR…

Welcome to the DENSEms tool! With this software, you can:
- Simultaneously access multiple slices of short-axis left-ventricular DENSE displacement data
- View multi-slice left-ventricular motion
- Quantify multi-slice twist and torsion

SYSTEM REQUIREMENTS

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

This tool has been tested using 64-bit Windows 7 and 64-bit MATLAB r2010. Other operating systems and newer MATLAB versions will probably still work, but no guarantees.

We assume users have knowledge of MATLAB as well as the look and feel of the acquired data. This document is not a primer on MATLAB or the acquisition system!

We also assume users are already familiar with the main DENSEanalysis software package. Please see the DENSEanalysis manual for more information.

TABLE OF CONTENTS

1. INSTALLATION & STARTUP

The DENSEms module is included with the latest version of the DENSEanalysis software. Simply unzip the `DENSEanalysis.zip` file to install.

1.1. PRIOR TO INSTALLATION

- Ensure you meet the aforementioned system requirements

- 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 software, remove any existing search paths pointing to that installation and restart MATLAB (from the MATLAB `File` Menu, choose `Set Path` and remove folders referring to the previous installation).
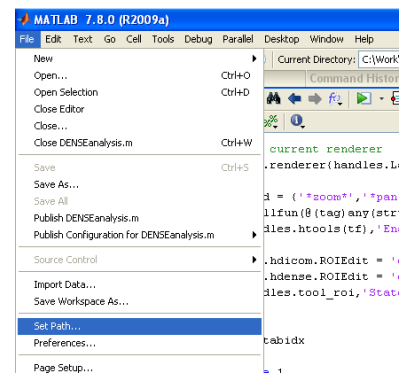
1.2. INSTALLATION

- Unzip the `DENSEanalysis.zip` file to a location of your choice

- Open MATLAB

- Navigate MATLAB to the new DENSEanalysis folder

- Run `DENSEsetup` in the MATLAB command window
 If `DENSEsetup` failed for any reason, the DENSEanalysis program will not function as expected!

1.3. STARTUP

- Open MATLAB

- Navigate MATLAB to the new `DENSEanalysis` folder

- Run `DENSEms` from the MATLAB command prompt

2. DENSE ANALYSES

Before we may access and evaluate multiple slices of short-axis left-ventricular DENSE data via the DENSEms utility, we must first recover tissue displacement from each individual slice via the DENSEanalysis tool. This section outlines a typical DENSEanalysis workflow; please refer to the DENSEanalysis manual for more information.

- Run **DENSEanalysis** from the Matlab command line

- Create a new patient workspace or access an existing patient workspace with one or more short-axis slices of DENSE data.

- For each short-axis DENSE slice, define a short-axis region of interest delineating cardiac anatomy.

- Select **Run Analysis** from the **Analysis** menu to estimate tissue displacement from the DENSE data.

- Explore the completed analysis to ensure accurate phase unwrapping and plausible displacement measurements.

- Access the cardiac model tool by exploring any strain visualization option or by selecting **Cardiac Model** within the analysis tab.

