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1. Overview

Retrospective is a software utility and graphical user interface to reconstruct self-gated cardiac or respiratory CINE MRI acquired with an MR Solutions preclinical MRI system.

Reconstruction is based on compressed-sensing after retrospective sorting of the data into cardiac and/or respiratory time frames, using a navigator signal for cardiac and respiratory synchronization.

2. Contact

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3. Disclaimer

The software has been extensively tested using mouse data acquired with an MR Solutions preclinical 7.0T/24cm system.

However, this does not warrant the functions contained in the program will meet your requirements or that the operation of the program will be uninterrupted or error-free.

In case of questions or issues, please contact Gustav Strijkers.

4. Citing the use of Retrospective

Retrospective is free of use. However, proper referencing the use of Retrospective in scientific publications is highly appreciated.

Citations to Retrospective can be done using the following reference ([link](#)):

Daal, M.R.R., Strijkers, G.J., Calcagno, C., Garipov, R.R., Wüst, R.C.I., Hautemann, D., Coolen, B.F. *Quantification of Mouse Heart Left Ventricular Function, Myocardial Strain, and Hemodynamic Forces by Cardiovascular Magnetic Resonance Imaging*. J. Vis. Exp. (171), e62595, doi:10.3791/62595 (2021).



5. Installation notes

Software download

Matlab source code and a Windows standalone version (using the free Matlab runtime engine) can be downloaded from github:

<https://github.com/Moby1971?tab=repositories>

Installation of the Windows standalone version

`MyAppInstaller_web.exe`

Will install the Matlab runtime engine and the Retrospective program.

Bart toolbox download

The advanced reconstruction options in Retrospective require the Bart reconstruction toolbox, which can be downloaded from:

<https://mrirecon.github.io/bart/>

Bart toolbox installation in OSX

(1) Install Xcode from the Mac App Store

(2) Install MacPorts (<http://www.macports.org/>)

It is recommended to install a newer version of gcc from MacPorts

(3) Installation

```
$ xcode-select --install
$ sudo port install fftw-3-single
$ sudo port install gcc6 (or newer, also change version in Makefile)
$ sudo port install libpng
$ sudo port install openblas
$ make all clean
$ make
```



Bart toolbox installation in Windows 10

(1) Install the Windows subsystem for Linux

Start a windows powershell and run the following command:

```
Enable-WindowsOptionalFeature -Online -FeatureName Microsoft-Windows-Subsystem-Linux
```

A system restart will be needed.

For more information, see:

<https://docs.microsoft.com/en-us/windows/wsl/install-win10>

(2) Download Ubuntu Linux 18.04

For more information see:

<https://docs.microsoft.com/en-us/windows/wsl/install-manual>

Install the appx file by double-clicking in Explorer or in a PowerShell command prompt:

```
Add-AppxPackage .\app_name.appx
```

You will be asked to create a user account the first time you start a Linux command prompt.

(3) Upgrade the Linux distribution

```
$ sudo apt-get update
$ sudo apt-get dist-upgrade
```

(4) Install Bart prerequisites

```
$ sudo apt-get install make gcc libfftw3-dev liblapacke-dev
libpng-dev libopenblas-dev gfortran
```

(5) Download Bart

```
$ wget https://github.com/mrirecon/bart/archive/v0.7.00.tar.gz
```

For WSL1 version 0.4.02 is recommended. Newer versions seem to compile but some functions which are required produce errors. Upgrade to WSL2 for higher versions (see e.g. <https://pureinfotech.com/install-windows-subsystem-linux-2-windows-10/> on how to upgrade).

(6) Build Bart

```
$ tar xvfz v0.7.00.tar.gz
$ cd bart-0.7.00
$ make
$ make utest
$ make test
$ sudo make PREFIX=/usr/local install
```



6. Running the software

Running in Matlab 2021a

The Retrospective software can be started from its root directory from the command line.

```
>> retrospective
```

Notes:

(1) The Retrospective root directory ~/Retrospective contains the following 2 text files:

- | | |
|---------------------------|--|
| <code>bartpath.txt</code> | Bart toolbox installation directory.
Delete this file if the Bart toolbox is not available on your system. |
| <code>mrddpath.txt</code> | Directory which is watched for new MRD files, when 'auto reco' is on.
On the scan computer, the preclinical MRD system directory takes priority.

