Table of contents

1. Overview

P2ROUD = Preclinical PROspective Undersampling in multiple Dimensions

P2ROUD is a software utility and graphical user interface to reconstruct MRI acquisition from data with k-space undersampling in one or more dimensions acquired with an MR Solutions preclinical MRI system.

2. Contact

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3. Disclaimer

The software has been extensively tested using mouse and rat 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 or Bram Coolen.

4. 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 P2ROUD program.

Bart toolbox download

The advanced reconstruction options in P2ROUD 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

Replace 'gcc-mp-6' with 'gcc-mp-10' in 'makefile'
```
$ make
```

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
```

Bart toolbox installation in Windows 10

(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://docs.microsoft.com/en-us/windows/wsl/install-win10
```

(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 gcc-10 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.

Recommended: Upgrade to WSL2 (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
$ sudo make PREFIX=/usr/local install
```

5. Running the software

Running in Matlab 2022a

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

```
>> retrospective
```

Notes when running from the Matlab prompt:

(1) The P2ROUD root directory `~/PROUD5` contains the following 2 text files:

```
bartpath_osx_arm.txt
bartpath_osx_intel.txt
```

> Bart toolbox installation directory for arm and intel based apple computers.

```
mrdpath.txt
```

> Directory which is watched for new MRD files, when 'auto reco' is on. On the MRI 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')
image_toolbox
matlab
phased_array_system_toolbox
signal_blocks
signal_toolbox
```

Running the Windows standalone

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

6. Basic operation

The P2ROUD program operates from a single window with 5 panels.
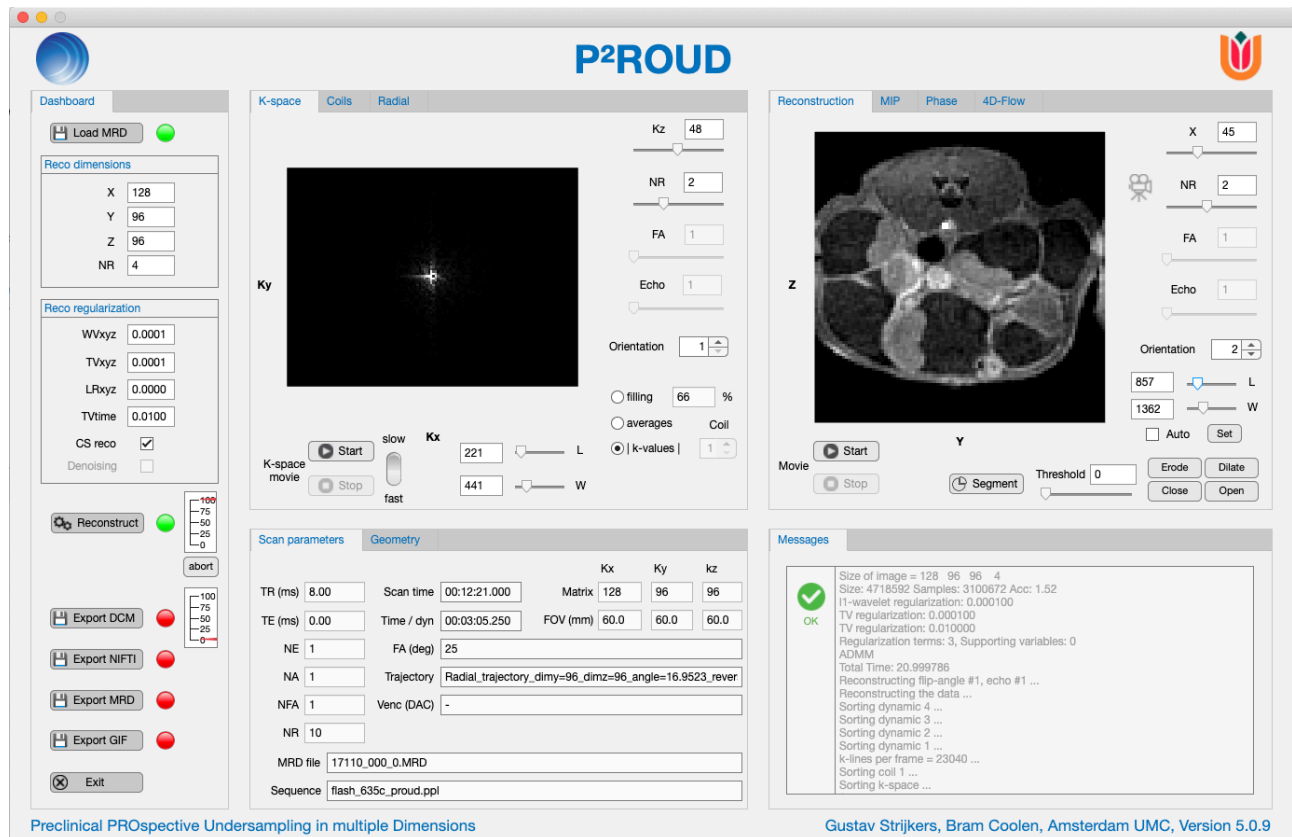
Panel 1: Dashboard

