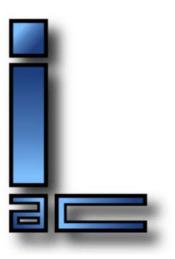
HARP

User Manual



HARP Group

Image Analysis and Communications Laboratory

June 2013

Table of Contents

Introduction	3
Overview	3
Starting HARP	3
Tagged MRI Processing Steps	4
Section I. Data Loading	4
STEPS:	5
Section II. Image Previewing	7
STEPS:	7
Section III. Data Pre-processing	10
ROI Properties	11
Filter Properties	11
Propagate ROI/Filter Settings	12
Section IV. Data Analyzing	12
Steps:	12
HARP Analysis	13
Pacis Eunstions	1.4

INTRODUCTION

Overview

Welcome to HARP. HARP is an image processing software written in MATLAB, a technical computing suite published by The MathWorks™. It was created to study and to characterize the mechanical function of muscles, specifically those in the heart and the tongue. The software does this by analyzing tagged magnetic resonance images. The various processing and analysis routines of the program include image filtering, displacement computation, strain calculation, motion tracking, and more. Current version for public release is 2.0.

Starting HARP

- 1. Open MATLAB.
- 2. Set Current Directory to the folder containing source files of HARP package. Current Directory may be changed by standard Matlab operations.
- 3. Type HARP into the MATLAB command line and hit Enter. HARP will run.

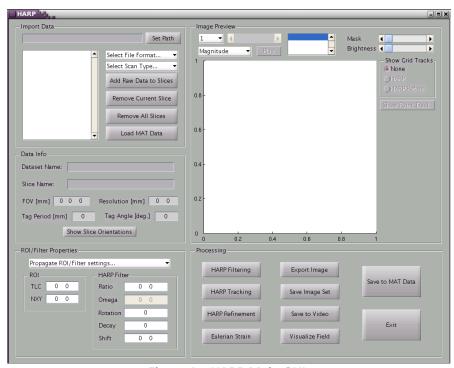


Figure 1 – HARP Main GUI

TAGGED MRI PROCESSING STEPS

This section describes the steps that are commonly carried out to process tagged MRI data sets. It is a good idea to start by setting the current path or working directory to the location where the MR data is stored. Press the "Set Path" button, as shown in Figure 2, and then navigate to the desired location.

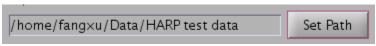


Figure 2 – Setting the working directory

Section I. Data Loading

The process starts by loading the tagged MR data in the Data Loading section, as depicted in Figure 3.

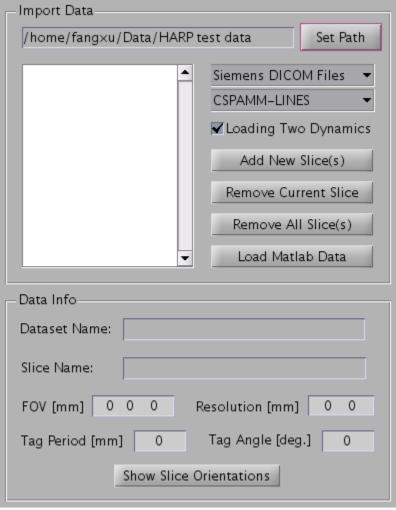


Figure 3 – Data Loading section.

STEPS:

1. Choose file format as shown in Figure 4. As shown, only two types are supported by this version. For the attached tongue test data, the File Format is Siemens DICOM. For the attached cardiac test data, the File Format is Philips PAR/REC.

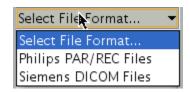


Figure 4 – File Format Selection.

2. Choose the Scan Type as shown in Figure 5. Use Table 1 as a guide to what to select for the scan type. It is expected that there are more than one orientation for tagged MRI data set (e.g., axial, sagittal, and coronal). Another orientation can be loaded with the same steps after one orientation is done loading. For each orientation, one or more data sets can be acquired as different Scan Types—these are called "dynamics". SPAMM only has one dynamic "A". CSPAMM and MICSR use two dynamics, "A" and "B". Note that for dicom data, image magnitude and image phase are saved separately. Both has to be loaded for CSPAMM. (e.g., For the test data containing only the magnitude image, the Scan Type is MICSR.) Keep the "loading two directions" button checked, as more functions are coming in future releases.

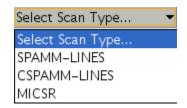


Figure 5 – Scan Type Selection.