Make sure that the text files contain exactly 1 line of text. |

(2) Additional licenses may be required.

```
>> license('inuse')
communication_toolbox
distrib_computing_toolbox
image_toolbox
matlab
signal_blocks
signal_toolbox
statistics_toolbox
```

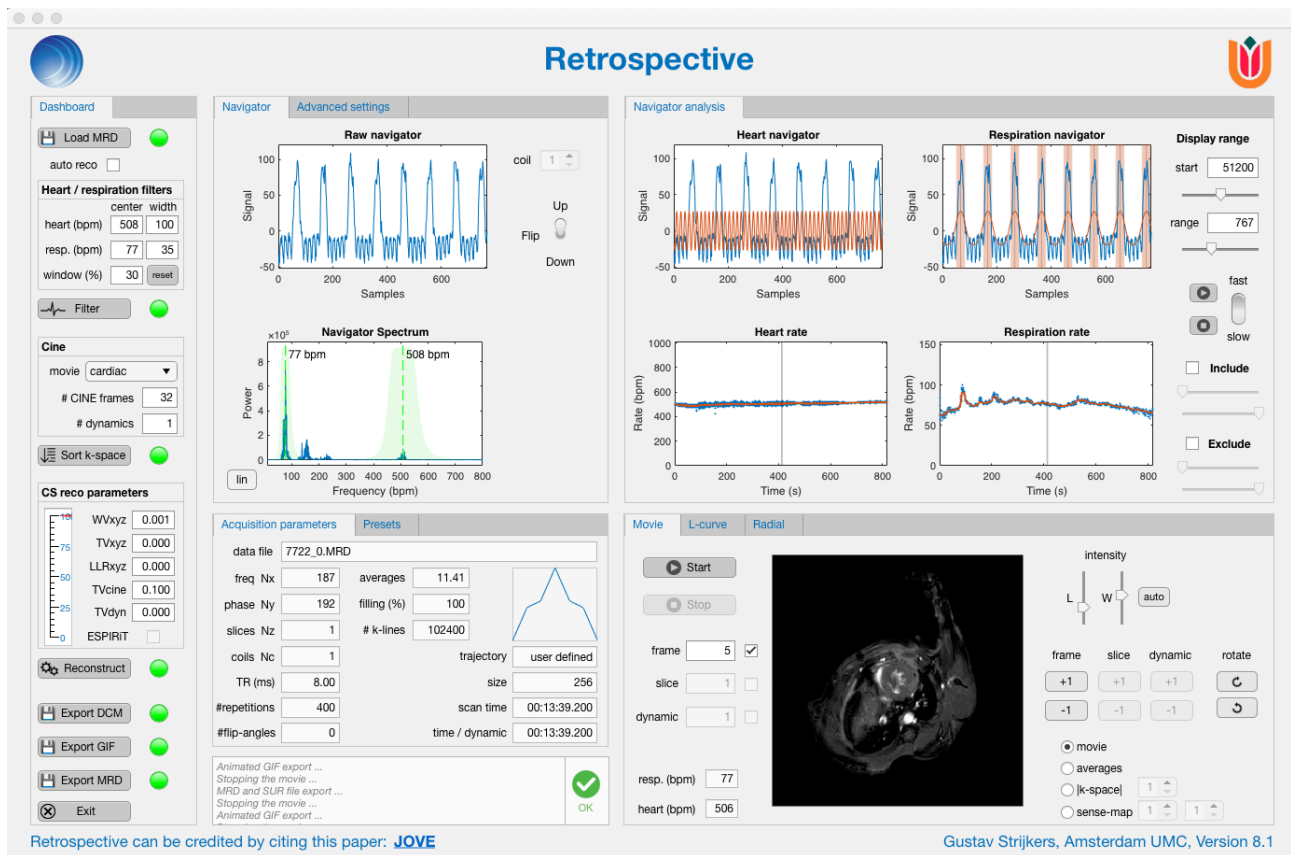
Running the Windows standalone

The Windows standalone version can be run from the start menu or the desktop icon.



