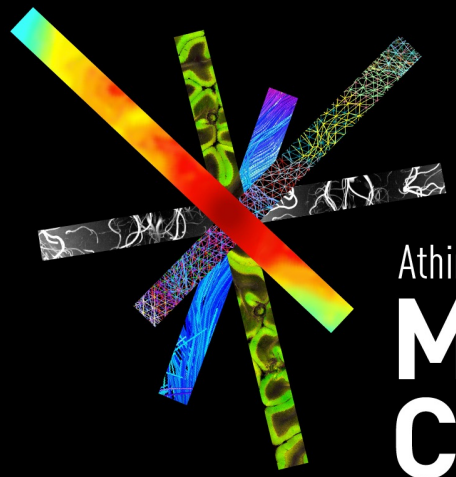

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Multiparametric mapping with Pulseq

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Objectives

1. Demonstrate the actual workflow of implementing and executing custom pulse sequences in Pulseq

2. Introduce an application of Pulseq for cross-platform, multiparametric mapping

Background

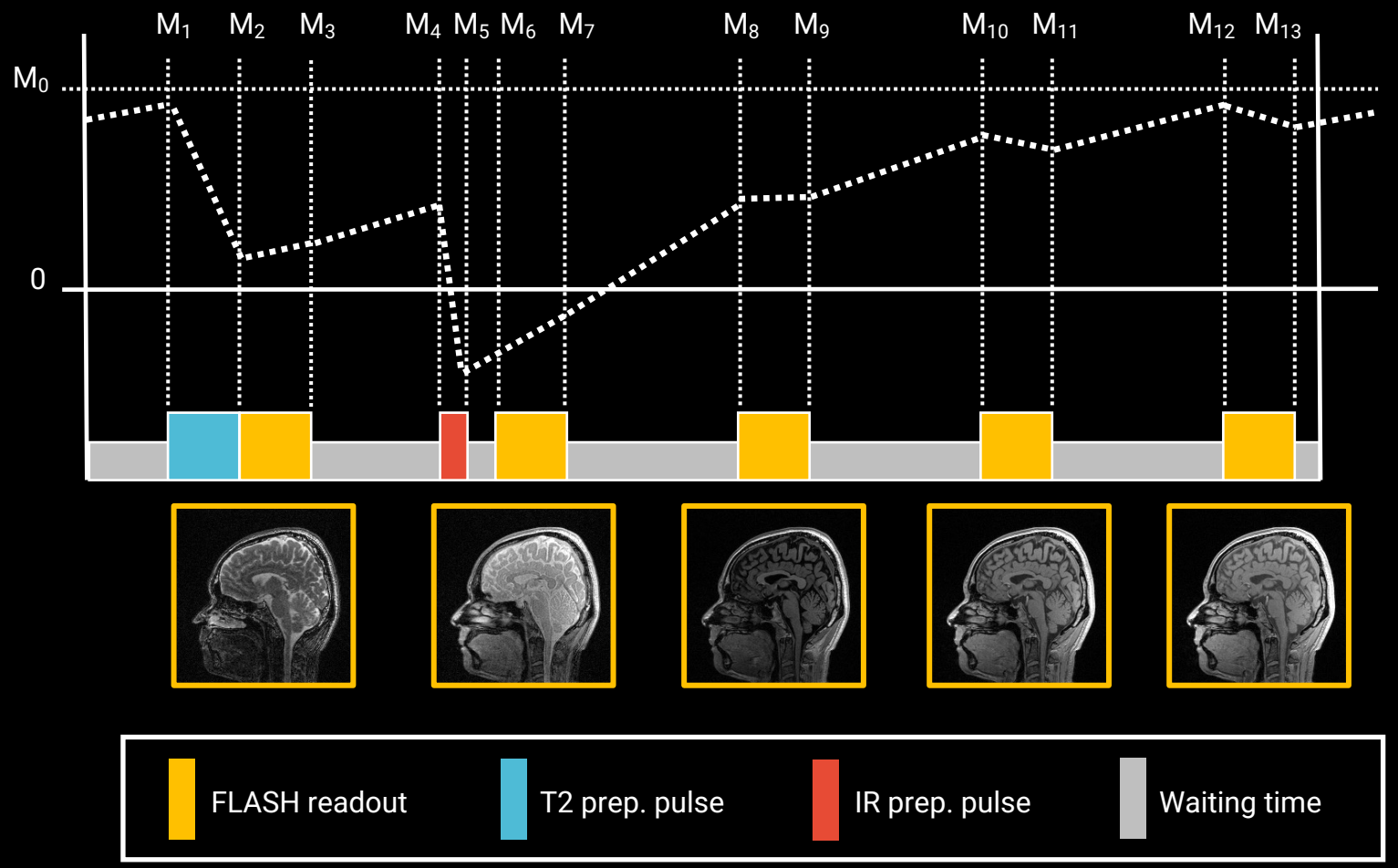
- Multi-site data cannot be naively pooled together for analysis due to large inter-scanner differences