- Define short-axis cardiac parameters, ensuring an appropriate cardiac model for the given slice (typically a four-element model for apical data and a six-element model for mid-ventricular and basal data).
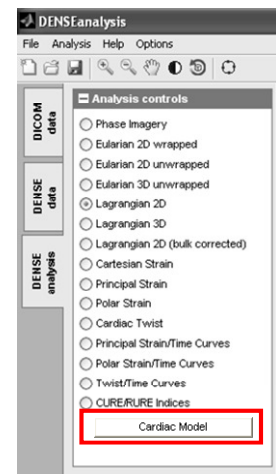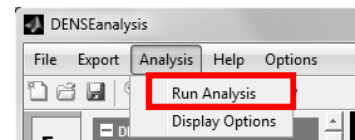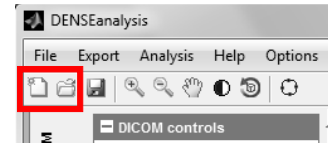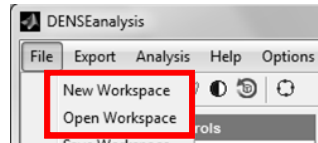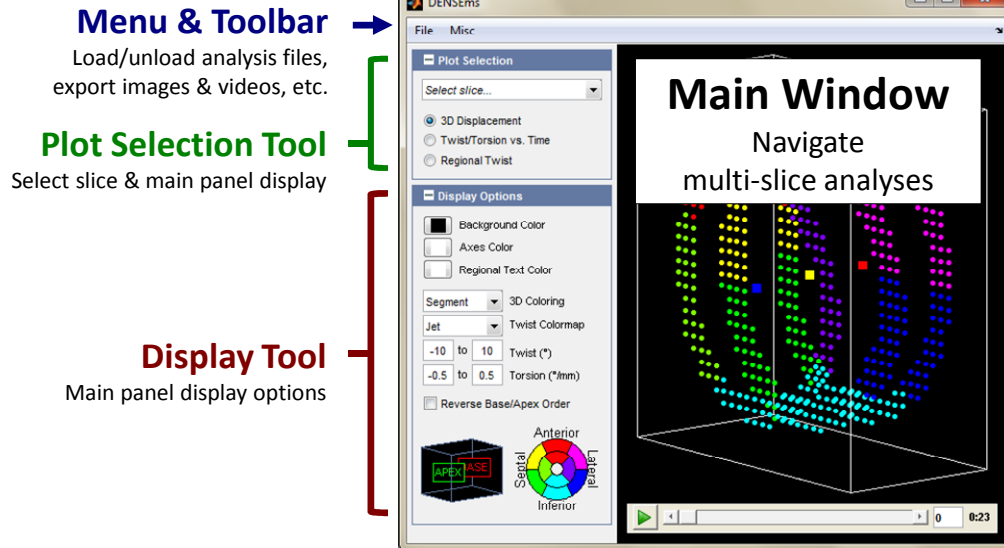
- Select **Export MAT** from the **Export** menu to export a Matlab compatible file containing the completed analysis.

- Repeat the analysis process for all parallel cardiac short-axis slices from a given study/patient.

- We suggest you gather all analysis files (.mat) in a single folder for easy bookkeeping.
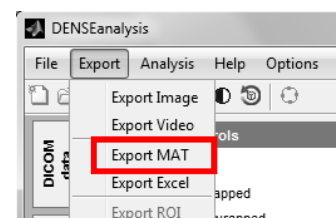
3. INTERFACE

Below is a snapshot of the DENSEms tool. For specific information on each available option, refer to the appropriate section of this manual.

Menu & Toolbar →
Load/unload analysis files, export images & videos, etc.

Plot Selection Tool
Select slice & main panel display

Display Tool
Main panel display options

4. FILES

To begin multi-slice analysis, we must load multiple short-axis analysis files exported from the DENSEanalysis tool into the DENSEms utility.

IMPORTANT NOTES REGARDING ANALYSIS FILES

- Analysis files must be generated using the latest version of the DENSEanalysis software. Previous exports are not compatible with the DENSEms utility.

- Files must be derived from a single study/patient (i.e. all image information must have the same StudyInstanceUID).

- All regions of interest must delineate short-axis left-ventricular cardiac anatomy.

- Slice planes must be unique and parallel.

- Frame indices are assumed to be perfectly aligned (i.e. we assume frame 1 was acquired at the same cardiac phase for all slices, as was frame 2, frame 3, etc.).

4.1. LOAD FILES

- Select `Load File(s)` from the `File` menu.
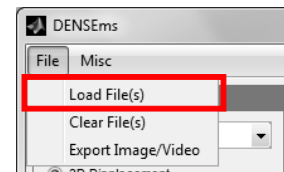
- Navigate to the appropriate directory and select one or more analysis export files generated using the DENSEanalysis software.

- Select `Open`.

- View the file load report.