Table 1. List of Scan Types and brief descriptions.			
Scan Type	Dynamics	Folder #	Load Order
SPAMM-LINES	1	2	A1 mag, A2 mag
CSPAMM-LINES	2	8	A1 mag, A1 phs, B1 mag, B1 phs, A2 mag, A2 phs, B2 mag, B2 phs
MICSR	2	4	A1 mag, B1 mag, A2 mag, B2 mag

3. Images can be loaded either directly from image files or from saved datasets.

Loading from Image Files

This must be done the first time a data set is examined. Click 'Add Raw Data to Slices.' HARP will open an image loading window (see Figure 6) "Folder #" times (see Table 1). Multiple files should be selected within each image loading window using Ctrl+A. For the tongue test data the MICSR loading order is: A1 mag -> B1 mag -> A2 mag -> B2 mag. According to the Dicom header, these files will be sorted into their physical location and time index. Precisely corresponding images must be loaded within each image loading window or an error will pop up and terminate the loading. (Errors are not always indicated to the user in the GUI, but are often simply appearing in the Matlab command window.) Mind the instructions at the top of pop-up window.

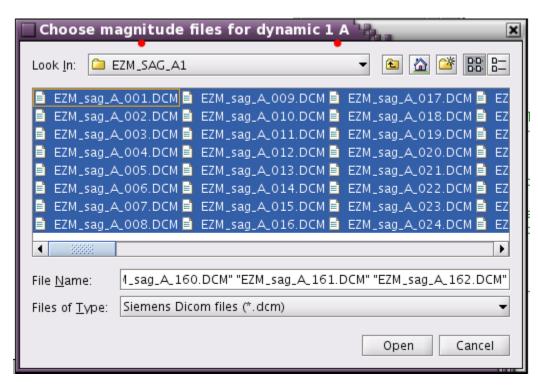


Figure 6 - Loading from MICSR Siemens DICOM files

Loading from Saved Datasets

If a dataset was previously saved, it can be loaded as a MAT file. Click 'Load MAT Data.' Open a dataset (*.MAT), saved during a previous session. After all necessary files have been opened, a loading bar will appear. When all files have been loaded, continue to Step 4.

4. You can remove unwanted slices by selecting the unwanted slice and clicking 'Remove Current Slice.' To remove all slices and start over again, click 'Remove All Slices.

Additional slices may be added to the current session by clicking 'Add Raw Data to Slices' or 'Load MAT Data'.

Once the desired slices are loaded, the Image Previewing phase begins.

Section II. Image Previewing

The Image Previewing GUI is shown below.

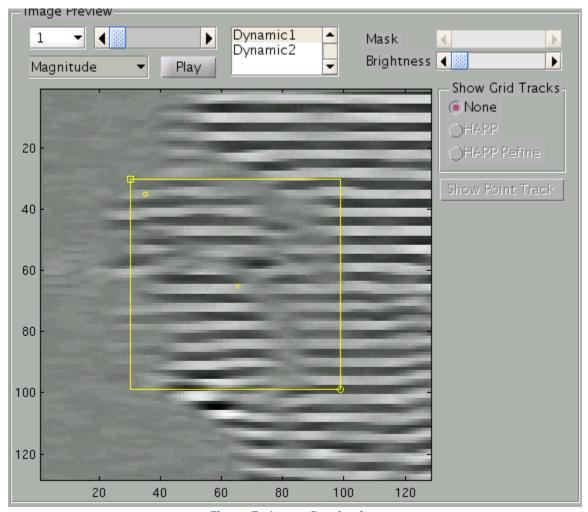


Figure 7 - Image Previewing

STEPS:

1. Select a slice and a dynamic to view from the Slices and Dynamics windows. The image slice and phases (if the slice has more than one phase) will appear in the Preview window (see Figure 7).

- 2. Select each slice, dynamic, and phase to ensure that all loaded images correct. For image slices with multiple phases, "Play" may be pressed to show a "video" of the sequential phases of the selected slice. The "video" will play once in the forward direction and once in the backward direction. Videos may be saved in *.GIF and *.AVI formats by clicking the "Save to Video" button in the Processing section (see Figure 1).
- 3. At any time, the contents of the Preview window may be exported to a MATLAB figure (*.FIG) by clicking the "Export Image" button in the Processing section. Alternatively, all phases of the currently selected image slice may be saved simultaneously in *.PNG, *.JPG, or *.FIG formats by clicking the "Save Image Set" button in the Processing section.
- 4. The Preview Options dropdown box contains various representations of the image slice and phases depending on the type of image and the Data Analysis operations which have been performed on the image. A list of possible representations is shown below (see Figure 8)

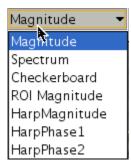


Figure 8 - Preview Options after filtering

5. ROI Specification

The Region of Interest (ROI) must be specified for each phase of each image by moving the yellow rectangle (see Figure 9).