7. Basic operation

The Retrospective program operates from a single window with 5 main panels.



Panel 1: Dashboard

This panel contains the task buttons that control the reconstruction process. The dashboard tasks need to be completed from top to bottom. A green light next to the task indicates that the task has been completed. When the light is yellow the task is busy. Red indicates not completed yet.

Panel 2: Acquisition parameters / Presets

This panel lists the relevant acquisition parameters and a few reconstruction presets.

Panel 3: Navigator / Advanced settings

This panel shows the raw navigator signal, the navigator frequency spectrum, and some advanced navigator analysis parameters.

Panel 4: Navigator analysis


This panel shows the navigator signals filtered for cardiac and respiratory motion, as well as the heart and respiratory rates as function of time.

Panel 5: Movie / L-curve / Radial

In this panel the reconstructed CINE movie is shown. There are advanced sub-panels for optimization of compressed-sensing reconstruction (L-curve analysis) and Radial reconstructions (work in progress).



Step 1: Loading data

Press  **Load MRD** to import load the MRD raw data file *.

The data should include navigator data for cardiac and respiratory synchronization.

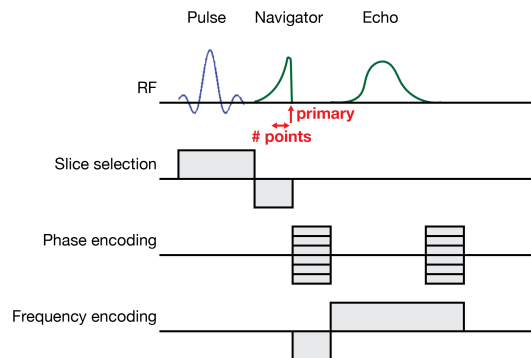
For data acquired with multiple receivers (phased-array RF coil) select 1 of the MRD files.

Relevant acquisition parameters will be shown in panel 2, including the k-space trajectory (linear, zigzag, or user defined).

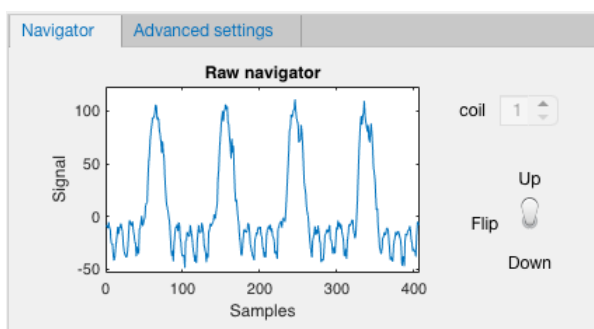
When **auto reco** ☒ is enabled, retrospective will watch the MRD datafile directory and start automatic reconstruction when a new MRD file is added.

Step 2: Inspecting the raw navigator signal

The in-slice navigator is generated by the refocusing properties of the slice selection gradient directly after the RF pulse, as shown in the figure below.



The raw navigator signal will contain rapid oscillations due to cardiac motion and slower periodic peaks due to respiration.



For multi receiver coil data, individual navigators can be inspected with the **coil** toggle switch.

The respiration peaks in the navigator should be positive; in case they are negative, flip the signal with the **Flip** switch.

If cardiac and respiratory oscillations are not clearly visible, change the **primary** point slightly and increase **# points** (typically **# points** = 1 to 5) to see whether the quality improves.



The panel also contains 2 presets for navigator filtering of mouse and rat data. These adapt the values **min/max heart** and **respiration rates**, which determine the search windows for the heart and respiration rate.

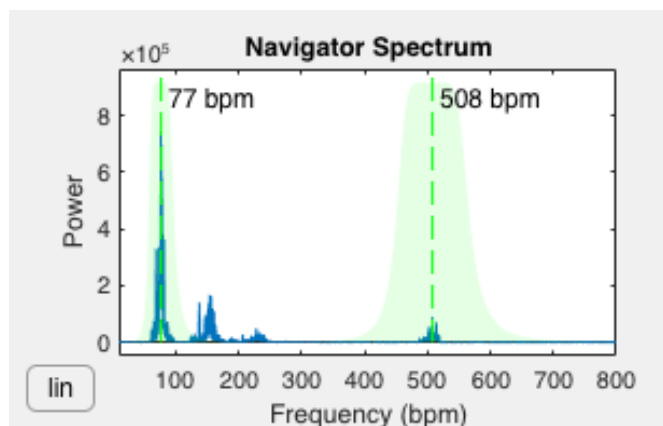
The parameter **freq Nx discard** determines the number of samples that are discarded between the end of the navigator and the beginning of the imaging echo. If an FID artifact is visible in the reconstructed images/movie, increase this number.