Address the unmet need for a cross-platform, multiparametric technique to facilitate data harmonization across different sites

3D-QALAS: Rapid whole-brain T1 and T2 mapping

3D-QALAS[1,2]:

- 3D-quantification using an interleaved Look–Locker acquisition sequence with a T2 preparation pulse
- Multi-acquisition 3D gradient echo
- Signal modeling-based parameter fitting on the five source images to derive quantitative maps



[1] Kvernby et al. *J Cardiovasc Magn Reson* 2014; [2] Fujita et al. *Magn Reson Imaging* 2019

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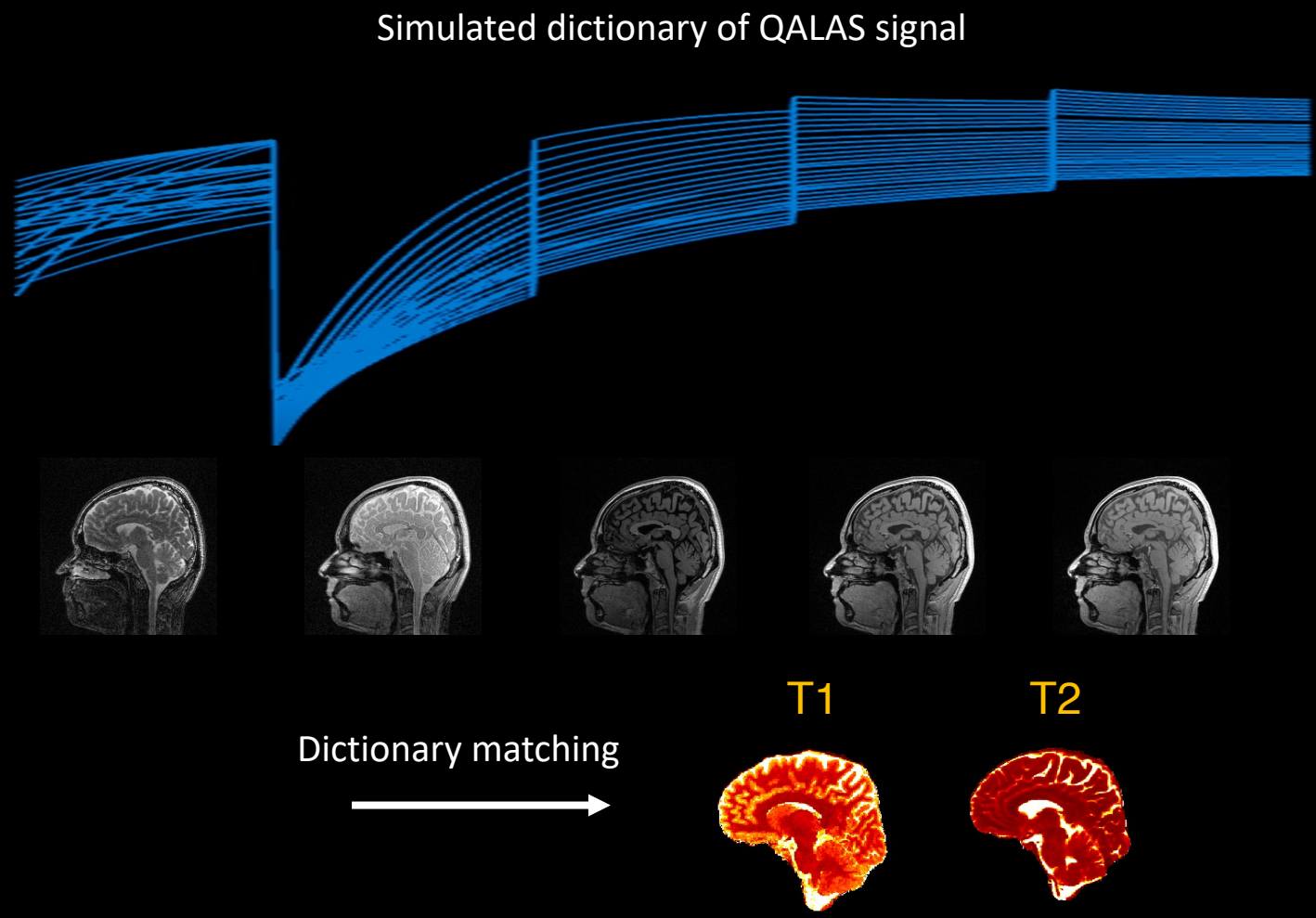
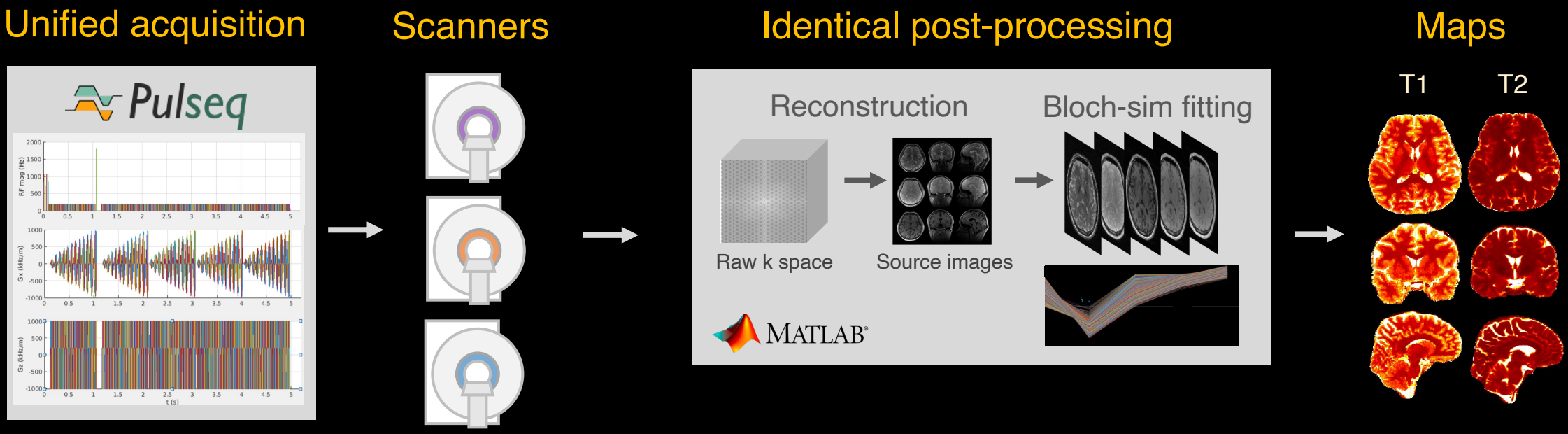


[1] Kvernby et al. *J Cardiovasc Magn Reson* 2014; [2] Fujita et al. *Magn Reson Imaging* 2019