This panel contains the task buttons and parameters 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: K-space / Coils / Radial

This panel shows the raw k-space data.

Panel 3: Scan parameters / Geometry

This panel displays the relevant acquisition and geometry parameters.

Panel 4: Reconstruction / MIP / Phase / 4D-flow

After reconstruction is completed this panel shows the reconstructed images.

Panel 5: Messages

Displays program status and messages.

Step 1: Loading data

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

P2ROUD in principle can reconstruct any spin-echo, fast-spin echo, and gradient-echo data (except epi).

However the program is particularly designed to reconstruct undersampled data with user-defined undersampling pattern (e.g. SENSE, random undersampling, pseudo-spiral or radial).

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

Relevant acquisition parameters will be shown in panel 3.

k-space trajectory

Currently there are 2 options to include a user-defined k-space trajectory in the FLASH (version 634) sequence.

(1) **2D-data**

pe1-order = 3

The k-space points for the 1st phase-encoding direction (views) are provided in the views-table in the sequence.

(2) **3D-data**

pe1-order = 4

The k-space points for the 1st and 2nd phase-encoding directions (views and views2) are provided in a text file (*.txt) as a list of points without comma separation.

For example:

```
-48        (views     k-point 1)
0          (views2    k-point 1)
-47        (views     k-point 2)
0          (views2    k-point 2)
-46        .
1          .
-45        .
.
.
etc...
```

The list has to be up-loaded to the EVO using c:\smis\UploadData.exe just before the acquisition is started.
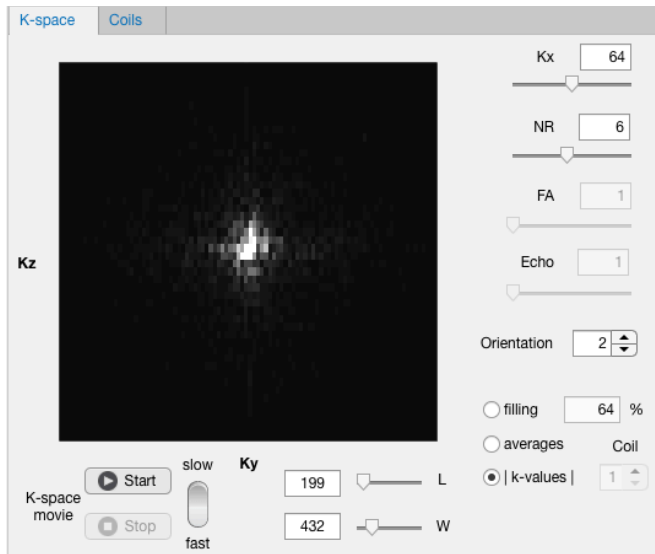
NOTE ! The list file has to be manually placed in the corresponding MRD directory when loading the data in P2ROUD.

A Matlab file (**radialtrajectory.m**) for making a pseudo-radial trajectory can be found in the directory /Trajectories.

Step 2: Inspecting k-space

The raw k-space data is displayed in panel 2.