Binning of cardiac and/or respiratory motion states can be done using a Gaussian soft weighting of k-lines from neighboring frames (see: Küstner et al., NMR Biomed e4409 (2020). doi:10.1002/nbm.4409) to increase k-space filling and SNR. The #frames value below **Sharing** indicates the number of shared frames. #frames = 0 is recommended in most cases to prevent temporal smoothing.

Step 3: Inspecting the navigator power spectrum

The bottom part of panel 3 shows the power frequency spectrum of the raw navigator signal.

Typically, the spectrum looks as the figure above, with peaks (and higher harmonics) corresponding to the respiratory and cardiac frequencies. The program automatically determines the most likely respiratory and cardiac frequency.




Green shaded areas indicate the position and width of the Butterworth filters, which are used to filter the raw navigator and extract the periodic cardiac and respiratory motion as function of time.

In case the automatic respiration and/or cardiac frequency detection fails, the **center** and **width** filter values can be adjusted in the heart/respiration filters panel, shown below.

Center and **width** determine the center-frequency and width of the Butterworth filters for navigator filtering.

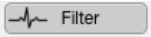
Window (%) determines the percentage of the data that is discarded during respiratory motion.

Press  to reset the values.

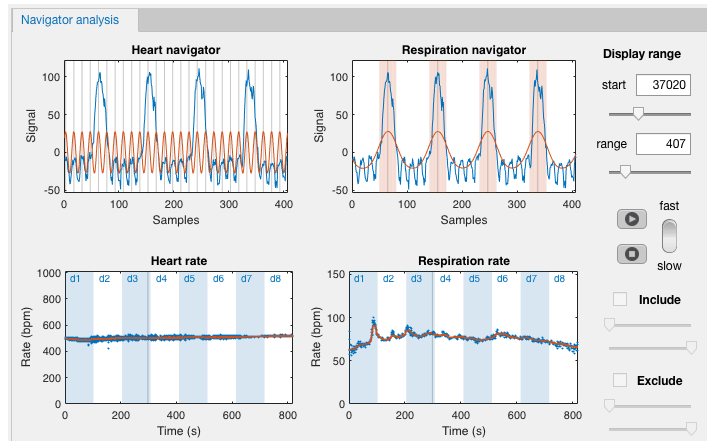
Heart / respiration filters		
	center	width
heart (bpm)	508	100
resp. (bpm)	77	35
window (%)	30	




Step 4: Filter the navigator

Press  to filter the raw navigator signal and extract cardiac and respiratory motion as function of time.

The result may look like this:



The sliders can be used to change the **display range** to inspect the full data set.

Use  buttons to automatically advance the navigator and inspect the data.

The top left figure shows in blue the raw navigator signal and in red the signal filtered for cardiac motion. The gray vertical lines indicate the peaks in the oscillations, which can be used to check the alignment between the red and blue signals.