Study overview

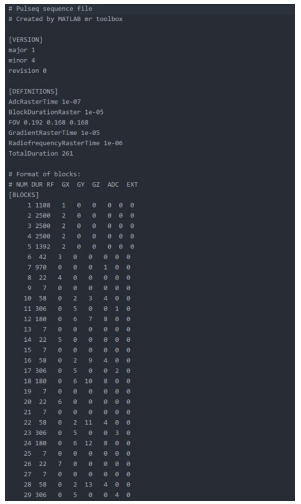


Site	Manufacturer	Scanner model	Software version	Evaluation
Site A	Siemens Healthcare, Erlangen, Germany	Prisma	VE11C	-
Site A	Siemens Healthcare, Erlangen, Germany	Prisma	XA30	Cross-software
Site A	Siemens Healthcare, Erlangen, Germany	Skyra	VE11C	Cross-scanner
Site B	Siemens Healthcare, Erlangen, Germany	Prisma	VE11C	Cross-site
Site C	GE HealthCare, WI, USA	Premier XT	MR30	Cross-vendor

Sequence implementation on Pulseq

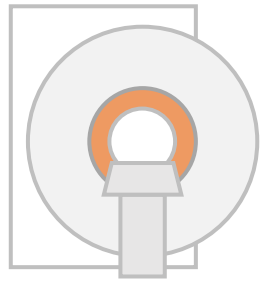
writeSeq.m

.seq



```
# Pulseq sequence file
# Created by MATLAB mr toolbox

[VERSION]
major 1
minor 4
revision 0

[DEFINITIONS]
AdcRasterTime 1e-07
BlockDurationRaster 1e-05
FOV 0.192 0.168 0.168
GradientRasterTime 1e-05
RadioFrequencyRasterTime 1e-06
TotalDuration 261

# Format of blocks:
# NUM DUR RF  GX  GY  GZ  ADC  EXT
[BLOCKS]
     1 1108   1   0   0   0 0   0
     2 2500   2   0   0   0 0   0
     3 2500   2   0   0   0 0   0
     4 2500   2   0   0   0 0   0
     5 1392   2   0   0   0 0   0
     6  42   3   0   0   0 0   0
     7 970   0   0   0   1 0   0
     8  22   4   0   0   0 0   0
     9   7   0   0   0   0 0   0
    10  58   0   2   3   4 0   0
    11 306   0   5   0   0 1   0
    12 180   0   6   7   8 0   0
    13   7   0   0   0   0 0   0
    14  22   5   0   0   0 0   0
    15   7   0   0   0   0 0   0
    16  58   0   2   9   4 0   0
    17 306   0   5   0   0 2   0
    18 180   0   6  10   8 0   0
    19   7   0   0   0   0 0   0
    20  22   6   0   0   0 0   0
    21   7   0   0   0   0 0   0
    22  58   0   2  11   4 0   0
    23 306   0   5   0   0 3   0
    24 180   0   6  12   8 0   0
    25   7   0   0   0   0 0   0
    26  22   7   0   0   0 0   0
    27   7   0   0   0   0 0   0
    28  58   0   2  13   4 0   0
    29 306   0   5   0   0 4   0
```

Scanner



Sequence implementation on Pulseq: writeSeq.m

```
%------------------------------------------------------------------------
% Define high-level parameters
%------------------------------------------------------------------------

% Set system parameters
sys = mr.opts('MaxGrad', 32, 'GradUnit', 'mT/m', ...
              'MaxSlew', 160, 'SlewUnit', 'T/m/s', ...
              'rfDeadTime', 100e-6, ...
              'rfRingdownTime', 60e-6, ...
              'adcDeadTime', 40e-6, ...
              'adcRasterTime', 2e-6, ...
              'gradRasterTime', 20e-6, ...
              'blockDurationRaster', 20e-6, ...
              'B0', 3.0);

% Create sequence object and define FOV, resolution, and other high-level
seq = mr.Sequence(sys);          % Create a new sequence object
fov=[192 168 168]*1e-3;          % Define FOV and resolution
N = [192 168 56];

Nx = N(1);
Ny = N(2);
Nz = N(3);

bandwidth = 340;                 % Hz/pixel
flip_angle = 4;                  % degrees
rfSpoilingInc=117;               % RF spoiling increment
dwell = 16e-6;
Tread = dwell*Nx;
```