  – Failure to meet the file criteria above (DENSEanalysis export files, single study, short-axis cardiac anatomy, unique and parallel slices) will result in a load failure.
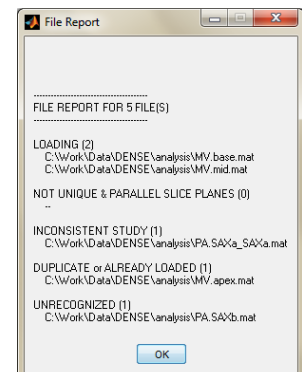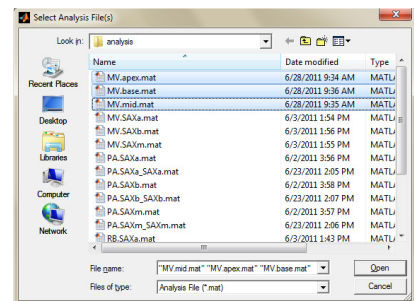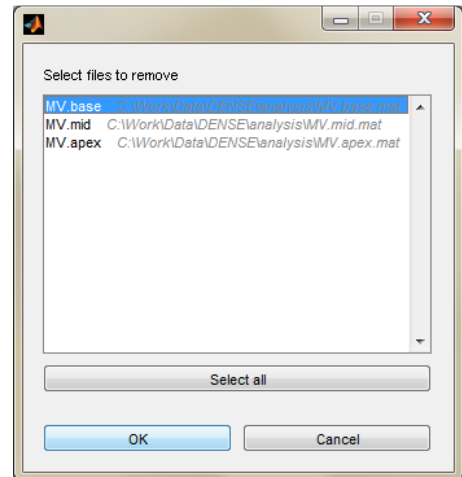
4.2. UNLOAD FILES

- Select **Clear File(s)** from the **File** menu.
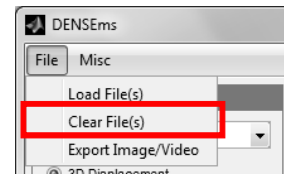
- Select files to remove.
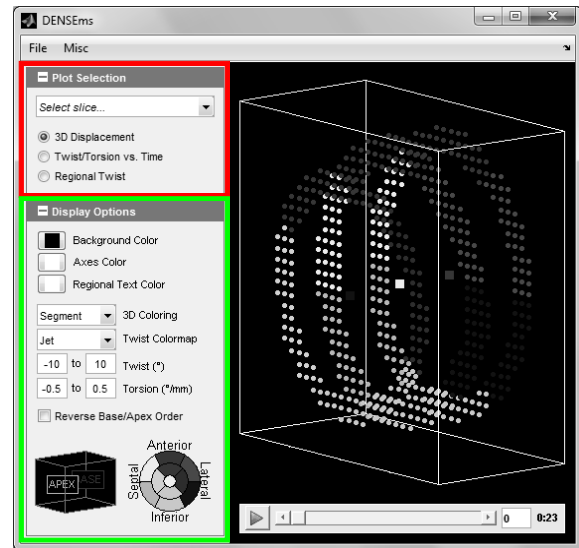- Select **OK**.

5. DISPLAY

Users have access to several multi-slice displays, accessible through the **Plot Selection** tool, including:
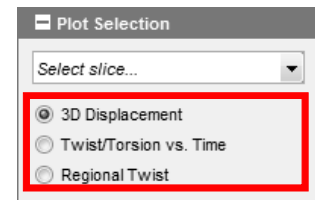
- 3D material point displacement
- Twist and torsion versus time
- Regional twist

Users may change the appearance of each display via the **Display Options** tool.
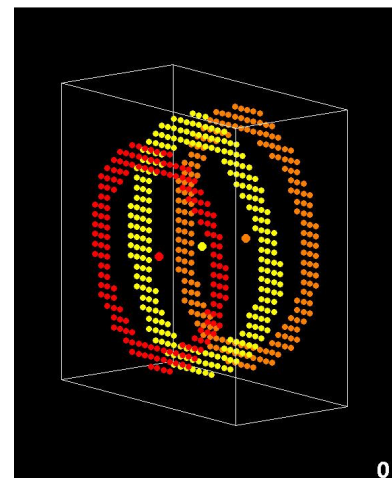

5.1. PLOT SELECTION

Access different displays through the **Plot Selection** buttons.

3D Displacement

This option allows users to navigate material point locations for all loaded slices for any frame of interest.

In addition to material point locations represented by small circles, the software displays the epicardial centroid as a small square.

Twist/Torsion vs. time

This option accesses average twist per slice as a function of time, and torsion as a function of time.

Twist quantifies material point rotation around the left ventricular centerline, measured in degrees.
- Material point rotation is measured with respect to the epicardial centroid of each slice for each frame.
- Positive twist is defined as a counter-clockwise material point rotation when viewed from the apex of the left ventricle (the traditional MR view).