The window displays either the acquired k-space points (**filling**), the number of averages per k-point (**averages**), or the absolute value of k-space (**|k-values|**). The percentage of k-space points acquired is indicated (64% for this dataset).

The sliders step through the 3rd k-space dimension, slices, repetitions (**NR**), flip angles (**FA**) and echoes (**Echo**), if applicable. You can toggle the orientation with the toggle buttons.

Step 3: Displaying the k-space trajectory
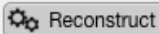
Press ▶ Start to start an animation of the k-space trajectory. An example for a pseudo-radial k-space trajectory is shown below
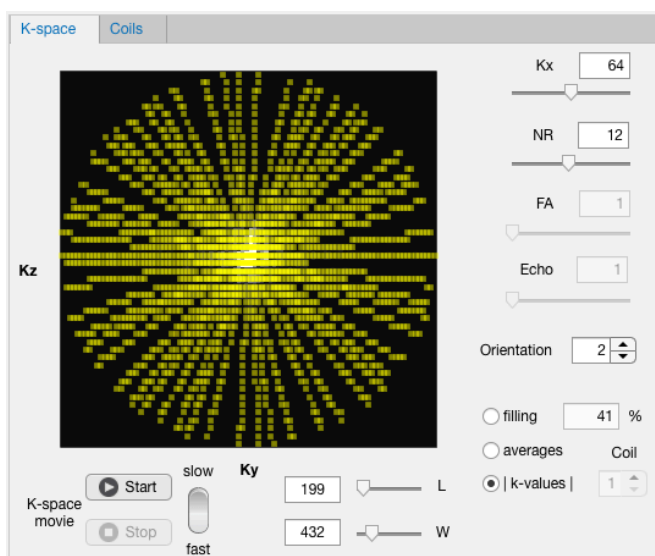
Press ⏹ Stop to stop the animation. Press fast ◯ slow to toggle between fast and slow animation speed.

Step 4: Fourier transform reconstruction

For a first quick inspection of the reconstructed images, a Fourier transform reconstruction of the data can be done by un-checking the **CS reco** box and pressing ⚙ Reconstruct .
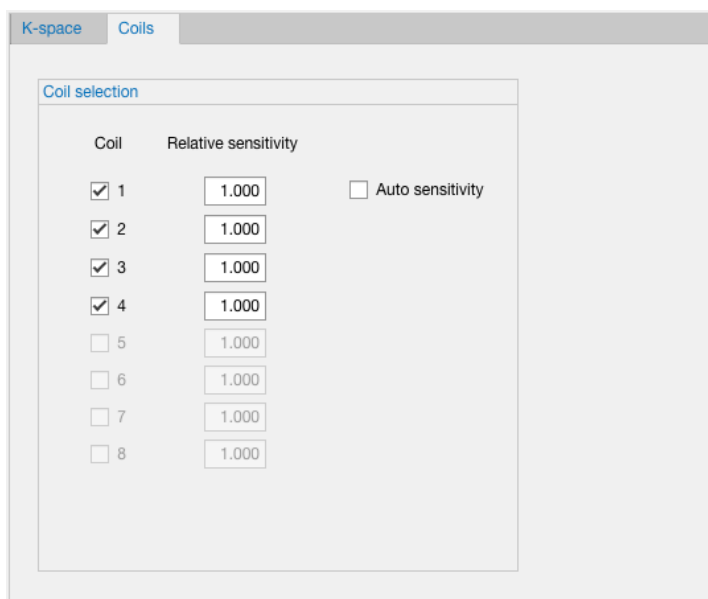
Reco dimensions	
X	128
Y	96
Z	96
NR	4

Reco regularization	
WVxyz	0.0001
TVxyz	0.0001
LRxyz	0.0000
TVtime	0.0100
CS reco	☐
Denoising	☐

The spatial dimensions of the reconstructed data can be increased or decreased, which will result in zero-padding or cropping of k-space. The number of repetitions (**NR**) cannot be changed when performing a Fourier transform reconstruction.

Step 5: Coils panel

For acquisitions performed with a phased-array coil the **Coils** panel gives access to the different channels. Here coils can be checked/unchecked to be considered/omitted in the reconstruction. Relative coil sensitivities can be changed or automatically determined by checking the Auto sensitivity checkbox.