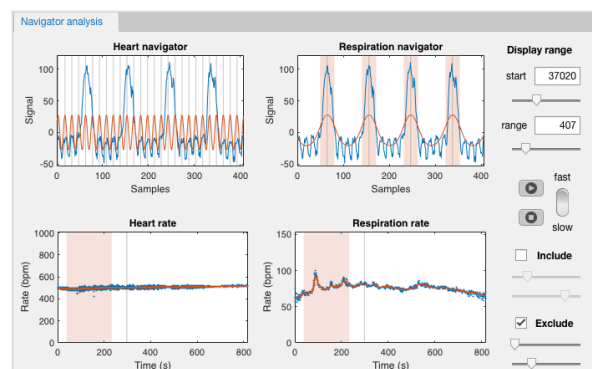
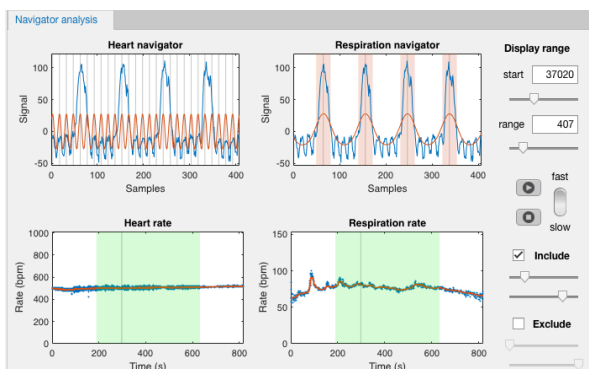
Bottom left is the resulting heart rate as function of during the full acquisition. The blue line is the heartbeat to heartbeat variation, whereas the red line is a smoothed trend-line.

The top right figure shows in blue the raw navigator signal and in red the signal filtered for respiratory motion. The gray vertical lines indicate the peaks in the oscillations, which can be used to check the alignment between the red and blue signals. The shaded red areas indicates the part of the data which is discarded during respiratory motion.


Bottom right is the resulting respiration rate as function of during the full acquisition. The blue line is the respiration to respiration variation, the red line is a smoothed trend-line.

Heart and respiration rates should be smoothly varying over time. If this is not the case, adjust the Butterworth filter settings.

Including / excluding data



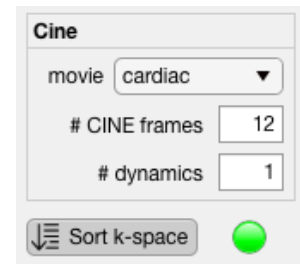
In case of irregular respiration or heartbeat part of the data can be included (green) and/or excluded (red) by checking the **Include** or **Exclude** boxes or both. Including or excluding data is not possible for multi-slice 2D data.

After this, press  again to filter the data with the new settings.



Step 5: Sort the k-space

Choose the desired sorting method, number of frames, and number of dynamics. In the presets panel you can select some pre-defined sorting options.



Sorting methods

(1) Cardiac

Cardiac phase-binning. Each heartbeat is divided into an equal number of cardiac CINE frames. The average time between cardiac frames is determined from the average heart-rate and the number of cardiac frames. This option is preferred for most applications, particularly for high frame-rate reconstructions for analysis of diastolic function.

(2) Cardiac abs.

Cardiac absolute-binning. A fixed frame time is predetermined from the average heart-rate and the number of cardiac CINE frames. This option could be more accurate for reconstruction of systolic function in the presence of heart-rate variations, but leads to temporal blurring in the diastolic phase.

(3) Respiratory

Respiratory phase-binning. Each respiration cycle is divided into an equal number of respiratory frames. The average time between respiratory frames is determined from the average respiration-rate and the number of desired respiration frames. When using this option, **window (%)** is neglected.

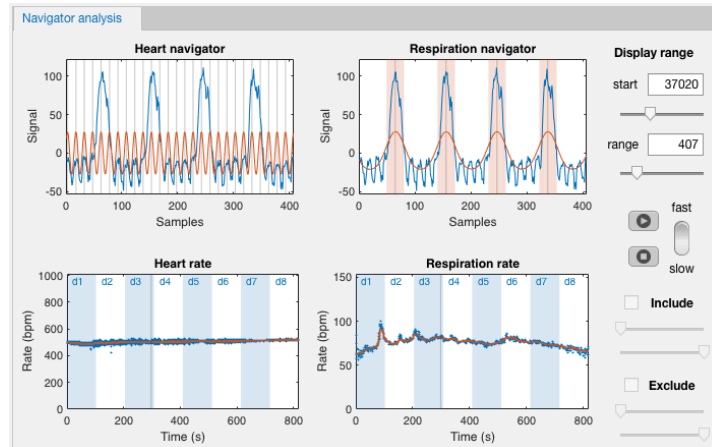
(4) Realtime

With the realtime option selected the data is sorted into 1 CINE movie per heart beat for fast dynamic imaging, for example during injection of a contrast agent. This option requires a short-as-possible TR and a suitable sparse k-space trajectory that results in sufficient k-lines per frame for compressed-sensing and/or parallel imaging image reconstruction. The number of dynamics will be automatically set to the total number of heartbeats in the acquisition and respiratory motion is disregarded. The parameter sharing in the advanced settings panel determines the number of k-lines that are shared from neighboring dynamics in order to increase k-space filling and image quality at the expense of temporal averaging.