Average Twist quantifies the average twist per slice among all material points for each frame, measured in degrees.

Torsion quantifies the change in average twist per unit longitudinal length, measured in degrees per mm of length.
- For each neighboring slice pair, we quantify the change in average twist over the distance between slices. We average these values to produce our torsion measurement.
- Positive torsion indicates a decrease in average twist from apex to base.
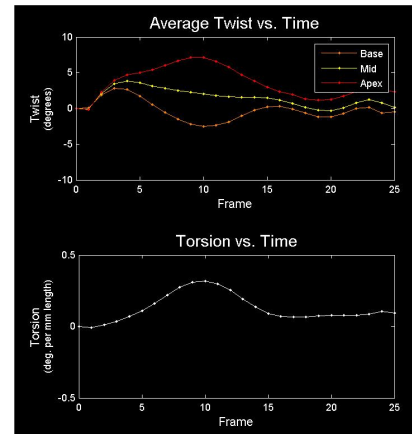
Regional Twist

This option allows users to visualize average twist values within radial segments of cardiac anatomy.

Regional Twist measures the average twist in a specific radial segment of cardiac anatomy, measured in degrees.

The displayed layers traverse slices of cardiac anatomy from the basal level in the outer layer to the apical level in the inner layer.

Slices are colored according to the twist range (Section 5.8) and twist colormap (Section 5.9).
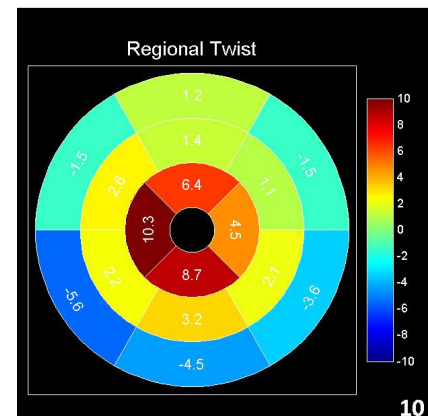
Radial segments are displayed according to the standard American Heart Association model, as viewed from the apex of the left ventricle. The anterior, septal, inferior, and lateral directions are at 12, 9, 6, and 3 o'clock, respectively.
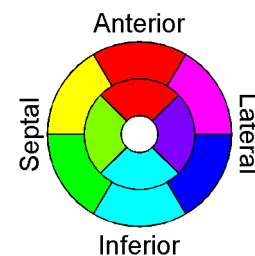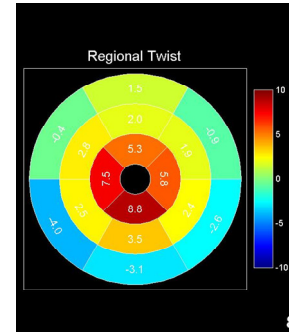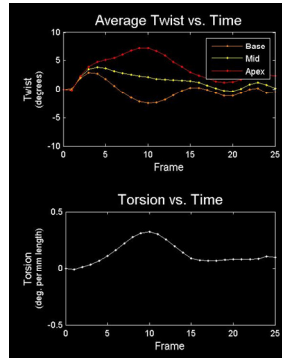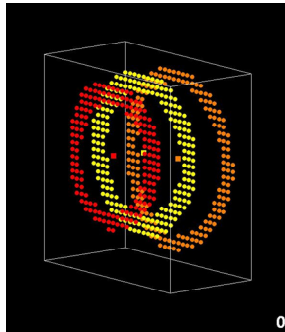
5.2. SLICE SELECTION

