

Table of contents

1. Overview
2. Contact
3. Disclaimer
4. Citing the use of Retrospective
5. Installation notes
6. Running the software
7. Basic operation



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

Retrospective and this manual is written by:

Gustav Strijkers
Amsterdam UMC
Biomedical Engineering and Physics
Amsterdam, the Netherlands
g.j.striekers@amsterdamumc.nl

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 with MacPorts

- (1) Install Xcode from the Mac App Store

```
$ xcode-select --install
```

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

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

- (3) Install packages

```
$ sudo port install fftw-3-single
$ sudo port install gcc10
$ sudo port install libpng
$ sudo port install openblas
```

- (4) Make

```
$ make
$ sudo make install
```

Bart toolbox installation in OSX with HomeBrew (for Mac with Apple Silicon)

- (1) Install Xcode from the Mac App Store

```
$ xcode-select --install
```

- (2) Install HomeBrew

```
$ /bin/bash -c "$(curl -fsSL https://raw.githubusercontent.com/Homebrew/install/HEAD/install.sh)"
```

- (3) Install packages

```
$ brew install --cask gcc-arm-embedded
$ brew install libpng
$ brew install fftw
$ brew install openblas
```

- (3) Make

```
- Use the provided makefile for Apple Silicon
$ make
$ sudo make install
```



Bart toolbox installation in Windows 11

(1) Install the Windows subsystem for Linux

Start a windows powershell as administrator and run the following command:

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

A system restart will be needed.

For more information, see:

<https://pureinfotech.com/install-wsl-windows-11/>

(2) Download Ubuntu Linux

Open PowerShell

To see a list of available Linux distributions for download, enter:

```
wsl -l -o
```

Install a Linux distribution:

```
wsl --install -d <distribution name>
```

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 gfortran
```

(5) Download Bart

```
$ wget https://github.com/mrirecon/bart/archive/v0.9.00.tar.gz
```

For WSL1 version 0.4.02 is recommended. Newer versions seem to compile but some functions which are required produce errors.

Recommended: Upgrade to WSL2 (see e.g. <https://pureinfotech.com/install-wsl-windows-11/> on how to upgrade).

(6) Build Bart

```
$ tar xvfz v0.9.00.tar.gz
```

```
$ cd bart-0.9.00
```

```
$ make
```

```
$ sudo make install
```



Required Python modules for Deep Learning Reconstruction

WSL:

```
$ sudo apt-get update
$ sudo apt install python
$ sudo apt install python-is-python3
$ sudo apt install python3-pip
$ sudo apt install unzip
$ pip install conda
$ pip install tensorflow
$ pip install imageio
$ pip install matplotlib
$ pip install matplotlib-inline
$ pip install opencv-python
$ pip install scikit-image
$ pip install torch
$ pip install torchvision
$ pip install torchmetrics
$ pip install tqdm
$ pip install pandas
$ pip install interval
$ pip install nibabel
```



6. Running the software

Running in Matlab 2023b

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