K-space	Coils

Coil selection		
Coil	Relative sensitivity	
☑ 1	1.000	☐ Auto sensitivity
☑ 2	1.000	
☑ 3	1.000	
☑ 4	1.000	
☐ 5	1.000	
☐ 6	1.000	
☐ 7	1.000	
☐ 8	1.000	

Step 6: Reconstruction

Checking the **CS reco** box gives access to the Compressed Sensing (CS) reconstruction parameters.

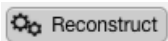| Reco dimensions	
X	128
Y	96
Z	96
NR	4

Reco regularization	
WVxyz	0.0001
TVxyz	0.0001
LRxyz	0.0000
TVtime	0.0100
CS reco	✓
Denoising	☐

The CS regularization parameters are:

(1) **WVxyz**

Wavelet regularization parameter in the spatial (x, y, and z) dimensions.

(2) **TVxyz**

Total variation constraint in the spatial dimensions.

(3) **LRxyz**

Locally Low Rank constraint in the spatial dimensions.

(4) **TVtime**

Total variation constraint in the dynamics (repetitions / **NR**) dimension.

The spatial dimensions of the reconstructed data can be increased or decreased. The number of repetitions (**NR**) can also be changed to undersample or average data in the dynamics dimension.

Pressing ⚙ Reconstruct will start the CS reconstruction with the BART toolbox.

If the BART toolbox is not available CS reconstruction will be done using a CS algorithm implemented in Matlab, which can be very slow for large datasets.

Denoising applies a basic denoising algorithm in Matlab.

Reconstruction of radial scans

The *Radial* tab gives access to advanced reconstruction parameters for radial (2D / 3D) scans.

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.

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 recontructions with *Bart*.

Step 7: Viewing the reconstructed images

After reconstruction the MR images are displayed in panel 4.
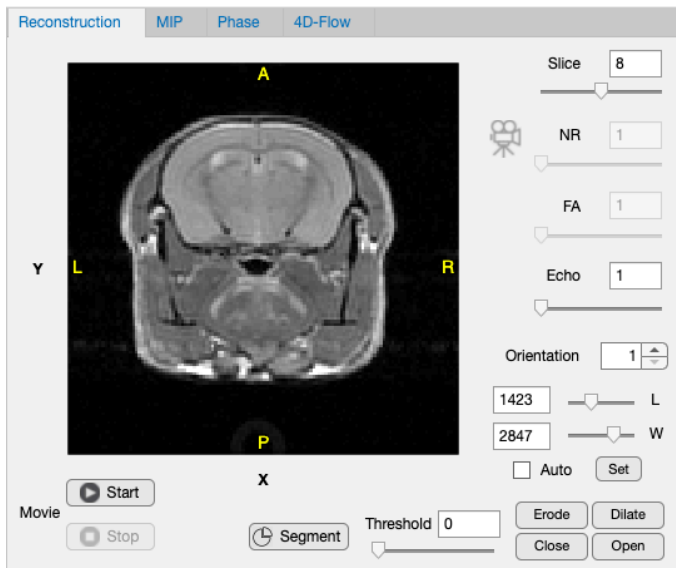
The image orientation can be changed by pressing the **Orientation** toggle buttons.

Image intensity can be adjusted with the **Level** and **Window** sliders. Checking **Auto level** will result in automatic intensity adjustment.

Press to start a movie of images as function of the dimension / parameter shown next to the camera icon .