Select a slice of interest via the `Slice Selection` dropdown box.
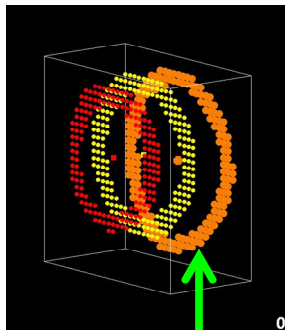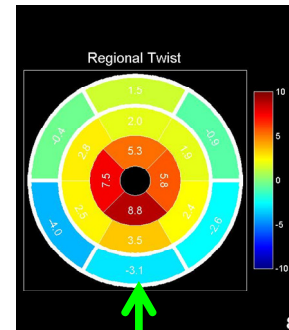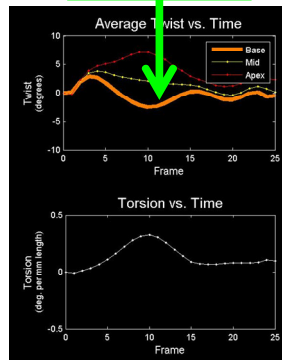This slice will be highlighted in each plot, as displayed below.
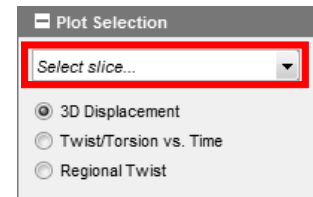

Selected Slice

Selected Slice

Selected Slice

5.3. BASE/APEX SLICE ORDER

The software has predefined basal and apical directions, enabling the regional twist display to place the apical-most slice on the inner-most level of the display. Users may reverse the slice order should the basal and apical slices not lie in the expected direction.

- Select the **3D displacement** display option.
- Compare the Base/Apex Orientation axes to the 3D Displacement display.
- Should the basal and apical slices not lay in the expected and labeled directions, select **Reverse Base/Apex Slice Order**.
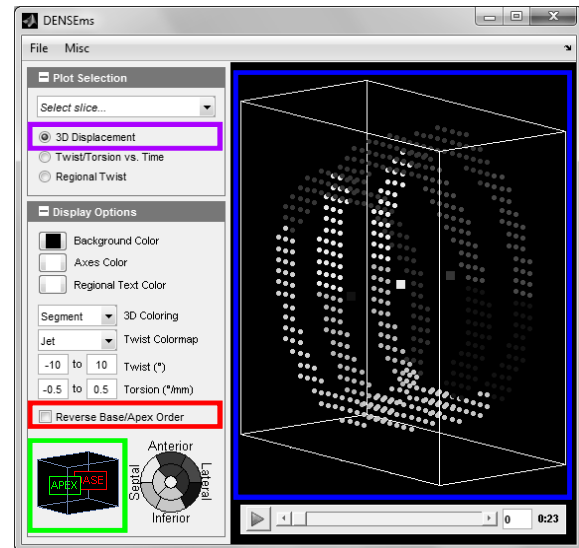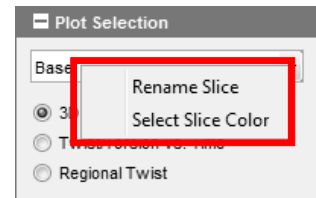
5.4. SLICE NAMES & COLORS

The name and color of each slice are important identifiers:

- – In the **3D Displacement** display, material points can be colored according to the slice color.
- – In the **Twist/Torsion vs. Time** display, lines are colored and labeled according to the respective slice color and name.

- Select a slice of interest.
- Right-click the Slice Selection dropdown box.
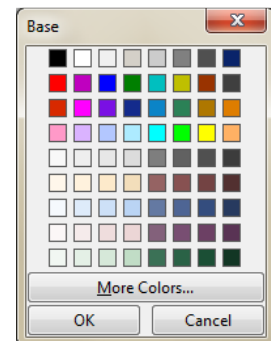- Select from the available options.

Rename Slice

- Modify the slice name.
- Select OK.
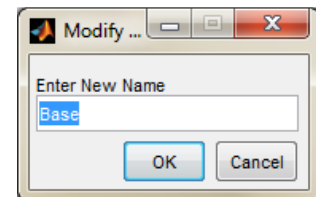
Recolor Slice

- Modify the slice color.
- Select OK.

5.5. ALTERNATIVE 3D COLORING

Users may select from alternative 3D material point color schemes, coloring points according to their radial segment or twist value rather than the slice color.

