

# ICMA 2.0

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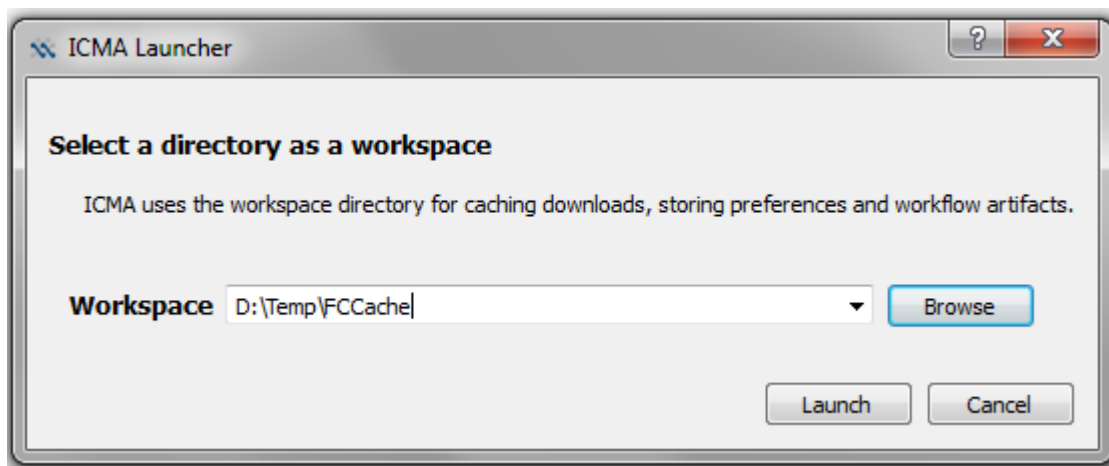
## Introduction

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The Integrated Cardiac Modelling and Analysis Module (henceforth referred to as ICMA), is a subject specific cardiac-ultrasound image based analysis and finite-element-model building software. The software is aimed to help perform strain analysis. It also enables them to compare the subject's cardiac geometry with a population or with that of the subject over time.

## Workspaces

Workspaces provide a convenient cache location to store preferences, past choices for directories, images etc. They are designed to reduce downloads from PACS, as studies are static and do not change. Consequently, US images are stored in the cache when accessed from a PACS. However, the number of images is limited by the cache size. Users can alter and clear the space through the preferences. A Fanout cache is created at the workspace location.



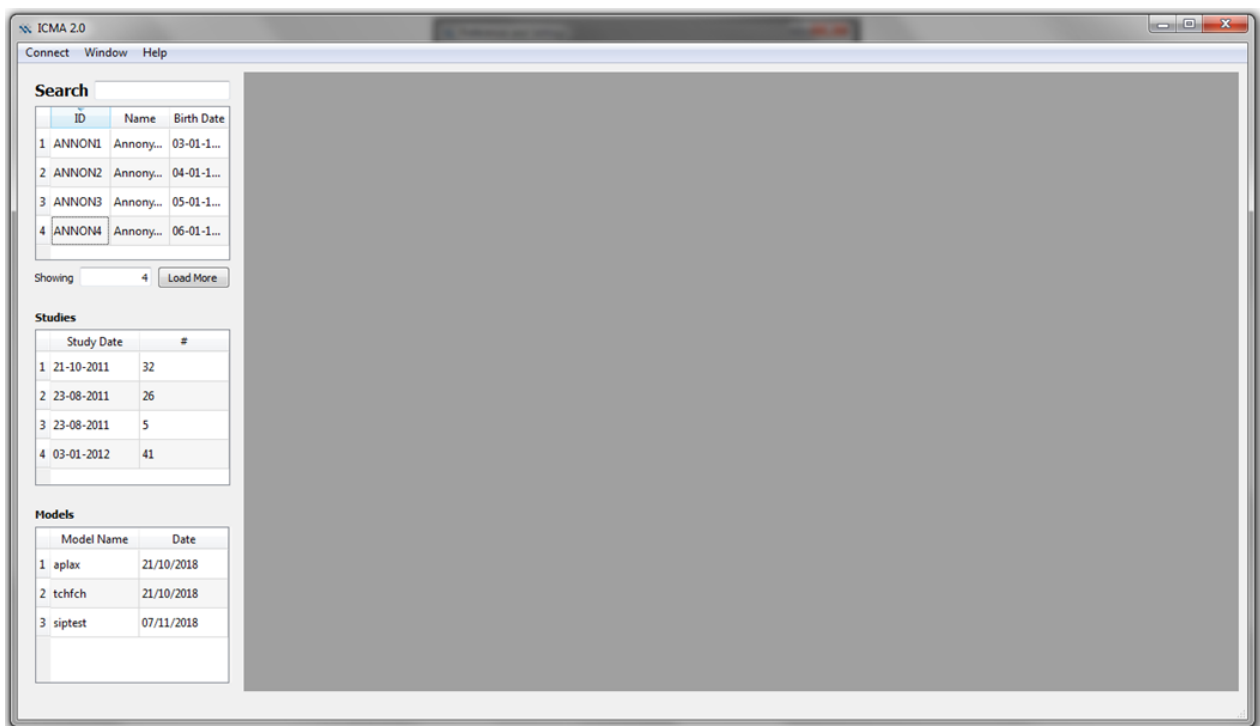
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## Loading data