```
>> retrospective
```

Additional licenses may be required.

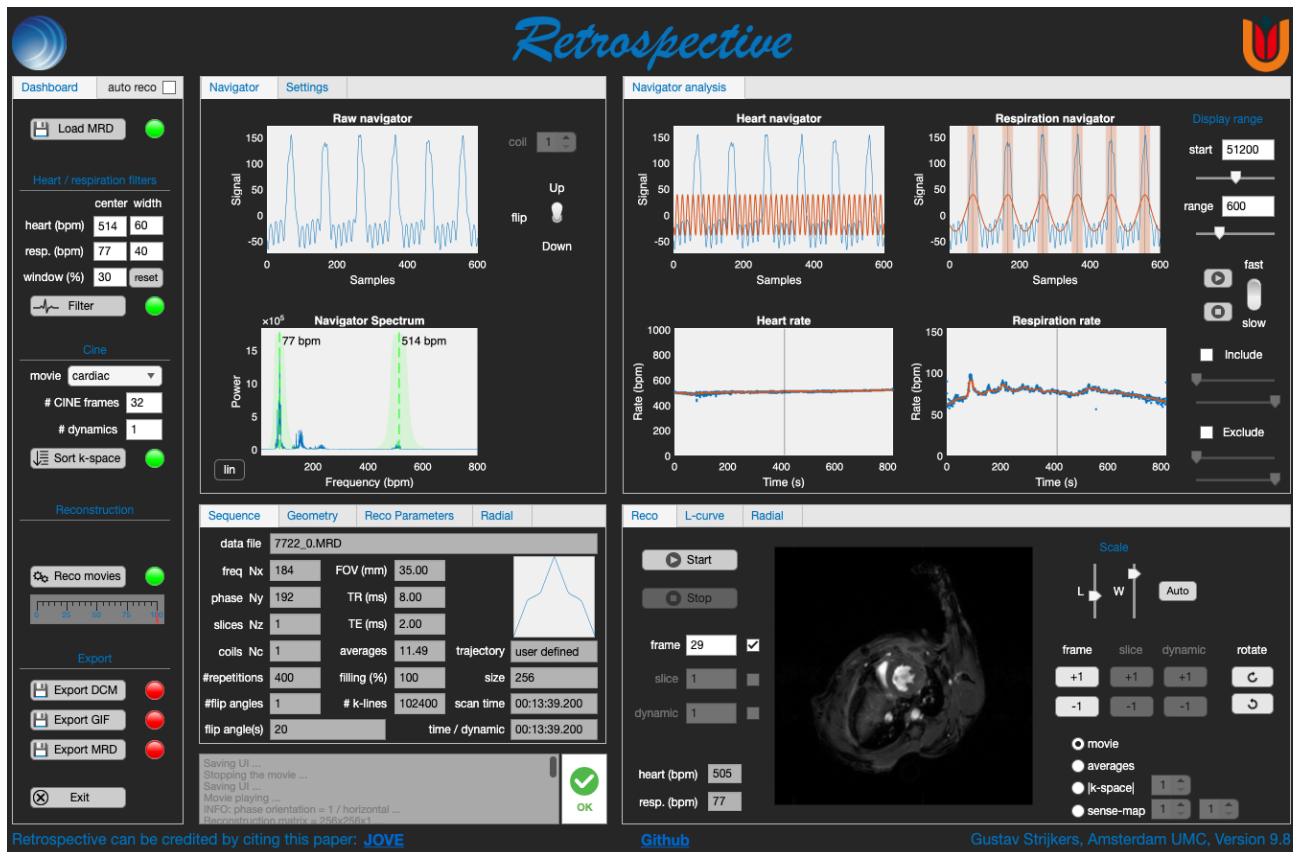
```
MATLAB  
Image Processing Toolbox  
Parallel Computing Toolbox  
Signal Processing Toolbox
```

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 a task has been completed. When the light is yellow the task is busy. Red indicates not completed yet.

Panel 2: Sequence / Geometry / Reco Parameters / Radial

This panel lists the relevant acquisition and reconstruction parameters.

Panel 3: Navigator / Settings

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

Panel 4: Navigator analysis

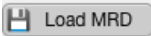
This panel shows the navigator signals filtered for cardiac and respiratory motion, as well as the heart and respiratory rates as function of time.

Panel 5: Reco / 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.



Step 1: Loading data

Press  to import load the MRD raw data file *.

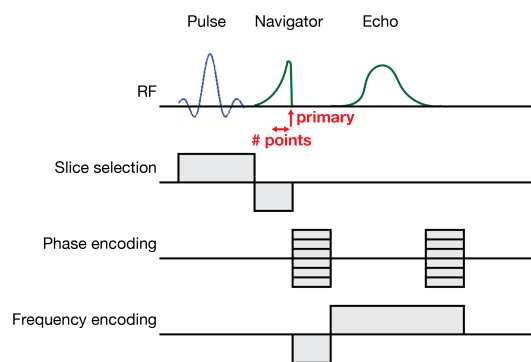
The data should include navigator data for cardiac and respiratory synchronization.

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

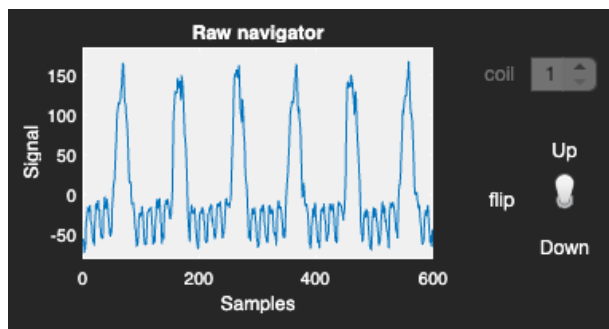
Relevant acquisition parameters will be shown in panel 2, including the k-space trajectory (linear, zigzag, or user defined).

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.



The settings panel is divided into two tabs: 'Navigator' and 'Settings'. The 'Navigator' tab is active. It contains the following settings:

- Navigator**
 - primary: 10
 - # points: 5
 - freq Nx discard: 38
- Presets**
 - ☐ mouse
 - ☐ rat
 - ☐ zebrafish
- Respiration**
 - toggle in/expiration: ☐
 - ignore respiration: ☐
- Sounds**
 - sounds on/off: ☒
- Colors**
 - ☐ classic
 - ☐ black/white
- Physio filtering**
 - filter order: 4
 - min heart rate: 300
 - max heart rate: 700
 - min resp rate: 30
 - max resp rate: 90

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/or increase **# points** (typically **# points** = 1 to 5) in the Settings tab to see whether the quality improves.

When **auto reco** ☒ is enabled, retrospective will watch the MRD datafile directory and start automatic reconstruction when a new MRD file is added for seamless integration with the MR Solutions preclinical imaging software.