Radial Segment Coloring

- Select the **3D displacement** display option.
- Select the **Segment** option from the 3D coloring dropdown menu.
- Compare the Radial Color Sample axes to the 3D Displacement display to locate each radial segment.
  - As the radial color sample is viewed from the apex, we suggest viewing the 3D display from the apex.
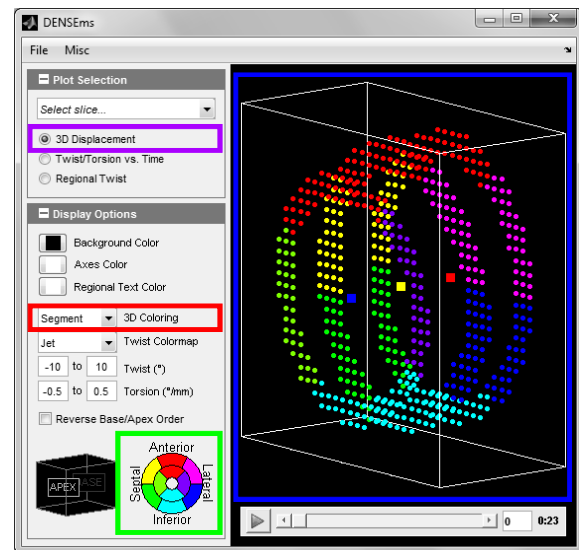
Twist Coloring

- Select the **3D displacement** display option.
- Select the **Twist** option from the 3D coloring dropdown menu.
- Each material point in the 3D Displacement display is colored by its twist value, according to the twist range (Section 5.8) and twist colormap (Section 5.9).
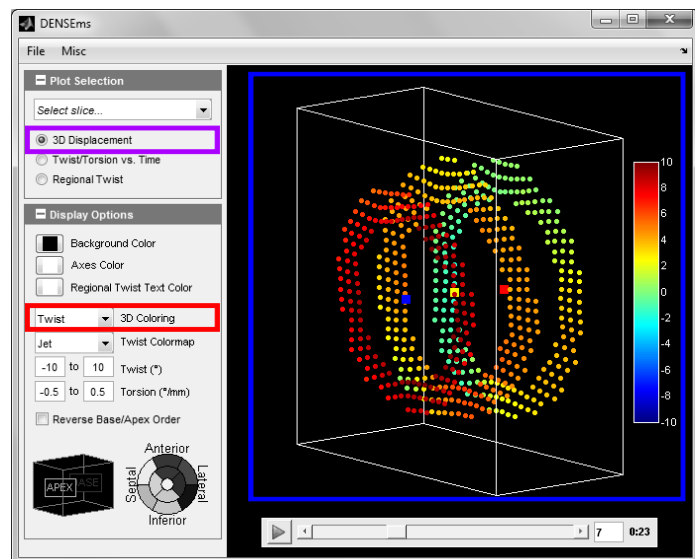
5.6. 3D VIEW OPTIONS

- Select the 3D Displacement display.
- Left-click, hold, and drag within the 3D box to rotate the 3D view
- Right-click within the 3D box to select from available views.
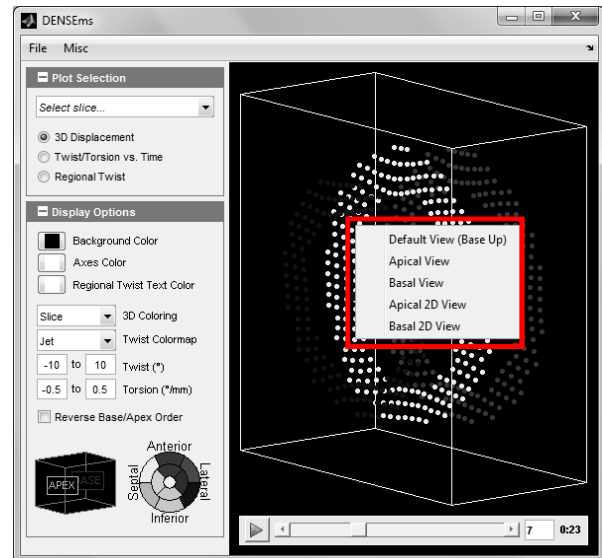
5.7. REGIONAL TWIST OPTIONS