DICOM data can be accessed from PACS, however, PACS needs to support WADO (Web Access of Dicom Objects) protocol. Opensource PACS like DCM4CHEE provide this. If your target PACS does not provide this, you may have to develop an interface or use DCM4CHEE as an intermediary.

Locally stored DICOM files can also be accessed either through the DICOMDIR file or by directly pointing to the directory. In the latter case, all the directories are recursively parsed and DICOM studies are loaded.

The data is organized per patient.



Double clicking on the patient name will list all the study instances associated with the patient. Also any models associated with the patient is also listed.

## Analysing Images and Creating Models

DICOM cine images associated with the study are loaded in a tabbed window.

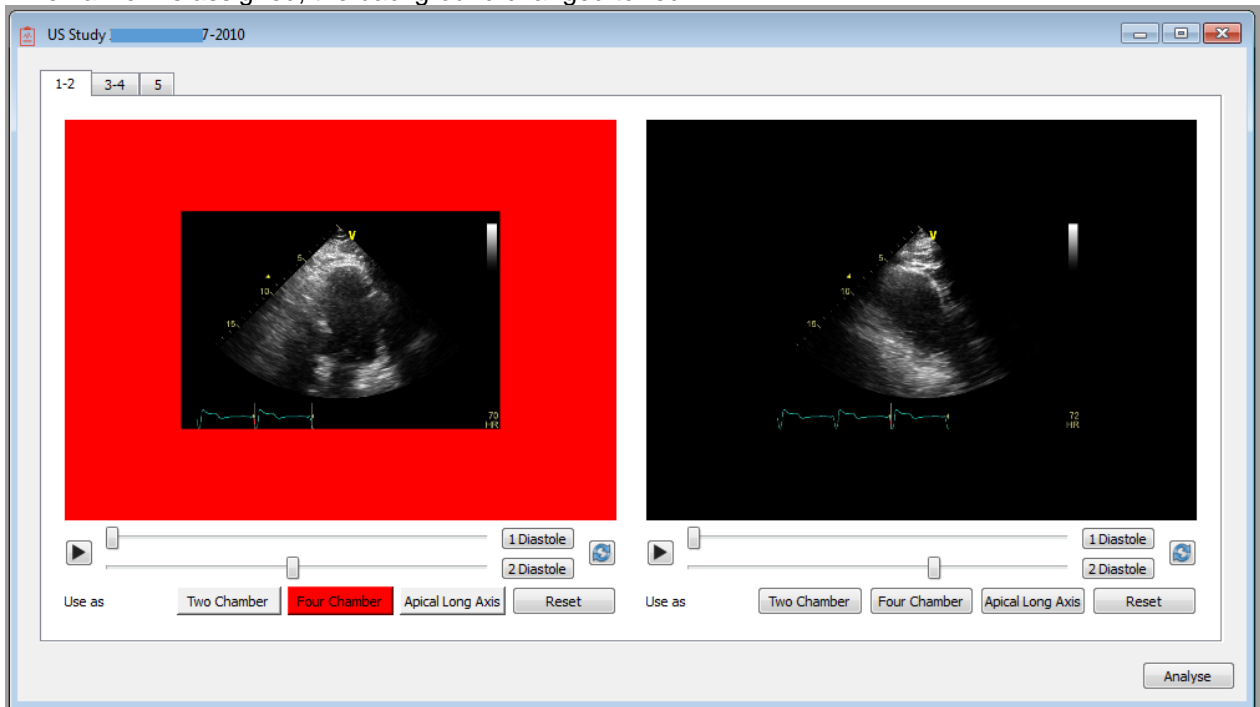


The number of images per tab and number of rows are configurable through the Preferences window.