Press  to start sorting the data into k-space.

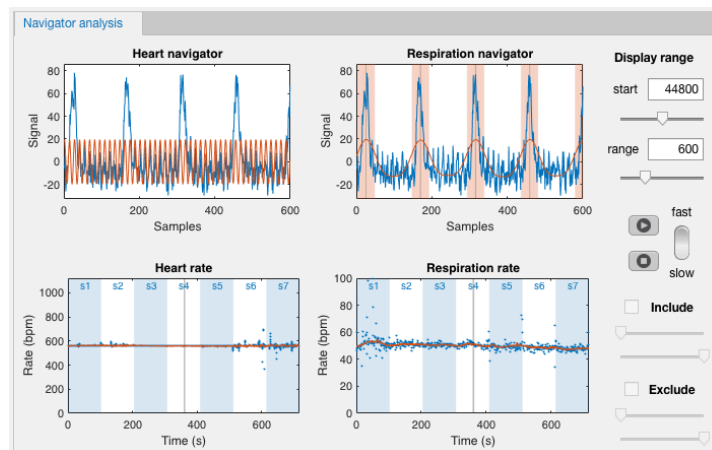
Dynamics

It is possible to reconstruct data in a dynamic time series, for example for dynamic-contrast enhanced acquisitions. Choose the desired number of dynamics, and continue with sorting k-space and reconstruction. The maximum number of dynamics is set to 600, but remember that k-space will become very sparse with high number of dynamics and reconstruction might take very long. The dynamic time-frames will be indicated in the heart rate and respiratory rate plots in blue/white shaded areas as shown below.



Multi-slice 2D data

For multi-slice 2D acquisitions, the heart rate and respiration rate plots show when the subsequent slices were acquired with blue/white shaded areas. For multi-slice 2D data it is not possible to reconstruct different dynamics nor is it possible to include or exclude part of the scan.

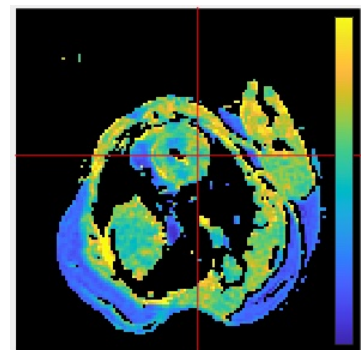


3D data

Version 8.1 of Retrospective supports reconstructions of 3D CINE data.

Variable flip-angle data for T1-mapping

Cardiac quantitative T1 maps can be acquired using the variable flip angle method (see: Coolen et al. NMR Biomed 24, 154–162 (2011)). This option requires a 3D self-gated T1-weighted (RF and gradient spoiled) acquisition with variable flip angle (typically 5 angles, for example 2°, 5°, 10°, 15°, 20°). The varying flip angles should be acquired in a single acquisition in which the flip angles are evenly distributed over the k-space repetitions. After reconstruction data should be exported as a new MRD file for T1 mapping using the **T1map** app available on GitHub.





Step 6: Reconstruction of the data

Before reconstruction, select the appropriate reconstruction settings and regularization parameters in the **CS reco parameters** panel.

Reconstruction is based on a compressed sensing algorithm with wavelet l1-norm regularization and total-variation regularization in spatial and time dimensions.

Some parameters are not available without the BART toolbox.

The **Presets** panel provides some pre-determined reconstruction settings for different applications.

CS reco parameters	
WVxyz	0.000
TVxyz	0.000
LLRxyz	0.000
TVcine	0.100
TVdyn	0.000
ESPIRiT	<input type="checkbox"/>

Parameters

(1) **WVxyz**

Wavelet regularization parameter in the spatial (x, y, and z) dimensions. For the mouse cardiac CINE, a low (0.001) or zero value resulted in the best movie quality.