The Settings tab contains 3 presets for navigator filtering of mouse, rat, and zebrafish 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.

Images can be reconstructed during in- or expiration. Default is reconstruction during expiration, in the intervals between breath-takes. For reconstruction of images during inspiration, tick the *toggle in/expiration* check box.

Discarding k-lines during respiration can be overruled by ticking the *ignore respiration* checkbox.

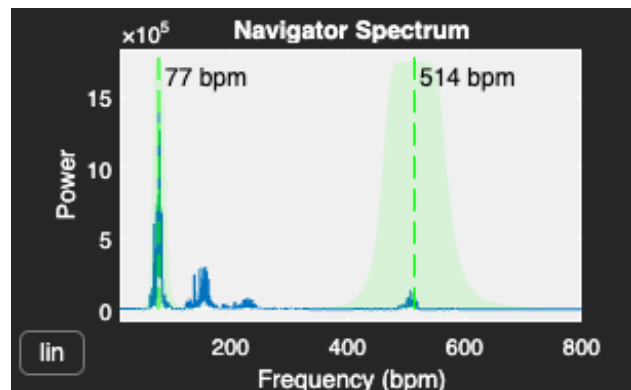
Error and warning sounds can be switched on or off with the *sounds on/off* checkbox.

Check the corresponding box to switch between *black/white* and *classic* user interface colors.

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.

Heart / respiration filters		
	center	width
heart (bpm)	514	100
resp. (bpm)	77	20
window (%)	30	<input type="button" value="reset"/>

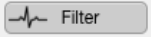
Center and **width** determine the center-frequency and width of the Butterworth filters for navigator filtering.

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

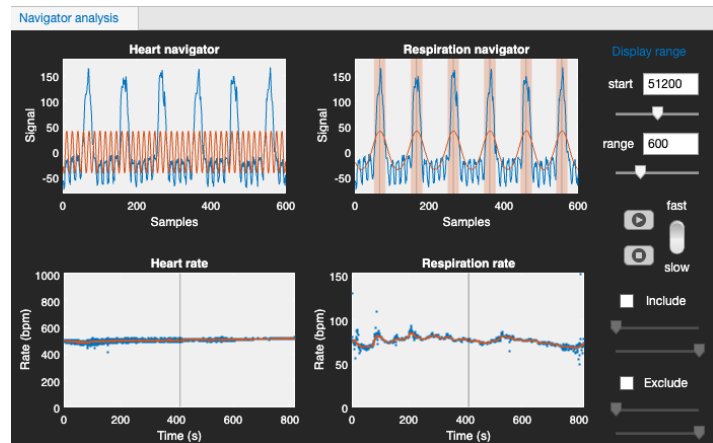
Press to reset the values.




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.

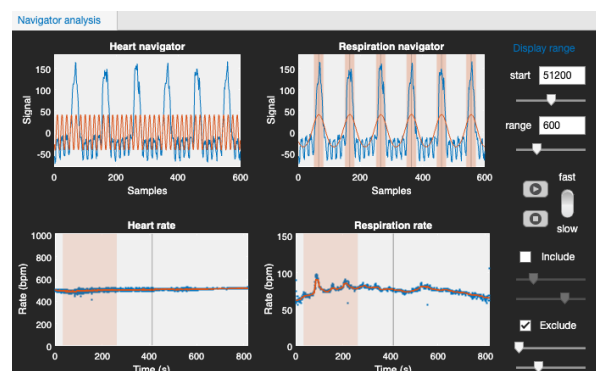
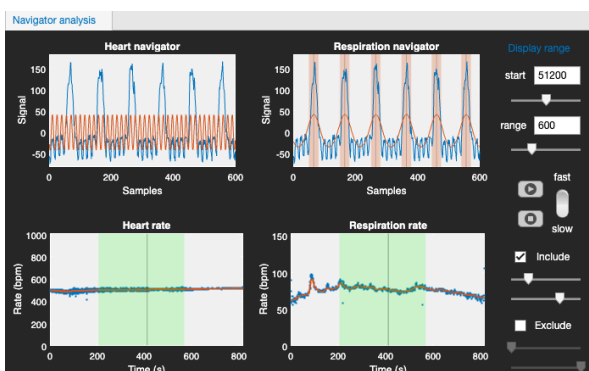
Bottom left is the resulting heart rate as function of during the full acquisition. The blue line is the heartbeat to heartbeat variation, whereas the red line is a smoothed trend-line.

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



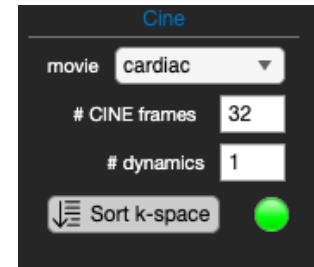
In case of irregular respiration or heartbeat part of the data can be included (green) and/or excluded (red) by checking the **Include** or **Exclude** boxes or both. Including or excluding data is not possible for multi-slice 2D data.

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.

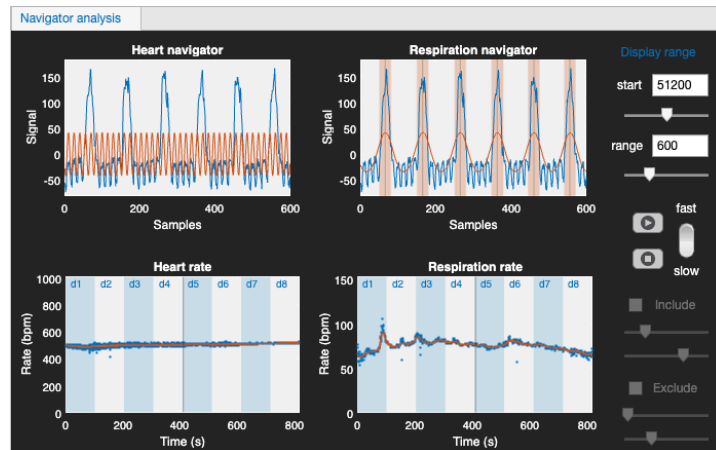
(4) Realtime

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.

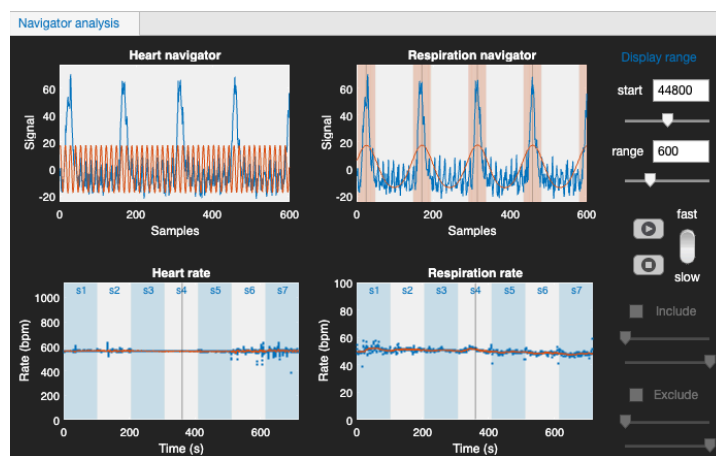
Dynamics

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.