## Setting up for speckle tracking

Images for Speckle tracking should be selected through this window. Users are expected to select the Long Axis view associated with the image and the start and end of a cardiac cycle.

The start and end diastole can be selected by moving the sliders. To lock in a selection, the Diastole button needs to be clicked. The reset icon next to these buttons can be used to return to the tool selected values. The long axis view can be specified by clicking the Chamber buttons. When a view is assigned, the background changed to red.



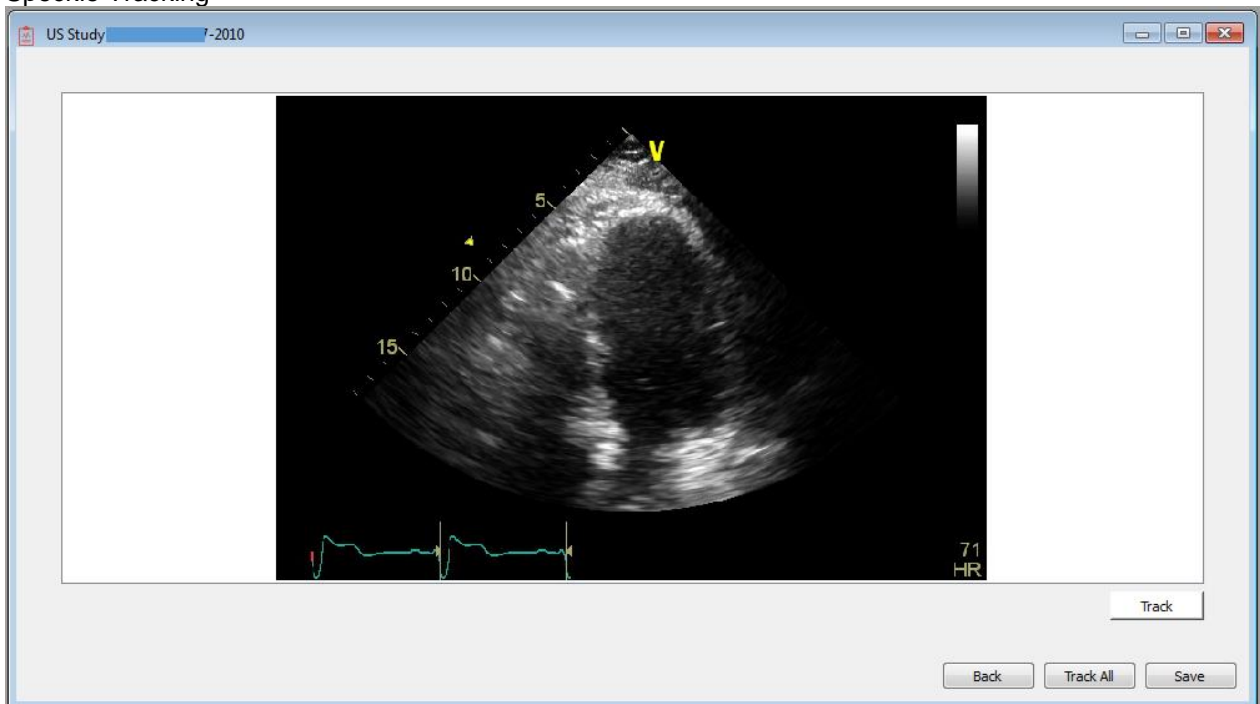
Only one image can be assigned to a view at a time. If an another image is selected for the view, the previous one is released.

View specification can be released by the 'Reset' button.