(4) **TVxyz**

Total variation constraint in the spatial dimension. Higher values smooth the movie in the spatial domain. For mouse CINEs, this parameter does not seem to improve image quality. Recommended value therefore is zero.

(2) **LLRxyz**

Locally Low Rank regularization parameter.

(3) **TVcine**

Total variation constraint in the CINE dimension. Higher values lead to improved image quality but increased temporal smoothing. For the mouse CINEs, a value of 0.1 seems a good compromise between image quality and temporal smoothing.

(5) **TVdyn**

Total variation constraint in the dynamics dimension.

For multi-coil data only

(5) **ESPIRiT**

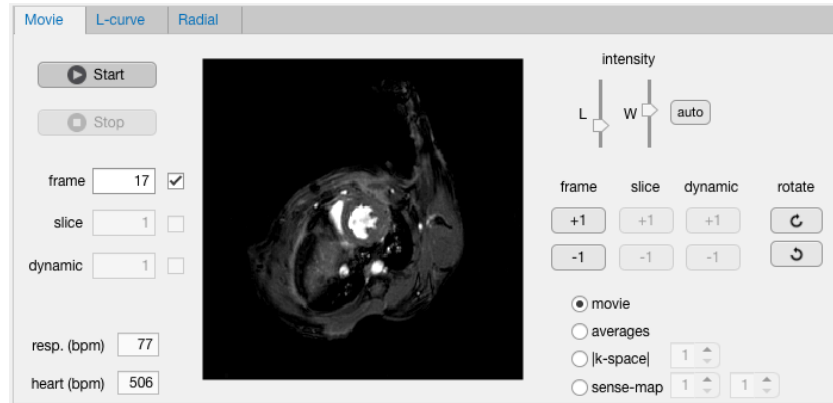
ESPIRiT reconstruction (Magn Reson Med. 2014 Mar 71(3): 990–1001.). This includes GRAPPA and SENSE reconstruction.

Press  **Reconstruct** to start the reconstruction.



Step 7: Viewing the movie

The resulting CINE MRI can be viewed in the Movie panel. Check the corresponding boxes to view the number of averages per k-line and cardiac frame, the k-space, or the coil sensitivity maps (ESPIRiT).





Press  to start the movie.



Press  to stop the movie.

Check the corresponding boxes to loop the movie over frames, slices, and/or dynamics.

Image intensity can be adjusted with the level (**L**) and window (**W**) sliders.

Press  or  to rotate the movie clockwise or counter clockwise (this will not affect the Dicom and MRD export orientations).




Press  or  below **frame** to advance or rewind the movie 1 time frame.

Different slices can be viewed with  or  below **slice**.

Advance dynamics with  or  below **dynamic**.

Synchronizing multi-slice 2D CINEs from one animal

Since the cardiac synchronization is not based on ECG triggering, CINEs from different slices or acquired in different orientations may not be synchronized with respect to each other, i.e. the end-systole and end-diastole might have different frame numbers.

To correct for this the following procedure can be followed. First stop the movie with the  button. Then set the frame number to 1 in the dialog **frame** . Then, advance or rewind the movie with  or  to the desired starting phase of the cardiac cycle, for example end-diastole.

The cardiac synchronization will also be taken into account with DCM, GIF and MRD export.



Step 8: Movie export

There are several ways to export the movies.



(1) Export DCM

Exports the data in Dicom format for further processing in 3rd party software. The program searches for the Dicom information. If this information is not found, tags will be generated by the program itself. In the latter case the correct image position and orientation information are lost.

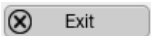
(2) Export GIF

Generates animated-gif movie or movies (3D, multi-slice) of the reconstructed CINE. Image intensity (window, level) and image rotations are preserved.

(3) Export MRD

The data will be stored as a new MRD data file in the same directory as the input MRD file. If the program finds an input rpr file, also a new rpr file will be generated. Additionally, when the program runs on the scanner computer, data will be reconstructed by the scanner software and new SUR files will be placed in the data directory for viewing and planning of next scans in the MR Solutions preclinical software.

Step 9: Exit

Press  to shut down the program.