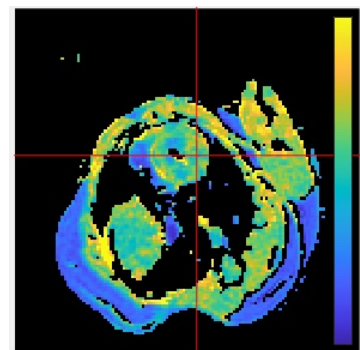


3D data

Version 9 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 **T1mapp** application available on GitHub.





Step 6: Reconstruction of the data

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

Sequence	Geometry	Reco Parameters	Radial
CS reco		Frame sharing	Reconstruction presets
WVxyz	0.0010	# frames	0
TVxyz	0.0000	Various	
LLRxyz	0.0050	guess reco	<input checked="" type="checkbox"/>
TVcine	0.1000	Matlab reco	<input type="checkbox"/>
TVdyn	0.0000	Reconstruction presets	
ESPIRiT	<input type="checkbox"/>	<input type="radio"/> scout <input type="radio"/> systolic function <input checked="" type="radio"/> diastolic function <input type="radio"/> respiratory function <input type="radio"/> realtime <input type="radio"/> variable flip-angle	
PCA	<input type="checkbox"/>	8	
ringing	<input type="checkbox"/>		

CS reco 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  to start the reconstruction.



Sequence / Geometry

The Sequence and Geometry tabs contain information on the sequence parameters and the image geometry.

Sequence	Geometry	Reco Parameters	Radial
data file 7722_0.MRD			
freq Nx 184	FOV (mm) 35.00		
phase Ny 192	TR (ms) 8.00		
slices Nz 1	TE (ms) 2.00		
coils Nc 1	averages 11.49	trajectory user defined	
#repetitions 400	filling (%) 100	size 256	
#flip angles 1	# k-lines 102400	scan time 00:13:39.200	
flip angle(s) 20		time / dynamic 00:13:39.200	

Sequence	Geometry	Reco Parameters	Radial
	FOV (mm) 35.00	offset X (mm) 0.00	
	aspect ratio 1.00	offset Y (mm) 0.00	
	phase orientation 1	offset Z (mm) 0.00	
	slice thickness (mm) 1.00	angle X (deg) 0	
	slice gap (mm) 0.00	angle Y (deg) 0	
		angle Z (deg) 0	

Reco Parameters

The Reco Parameters tab contains additional reconstruction settings.

Sequence	Geometry	Reco Parameters	Radial
<div>CS reco</div> <div>WVxyz 0.0010</div> <div>TVxyz 0.0000</div> <div>LLRxyz 0.0050</div> <div>TVcine 0.1000</div> <div>TVdyn 0.0000</div> <div>ESPIRIT <input type="checkbox"/></div> <div>PCA <input type="checkbox"/> 8</div> <div>ringing <input type="checkbox"/></div>			
<div>Frame sharing</div> <div># frames 0</div> <div>Various</div> <div>guess reco <input checked="" type="checkbox"/></div> <div>Matlab reco <input type="checkbox"/></div>			