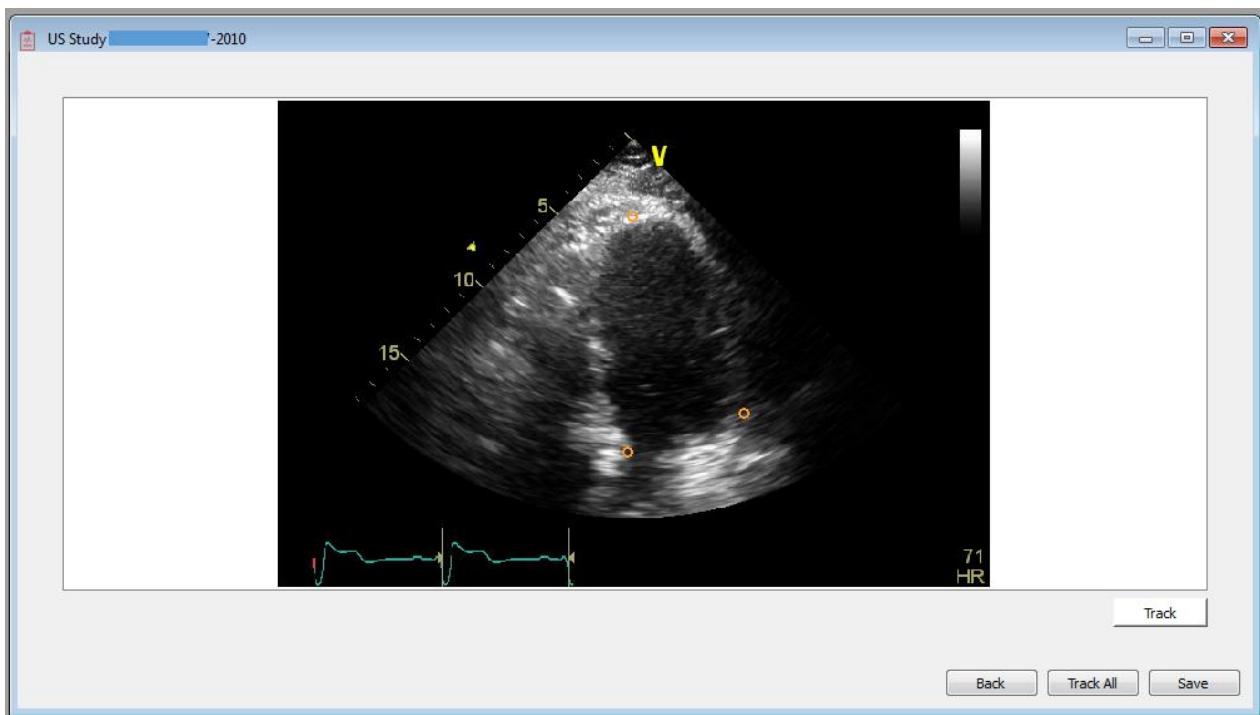
One or more (up to three) views can be selected for speckle tracking and model fitting.

After providing the cardiac cycle, view details. The process can be started using the Analyse button.

