

MRVIEWER MANUAL

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GUI MANUAL

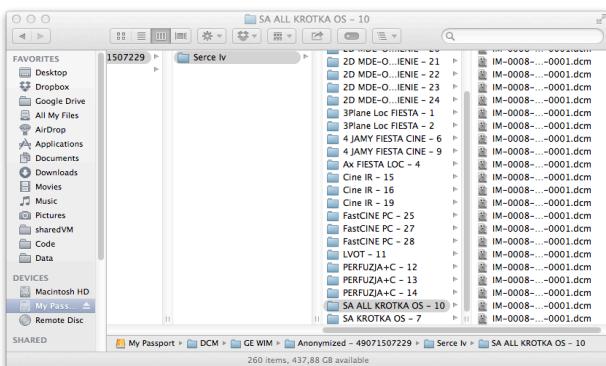
Matlab data from DICOM data

Input

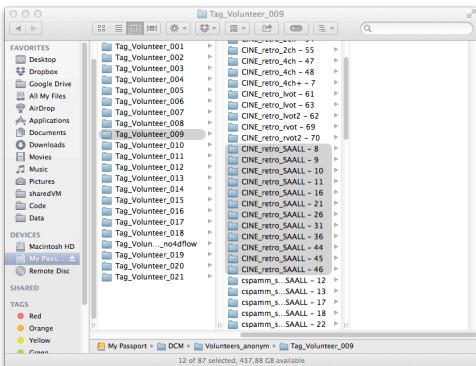
Arranging data is the most crucial part of working with mrviewer.

To convert data from DICOM to Matlab we can work only on one study at a time. We are using just CINE SAX (short axis images). We can use Dicom files that are located in two types of directories:

1. All CINE SAX Dicom files in one directory



2. Different series in different directories, but all directories in the same parent directory



To get this type of folder structure Osirix software can be used.

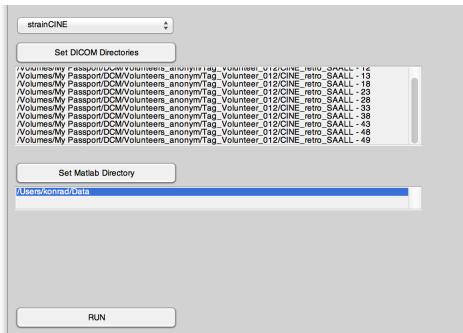
Output

Data will be put in defined ‘Matlab directory’/‘patient name’. ‘Matlab directory is defined in `mrdicom2matlab`, ‘patient name is taken from Dicom files.

Processing

IMPORTANT! You may have problems if there are non-English letters in the path to any of the folders.

1. Run `mrviewer`, choose `Menu -> Create folder with MAT from DICOM folder` (`mrdicom2matlab`).



2. Use the button ‘Set Dicom Directories’. Choose Dicom directories as explained previously (not files)
3. Use the button ‘Set MAT Directories’. Choose Matlab directory and run. This is a directory where all the processed data will be stored. Remember it because it is used in the next steps of the processing.
4. Hit ‘RUN’ button.

Run mrviewer

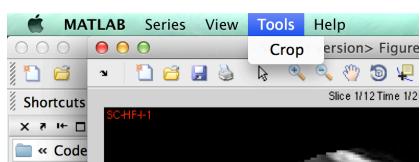
Run `mrviewer`. Choose working (MAT) directory (Menu → Open folder with MAT data)

Hot keys

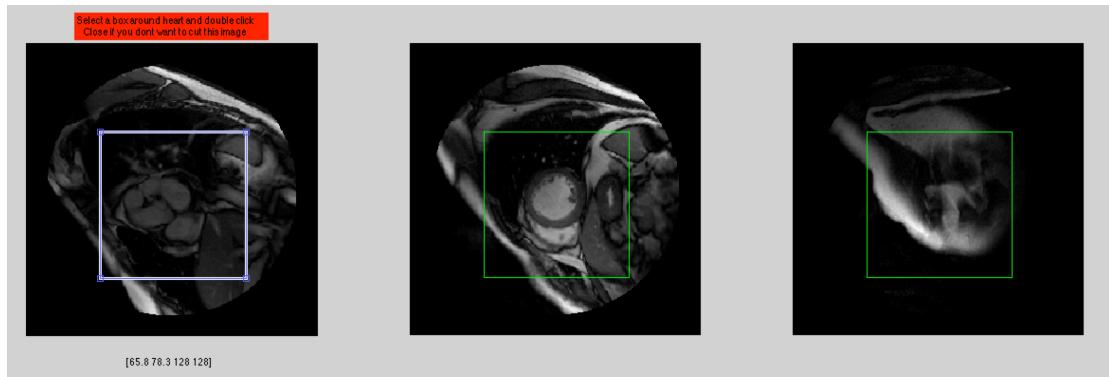
Left/right	Previous/next timeframe
Down/up	Previous/next slice
;/'	Go to end systole/end diastole frame
s	Choose series
v	Choose view
r	Reload series and view lists
Space/.	Play movie/slower/faster
m	Different mask modes
g	Export to gif
enter	Copy current study path to clipboard
Command w	close

Crop data

Choose crop from tools menu

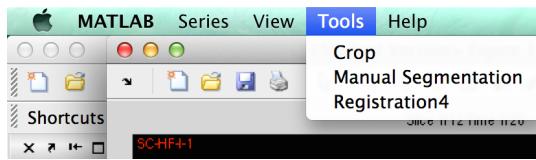


Drag the rectangle, and then double click on it.



You can see results by selecting mrData view (from menu or keyboard 'v')

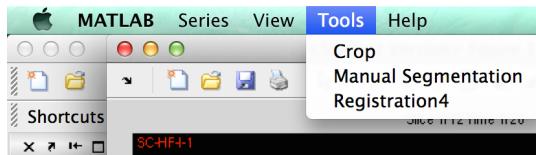
Registration



Necessary step to calculate strain and to do propagation of contours in segmentation.

Longest (~1min per slice) step.

Segmentation



1. Browse through the series. Find end systole (ES) and end diastole (ED) frames. Enter values in menu -> set some parameters or keyboard 's'
2. Segment the data. There two ways to make it semi-automatic:
 - a. Approximation (Auto operations -> **Auto (approximation)**).
 - i. If manual segmentations was performed in one frame, it copies segmentation to all frames
 - ii. If manual segmentation was performed two or more frames, frames in between are approximated based on the two.
 - b. Displacement field (Auto operations -> **Auto (track based on displacement field)**). Registration has to be performed before using this step. Takes manual segmentation from ED and tracks it based on displacement field.
 - c. Do **NOT** use Auto operations -> Auto (register based on displacement field).
3. Close segmentation window. Results will be saved automatically. If you don't want to save results select Menu -> Quit (do not save)
4. In mrviewer you can see results by selecting Segmented view (from menu or keyboard 'v').

Hot keys

Left/right	Previous/next timeframe
Down/up	Previous/next slice
1	ENDO - new/modify point segmentation
2	EPI – new/modify segmentation
x	Choose point in between first and last sector (RVLV point) to AHA 16 sectors.
s	Setting dialog
d	Delete contours from displayed frame

Strain calculation