<div>Reconstruction presets</div> <div><input type="radio"/> scout</div> <div><input type="radio"/> systolic function</div> <div><input checked="" type="radio"/> diastolic function</div> <div><input type="radio"/> respiratory function</div> <div><input type="radio"/> realtime</div> <div><input type="radio"/> variable flip-angle</div>			

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 **Frame sharing** indicates the number of shared frames. #frames = 0 is recommended in most cases to prevent temporal smoothing.

Reconstruction presets provides some pre-determined reconstruction settings for different applications.

Check the *guess reco* checkbox for the application to make an educated guess what type of reconstruction is appropriate. This is especially useful when doing automatic reconstruction.

PCA applies a principal-component-analysis noise filtering to the data. The **ringing** checkbox switches on a anti-ringing filter.

One can force a Matlab-based reconstruction by checking the **Matlab reco** checkbox.

The Presets tab contains also 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.



Radial

The radial tab contains additional settings for radial and UTE reconstructions.

Sequence Geometry Presets **Radial**

Gradient delays

calibration ☒

ring method ☒

Gx delay 0.00000

Gy delay 0.00000

Gz delay 0.00000

data offset 0

Radial trajectory

☐ half circle

☐ full circle

☒ user defined 1.00

center echo ☐

phase correction ☒

density correction ☒

Tick the *calibration* checkbox for automatic adjustment of the gradient delays. When the *ring method* checkbox is ticked, the RING method described by Rosenzweig et al. is used [Rosenzweig, S., Holme, H. C. M. & Uecker, M. Simple auto-calibrated gradient delay estimation from few spokes using Radial Intersections (RING). Magn Reson Med 81, 1898–1906 (2019)]. When *ring method* is unchecked, a recursive image-based gradient delay optimization is performed. The latter method is much slower.

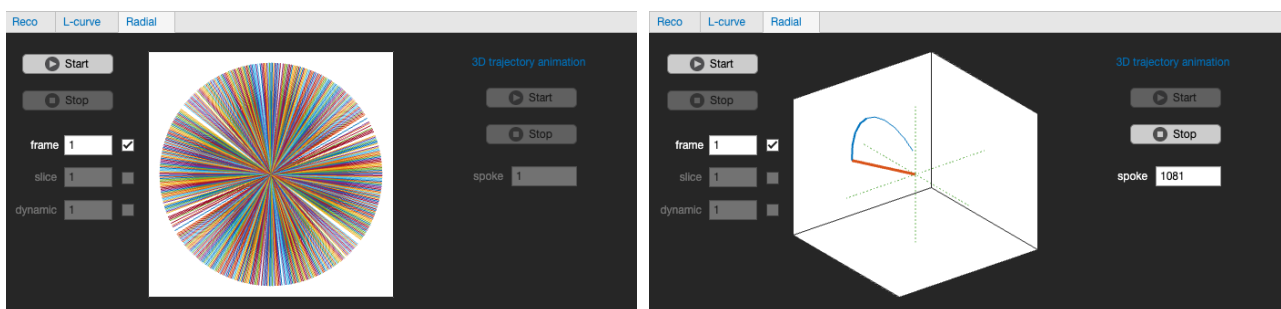