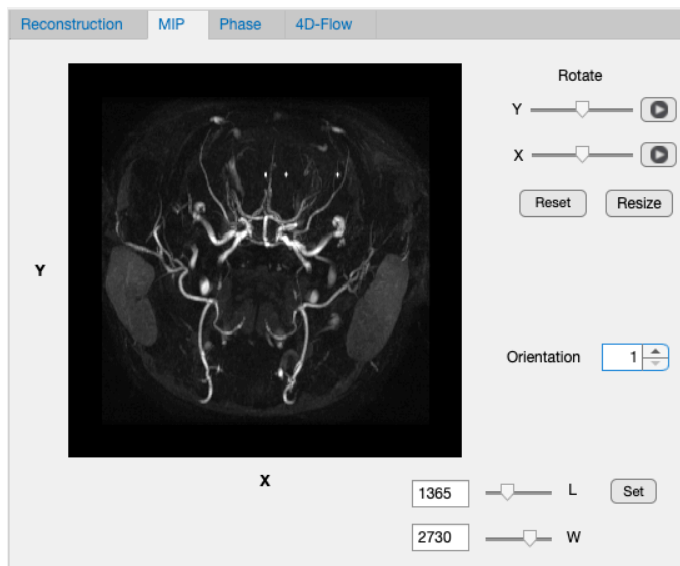Images can be segmented (on the basis of a threshold) by pressing .
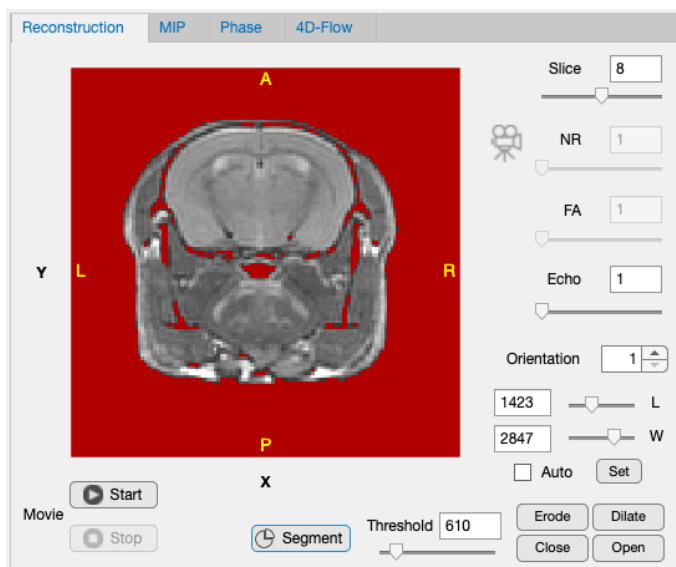
Use the threshold slider or morphological operations to fine-tune the segmentation.
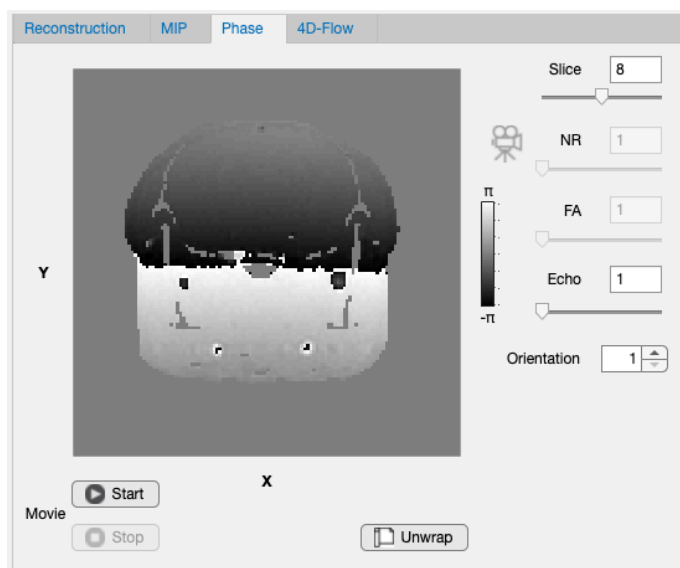
Maximum intensity projection (MIP)

In the *MIP* tab a maximum intensity projection is shown. The MIP can be rotated and animated using the available sliders and buttons.

Phase images

The phase tab shows the phase images.

Phase can be unwrapped by pressing the button.

Step 8: Image export

There are several ways to export the images.

(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 NIFTI**

Exports 3D and 3D-time data in NIFTI format for further processing in 3rd party software.

(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.

(4) **Export GIF**

The data will be exported as (animated) gif files.

Step 9: Exit

Press ⊗ Exit to shut down the program.