- Select the `Regional Twist` display.
- Right click any regional twist layer.
- Select from the available options:
  - Toggle text for all layers on and off via the `Display Text` option
  - Adjust the number of segments in the selected layer.
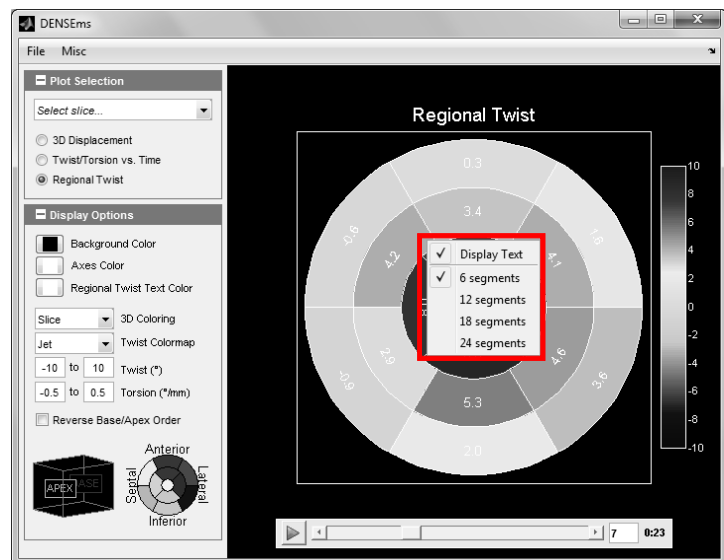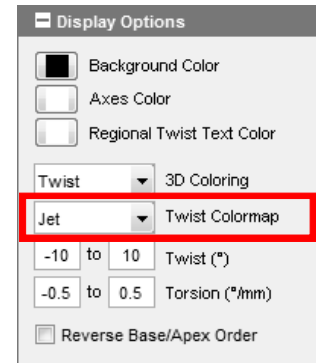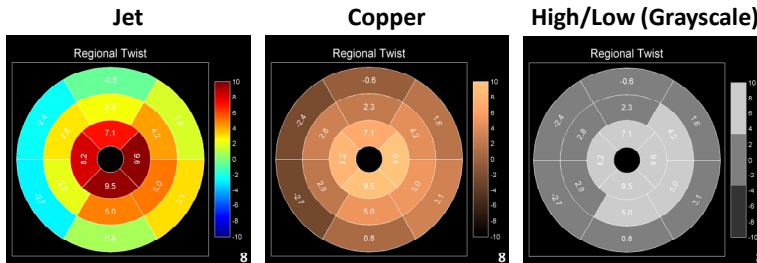
5.8. TWIST/TORSION RANGE

- Enter new range values to adjust the twist and torsion ranges within the Twist/Torsion vs. Time and Regional Twist displays.

Twist/Torsion vs. Time
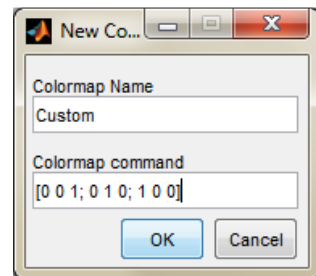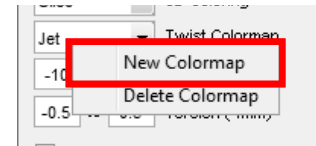
Regional Twist

Twist Range

Torsion Range

Twist Range
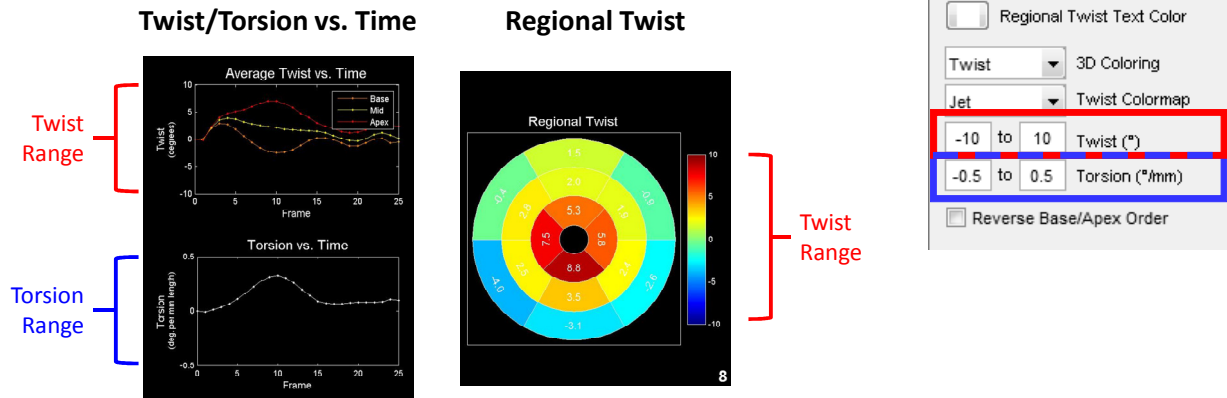
5.9. TWIST COLORMAP

Select Colormap

- Select a colormap from the **Twist Colormap** dropdown menu.