Currently three 2D radial trajectories are supported: half-circle (0:1:180 degrees), full-circle (0:1:360 degrees), and user defined (reading from MRD file, work in progress).

With *center echo* checked, the echoes are centered before reconstruction.

Phase correction performs a phase correction of the echoes before reconstruction.

Density correction performs a 2D or 3D density correction in k-space to account for non-uniform sampling. This setting only applies to reconstructions with *Bart*.

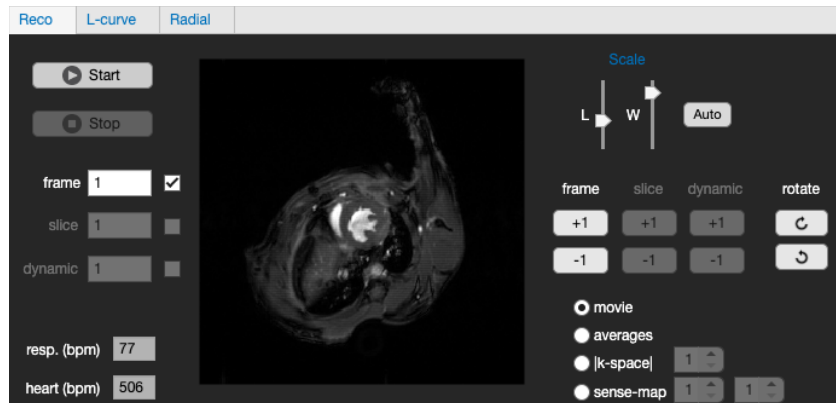
In the **Radial** tab in panel 5 one can view the 2D or 3D radial k-space filling and animate the 3D radial trajectory





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. Dicoms will be saved to /smis/dev/data if found.


(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. Gifs will be saved to /smis/dev/data if found.

(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  Exit to shut down the program.



Credits

- BART toolbox and compressed sensing algorithms

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

Michael Lustig, David Donoho, John M. Pauly, Sparse MRI: The application of compressed sensing for rapid MR imaging, Magn Reson Med 58, 1182-1195 (2007).

- Automatic gradient delay estimation algorithm

Rosenzweig, S., Holme, H. C. M. & Uecker, M., Simple auto-calibrated gradient delay estimation from few spokes using Radial Intersections (RING). Magn Reson Med 81, 1898–1906 (2019)

- Gibbs ringing suppression

Kellner, E, Dhital B., Kiselev VG and Reiser, M., Gibbs-ringing artifact removal based on local subvoxel-shifts. Magn Reson Med, 76(5), 1574-1581.

- NUFFT

<https://web.eecs.umich.edu/~fessler/>

- Phase unwrapping

M. A. Herráez, D. R. Burton, M. J. Lalor, and M. A. Gdeisat, "Fast two-dimensional phase-unwrapping algorithm based on sorting by reliability following a noncontinuous path", Applied Optics, Vol. 41, Issue 35, pp. 7437-7444 (2002),

H. Abdul-Rahman, M. Gdeisat, D. Burton, M. Lalor, "Fast three-dimensional phase-unwrapping algorithm based on sorting by reliability following a non-continuous path", Proc. SPIE 5856, Optical Measurement Systems for Industrial Inspection IV, 32 (2005).

- Frame sharing

Küstner et al., NMR Biomed e4409 (2020). doi:10.1002/nbm.4409