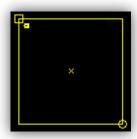


Figure 9 - Region of Interest Rectangle

a. The ROI settings are automatically copied to all the phases and all the dynamics of the current slice.

- b. The ROI rectangle is *translated* by clicking and dragging the tiny square in the upper left hand corner of the ROI rectangle.
- c. The ROI rectangle is *scaled* by clicking and dragging the tiny circle in the lower right hand corner.
- d. The *seed point* is the tiny yellow dot near the upper left hand corner of the ROI rectangle. It should be placed in a region of the tissue that moves without tag jumping. Position it within the muscle and then watch it move as you scroll through the frames using the scroll bar in the top of Figure 7. If it jumps across tags, change it.
- e. The *center point* is the tiny x in the center of the ROI rectangle. In cardiac studies, it should be clicked and dragged to the center of the myocardium for two phases of the slice. Ignore it for tongue studies.
- f. Use "Propagate current ROI to all parallel slices" to copy the ROI to the other slices, as shown in

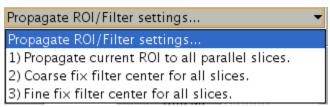


Figure 10 – Propagate settings window.

g. Verify the ROIs by selecting 'ROI Magnitude' in the Preview Options dropdown box. The Preview window will then show only the ROIs defined in next steps (Steps 6-10).

6. Filter Specification

The filter is specified by selecting 'Spectrum' in the Preview Options dropdown box. The filter size and shape are defined in the Preview window by the yellow circle (see Figure 11).



Figure 11 - Filter Ellipse

a. Place the filter circle on one peak in the spectrum view. Don't forget to specify filter placement for both dynamics.

- b. It is possible to manually alter the position and shape of the filter, but it is not recommended. The filter circle may be *translated* by clicking and dragging the tiny + at the center of the filter ellipse.
- c. The filter circle may be *scaled* by clicking and dragging the tiny circle at the right of the filter circle or the tiny square at the bottom of the filter ellipse. Or type size numbers in the HARP Filter boxes.
- d. The filter circle may be *rotated* by clicking either the square or the circle and dragging along the periphery of the filter ellipse. Not necessary when it is a circle.
- e. Once the filter circle encloses a peak, the Preview window should look approximately like Figure 12.

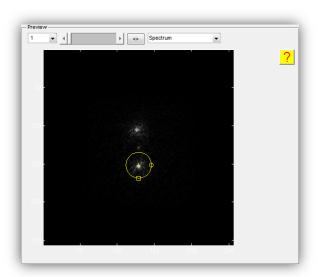


Figure 12 - Centering the filter ellipse

After the ROIs and filters have been defined, the Data Pre-processing phase begins.

Section III. Data Pre-processing

The Pre-processing and Properties subsections of the Data Pre-processing graphical user interface are shown below (Figure 13).

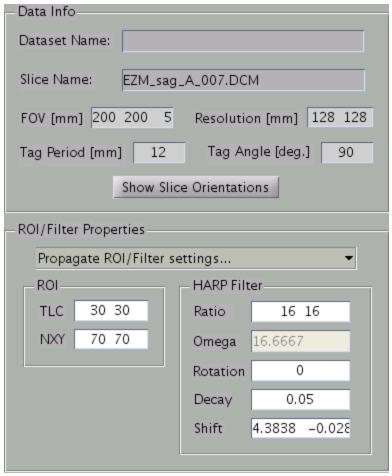


Figure 13 - Properties subsection

ROI Properties

- a. FOV and RES give the Field of View and Resolution of the phase, respectively, and cannot be edited.
- b. TLC gives the "top left corner" of the ROI rectangle and may be adjusted precisely.
- c. NXY gives the number of pixels that the ROI rectangle extends to the right of and below its top left corner and may be adjusted precisely.

Filter Properties

a. 'RATIOS' gives the magnitude of the major and minor axes of the filter circle. They are automatically forced to be equal.

- 'OMEGA' gives the center of the filter in Fourier space, as determined by tag spacing, tag angle, and FOV, for the currently selected dynamic. It should not be adjusted manually.
- c. 'Rotation' gives the rotation value of the filter ellipse in degrees and may be adjusted precisely.
- d. 'Decay' gives the erosion factor of the filter used during filtering and may be adjusted precisely.
- e. 'Shift' gives the coordinate location of the filter ellipse center and may be adjust precisely.