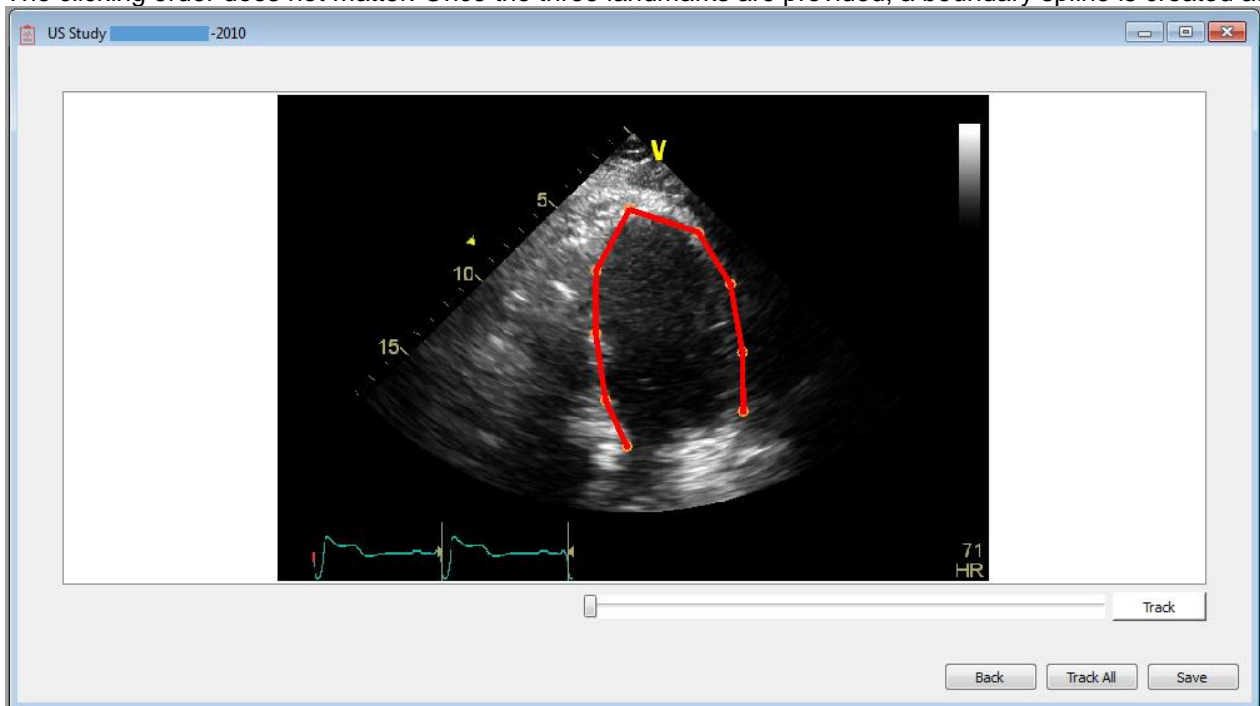
### Speckle Tracking



For each selected view a tracker column is created. Landmarks can be created by clicking on the images. The first frame corresponds to the start End Diastole image. You are required to provide the base plane and Apex locations by clicking. The view allows for three points to be created

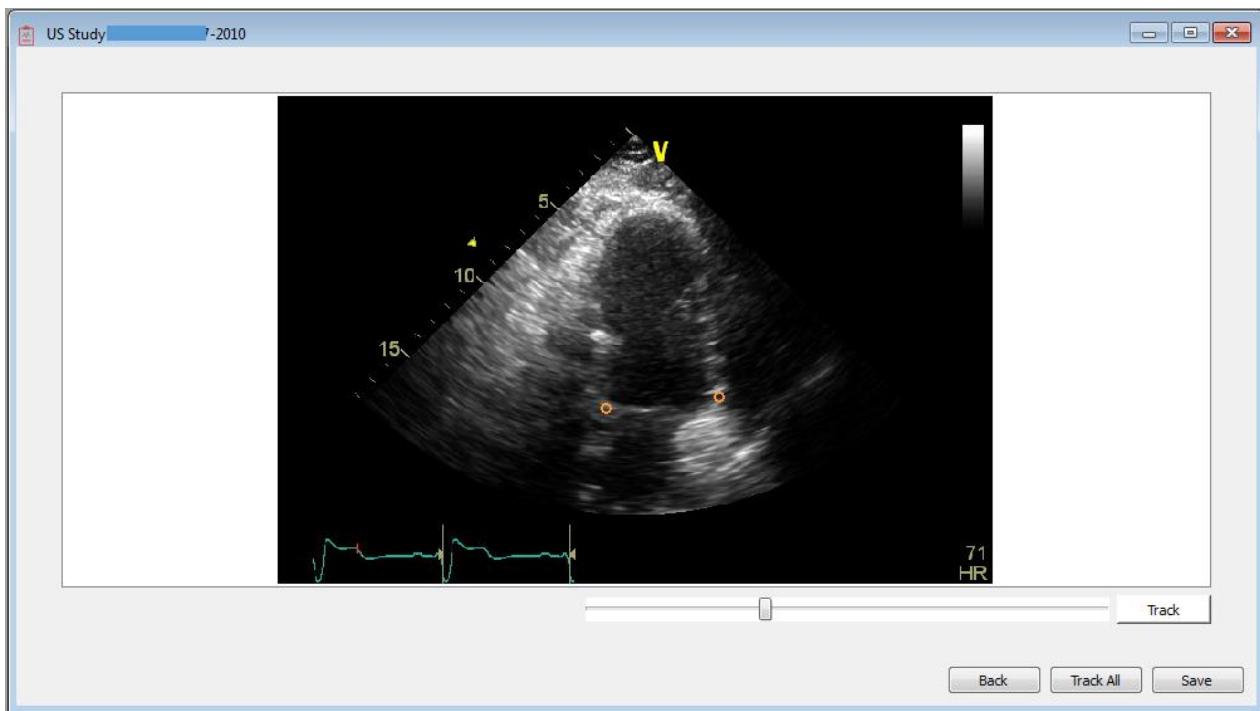


The clicking order does not matter. Once the three landmarks are provided, a boundary spline is created as



Additional landmarks are also provided. User can move these points to capture the boundary as desired. The boundary profile is used to create and track speckles, so the boundary affects the final results.