| **Jet**	**Copper**	**High/Low (Grayscale)**

New Colormap

- Right click the **Twist Colormap** dropdown menu.
- Select **New Colormap**.

- Enter a name for your colormap.
- Enter a matlab command for your colormap.
  - The matlab command must evaluate to an [Nx3] matrix, where N is between 1 and 128. The colormap spans the minimum to the maximum of the twist range.
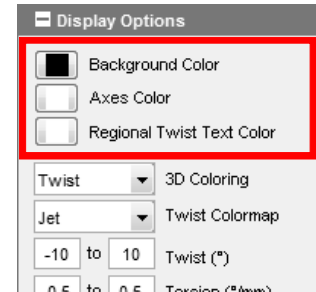- Select **OK**.

Delete Colormap

- Right-click the **Twist Colormap** dropdown menu.
- Select **Delete Colormap**.
- Select **OK**.
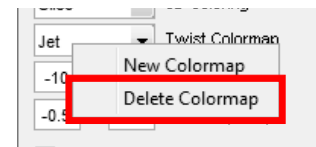
5.10. Background/Axes/Text Color

- Select a color option:

  - **Background Color**
  - **Axes Color**
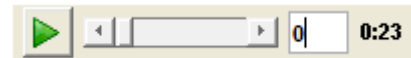 - **Regional Twist Text Color**

- Modify the color.
- Select **OK**.

5.11. Playbar

- Navigate through time via the playbar:
  - Scroll through the frames
  - Enter a specific frame of interest
 - Play all frames in a continuous loop.

6. EXPORT

Users may export high-resolution images and videos of the main display window, suitable for inclusion in papers and presentations. Users may also export twist & torsion measurements to a data file.

Image/Video export

Images and videos are captured directly from the current display. Videos traverse all available frames. Users may select from a number of image and video formats, including:

- Bitmap image (*.bmp)
- Enhanced Metafile (*.emf)
- EPS file (*.eps)
- JPEG image (*.jpg)
- Portable Document Format (*.pdf)

- Portable Network Graphics image (*.png)
- TIFF image (*.tiff)
- Uncompressed TIFF image (*.tiff)
- AVI file (*.avi)
- Animated GIF file (*.gif)

- Select `Export Image/Video` from the `File` menu

  - Navigate to the appropriate directory
  - Enter the file name to be exported
  - Select the appropriate file type

- Select `OK`.

- Select from the available export options

  - Size
    Select the screen size, or enter the height & width in inches
  - Resolution
    Select the screen resolution, or enter resolution in dpi
  - Video speed:
    Frames Per Second (for AVI/GIF only)
  - Compression
    AVI compression (for AVI only)

- Select `OK`.
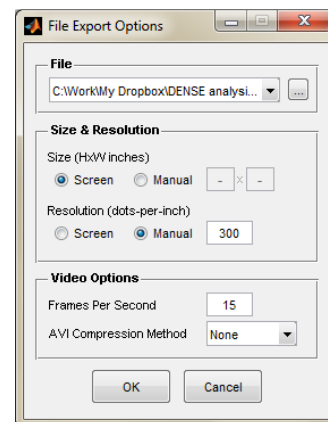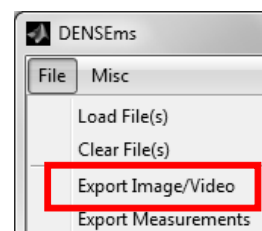
Measurement Export

Users can output a comma delimited text file (csv) or a Microsoft Excel spreadsheet (.xls) of the average twist, torsion, and regional twist values per frame.

- Select `Export Measurements` from the `File` menu

  - Navigate to the appropriate directory
  - Enter the file name to be exported
  - Select the appropriate file type

- Select `OK`.