Propagate ROI/Filter Settings...

1) Propagate current ROI to all parallel slices

Copies the current ROI rectangle to all dynamics and phases of all parallel slices.

2) Coarse fix filter center for all slices

Automatically **centers** the filter circle (based on FOV and tag spacing) on a peak of the spectrum for all dynamics and phases of all slices. This option also propagates the filter ratios to all slices.

3) Fine fix filter center for all slices

Automatically centers the filter circle based on the position of the peak of the spectrum and corrects for tag spacing errors. Use this after coarse fix, not before.

After all settings have been finalized, the Data Analyzing phase begins.

Section IV. Data Analyzing

The Data Analyzing GUI functions are listed in the Processing session.

Steps:

1. Click the 'Export Image,' 'Save to Video,' or 'Save Image Set' buttons to export images and videos of the Preview window contents.

- 2. Click the "HARP Filtering" button to automatically filter the spectral peaks of the image slices. Do after setting filters with yellow circle, propagating them to all slices, and checking that they appear on a peak. A loading bar will appear showing each slice being filtered. Once the filtering process is complete, new options will appear in the Preview Options dropdown box.
- 3. Click the "Save to MAT Data" button to save the current session as a *.MAT file to be loaded during a future session. The program auto-adds the date. Save often!
- 4. Click the "HARP Tracking" button to perform traditional HARP method in the selected ROI.
- 5. Click the "HARP Refinement" button to perform SP-HR refinement method. It is able to track large motions in the tongue when traditional HARP tends to suffer from large errors. It uses the seed point you selected earlier on every slice. Therefore you must choose the seed carefully before you use refinement method.
- 6. Click the "Eulerian Strain" button to generate the following Preview Option results for 2D Eulerian strain:
 - a. Ecc Circumferential Strain (Cardiac)
 - b. Err Radial Strain (Cardiac)
 - c. Exx Horizontal Strain
 - d. Eyy Vertical Strain
 - e. CircAng1_2D Angle between 1st Principal Strain and the Circumferential Direction (Cardiac)
 - f. CircAng2_2D Angle between 2nd Principal Strain and the Circumferential Direction (Cardiac)
 - g. Ep1_2D 1st Principal Strain
 - h. Ep2 2D-2nd Principal Strain
- 7. Click the "Show Slice Orientations" button to render the image slices as planes in 3D space and compare their orientations.
- 8. If desired, click the "Exit" button to end the current session and close HARP.
- 9. Continue analysis in the Visualization window by clicking the "Visualize Field" button after HARP tracking or refinement is performed. A new Window will appear. This is the Visualization Window, which is used for both HARP Analysis and Visualization.

HARP Analysis

The Visualization Window looks like this (Figure 14):

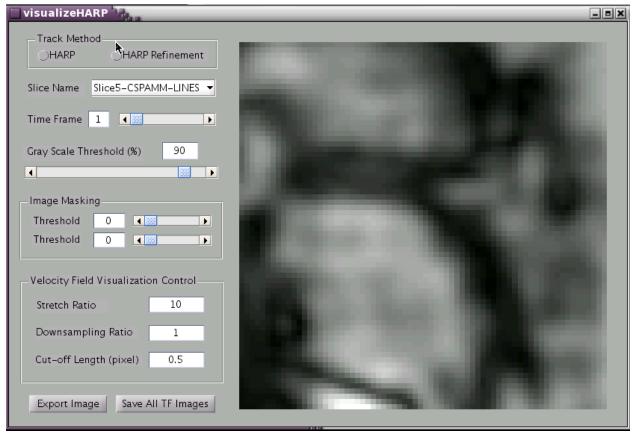


Figure 14 – The Visualization Window

Basic Functions

- 1. Select the desired slice, frame and tracking method.
- Apply a mask to the image by changing the two thresholds in Image Masking session.
 The first threshold is for the first phase and the second for the last phase. The middle
 phases are masked according to the corresponding linear value between these two
 thresholds.
- 3. Change the gray scale threshold to adjust the brightness.
- 4. Stretch ratio scales the motion arrow size.
- 5. Downsampling ratio is an integer to downsample the number of arrows being visualized.
- 6. Use cut-off length to remove any outliers or noises.
- 7. Click the "Export Image" button to export the currently displayed plot as a MATLAB figure (*.FIG).
- 8. All phases of the currently selected image slice may be saved at once in *.PNG, *.JPG, *.GIF, and *.FIG formats by clicking the "Save All TF Images" button.