Following this, the baseplane location for the end systole frame should be provided. This frame can be reached by moving the slider, and clicking two landmarks to identify the baseplane location, as

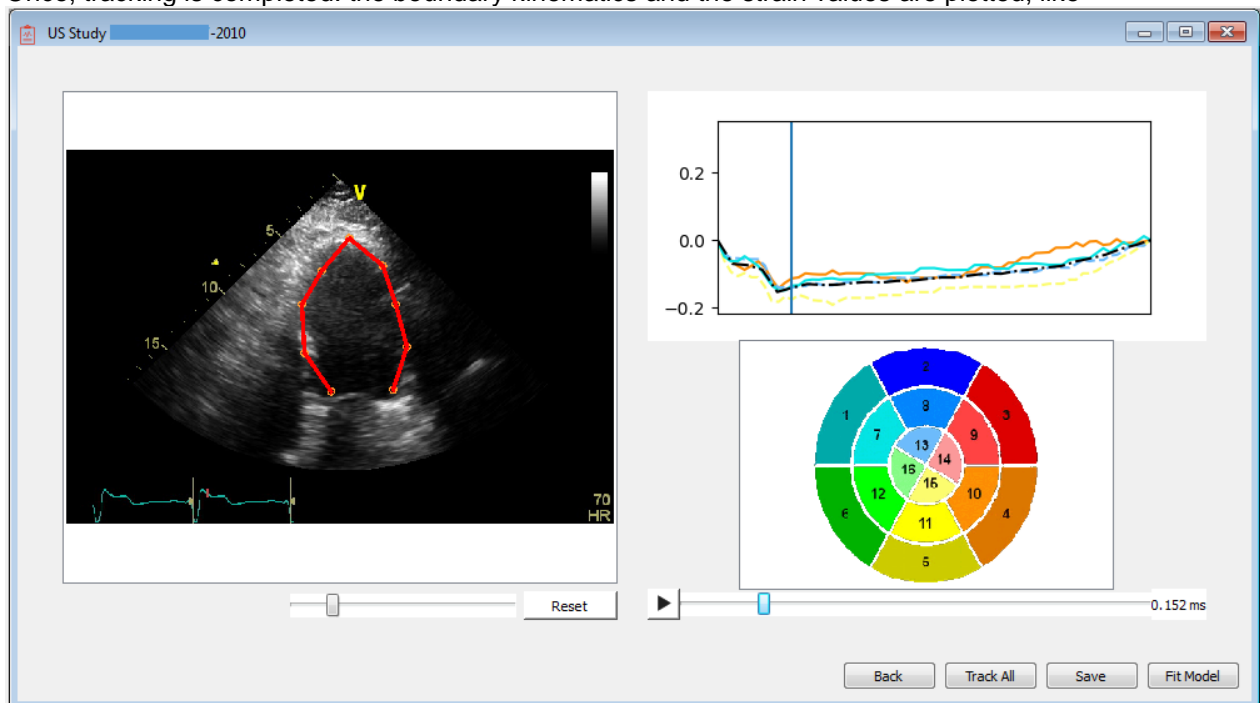


Speckle tracking can then be performed individually (by clicking the Track button) or for all views (Track All) button.

Speckle tracking uses many parameters that can be configured via Preferences.

These parameters include number of frames to be tracked, the number of speckles to be used, inter timeframe smoothing coefficient and weightage for model predicted vs tracked results.

Once, tracking is completed, the boundary kinematics and the strain values are plotted, like

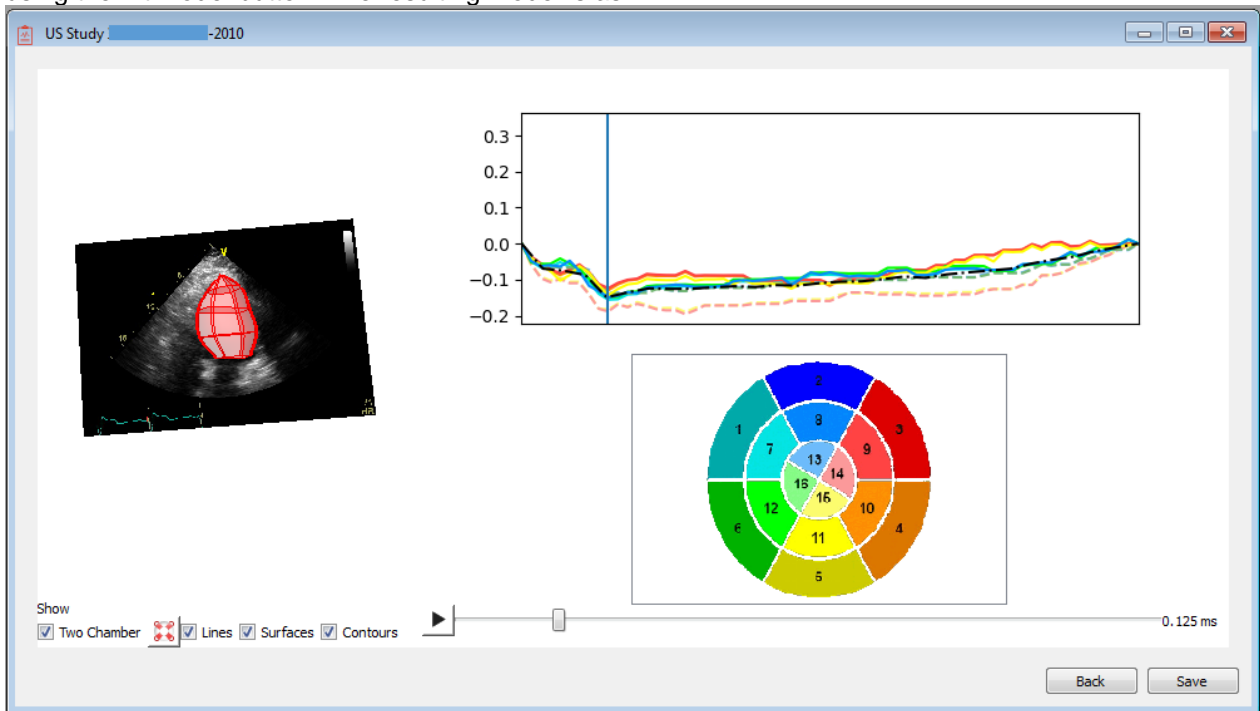


The play button can be used to view the boundary spline motion. The boundary for each frame can be investigated by moving the time slider. The boundaries can be manually modified per frame if necessary. Reset will discard the speckle tracking results and return to the initial state where the landmarks need to be specified.

The speckle tracking results which include the location of the landmarks per frame, per view, strain values

and details regarding the DICOM image can be saved to disk as a xlsx file using the Save button.

A finite element model capturing the chamber geometry based on the tracked boundary can be created using the Fit Model button. The resulting model is as



There is a 3D view on the left, where the mesh and the images are rendered. Check boxes to show and hide the available view are provided. The view can be recentered to the original configuration using the compress button.

Different graphics like lines, surfaces and the contours of intersection between the mesh and an image plane can also be shown and hidden. The bullseye view can be used to select (by clicking on the coloured area with the strain number) the strain values that are rendered.

Models can also be saved using the save button. Note that the parent directory where the model files should be stored needs to be provided, for instance

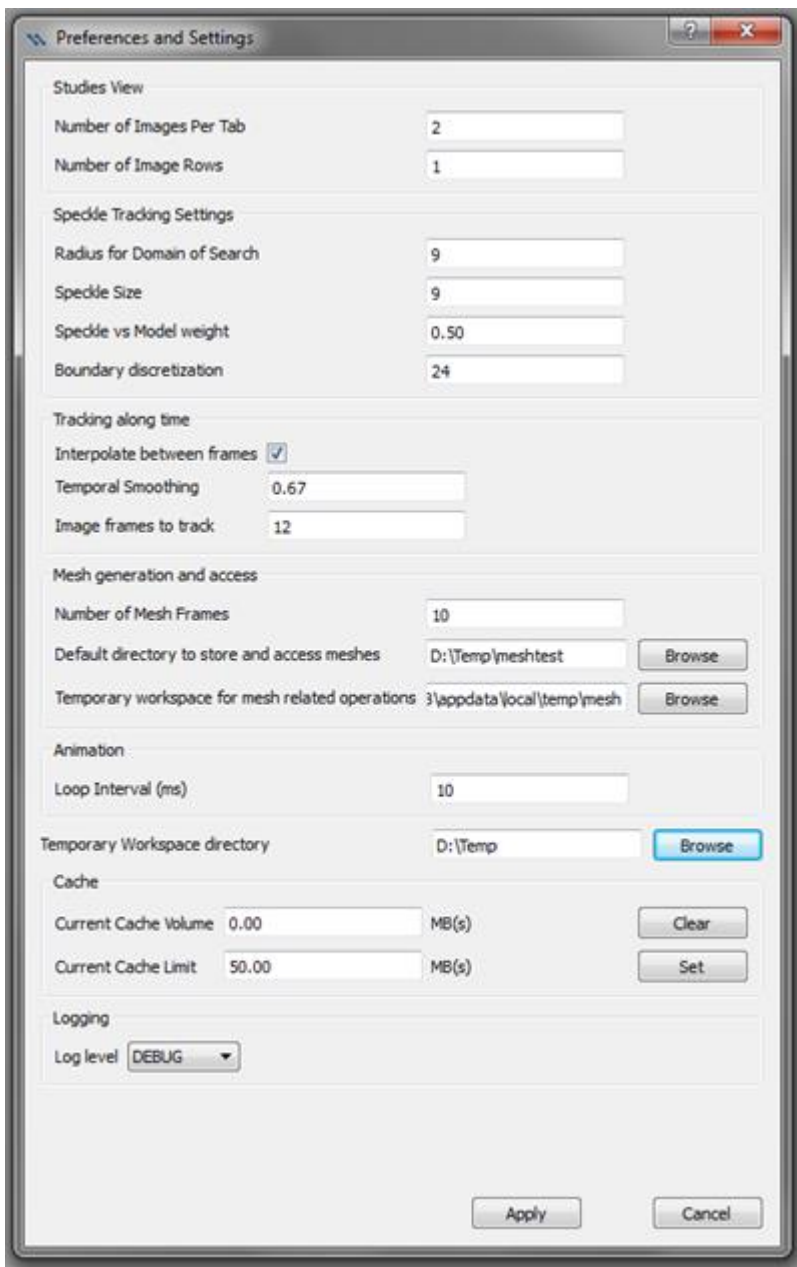


Local Storage (D:) ▶ Temp ▶ meshtest ▶ siptest				
ary ▼ Share with ▼ Burn New folder				
Name	Date modified	Type	Size	
Endo0	7/11/2018 9:48 p.m.	EX2 File	30 KB	
Endo3	7/11/2018 9:48 p.m.	EX2 File	30 KB	
Endo6	7/11/2018 9:48 p.m.	EX2 File	30 KB	
Endo10	7/11/2018 9:48 p.m.	EX2 File	30 KB	
Endo13	7/11/2018 9:48 p.m.	EX2 File	30 KB	
Endo16	7/11/2018 9:48 p.m.	EX2 File	30 KB	
Endo20	7/11/2018 9:48 p.m.	EX2 File	30 KB	
Endo23	7/11/2018 9:48 p.m.	EX2 File	30 KB	
Endo26	7/11/2018 9:48 p.m.	EX2 File	30 KB	
Endo30	7/11/2018 9:48 p.m.	EX2 File	30 KB	
ICMA.model	7/11/2018 9:48 p.m.	JSON File	3 KB	
Endo0	7/11/2018 9:48 p.m.	Meshmixer Docu...	891 KB	
Endo3	7/11/2018 9:48 p.m.	Meshmixer Docu...	895 KB	
Endo6	7/11/2018 9:48 p.m.	Meshmixer Docu...	896 KB	
Endo10	7/11/2018 9:48 p.m.	Meshmixer Docu...	893 KB	
Endo13	7/11/2018 9:48 p.m.	Meshmixer Docu...	897 KB	
Endo16	7/11/2018 9:48 p.m.	Meshmixer Docu...	894 KB	
Endo20	7/11/2018 9:48 p.m.	Meshmixer Docu...	891 KB	
Endo23	7/11/2018 9:48 p.m.	Meshmixer Docu...	894 KB	
Endo26	7/11/2018 9:48 p.m.	Meshmixer Docu...	897 KB	
Endo30	7/11/2018 9:48 p.m.	Meshmixer Docu...	890 KB	
ICMAModelStrains	7/11/2018 9:48 p.m.	Microsoft Excel W...	22 KB	
computedstrains.pkl	7/11/2018 9:48 p.m.	PKL File	5 KB	
APLAX0	7/11/2018 9:48 p.m.	PNG File	75 KB	
APLAX1	7/11/2018 9:48 p.m.	PNG File	75 KB	
APLAX2	7/11/2018 9:48 p.m.	PNG File	74 KB	
APLAX3	7/11/2018 9:48 p.m.	PNG File	75 KB	
APLAX4	7/11/2018 9:48 p.m.	PNG File	74 KB	
APLAX5	7/11/2018 9:48 p.m.	PNG File	73 KB	
APLAX6	7/11/2018 9:48 p.m.	PNG File	72 KB	
APLAX7	7/11/2018 9:48 p.m.	PNG File	72 KB	
APLAX8	7/11/2018 9:48 p.m.	PNG File	73 KB	
APLAX9	7/11/2018 9:48 p.m.	PNG File	74 KB	

The project named siptest is created under the parent directory D:\Temp\meshtest

The folder contains the images associated with the model, opencmis-zinc format model files, stl files for each geometric configuration within the cycle and the strain values in the form of xlsx file. The json and pkl files are required to reload the model in the tool.

The preferences can be altered using  
Windows->Preferences Action



Log of the events are output and can be used for debugging and analysis purposes.

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## Disclaimer

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