gradRasterTime (Siemens) = 10us
gradRasterTime (GE) = 4us

Sequence implementation on Pulseq: writeSeq.m

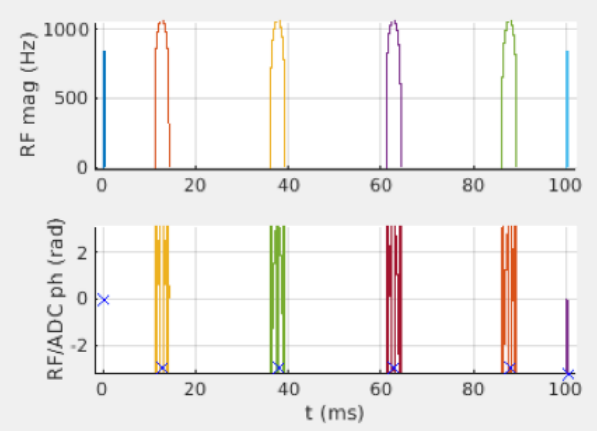
```
%--------------------------------------------------------------------------
% Prepare sequence blocks
%--------------------------------------------------------------------------

deltak = 1 ./ fov;
gx = mr.makeTrapezoid('x',sys,'Amplitude',Nx*deltak(1)/Tread,'FlatTime',ceil(Tread/sys.gradRasterTime)*sys.g
gxPre = mr.makeTrapezoid('x',sys,'Area',-gx.area/2);       % Gx prewinder
gxSpoil = mr.makeTrapezoid('x',sys,'Area',gx.area);         % Gx spoiler

% Make trapezoids for inner loop to save computation

gyPre = mr.makeTrapezoid('y','Area',deltak(2)*(Ny/2),'Duration',mr.calcDuration(gxPre), 'system',sys);
gzPre = mr.makeTrapezoid('z','Area',deltak(3)*(Nz/2),'Duration',mr.calcDuration(gxPre), 'system',sys);

gyReph = mr.makeTrapezoid('y','Area',deltak(2)*(Ny/2),'Duration',mr.calcDuration(gxSpoil), 'system',sys);
gzReph = mr.makeTrapezoid('z','Area',deltak(3)*(Nz/2),'Duration',mr.calcDuration(gxSpoil), 'system',sys);

stepsY=((traj(:,2)-1)-Ny/2)/Ny*2;
stepsZ=((traj(:,1)-1)-Nz/2)/Nz*2;

% Create non-selective pulse
rf = mr.makeBlockPulse(flip_angle*pi/180, sys, 'Duration', 0.1e-3);
```

Sequence implementation on Pulseq: writeSeq.m

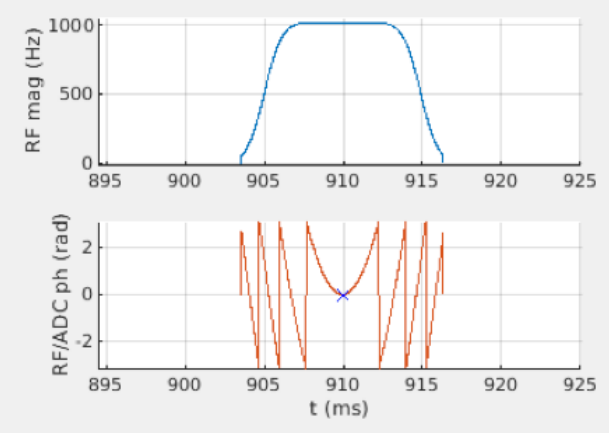
```
% Prep pulses
% T2 prep and IR prep pulse are imported from external txt files
% txt file is in mag and phase, while mr.makeArbitraryRf assumes real and
t2prep = readmatrix('csv_imports/T2prep.txt');
Re = t2prep(:,1) .* cos(t2prep(:,2));
Im = t2prep(:,1) .* sin(t2prep(:,2));
t2prep_pulse = mr.makeArbitraryRf((Re+Im*1i).', 380.4*pi/180, 'system',sy

IRprep = readmatrix('csv_imports/IRprep.txt');
Re = IRprep(:,1) .* cos(IRprep(:,2));
Im = IRprep(:,1) .* sin(IRprep(:,2));
IRprep_pulse = mr.makeArbitraryRf((Re+Im*1i).', 850*pi/180, 'system',sys,
```

mr.makeArbitraryRF

T2prep



IR



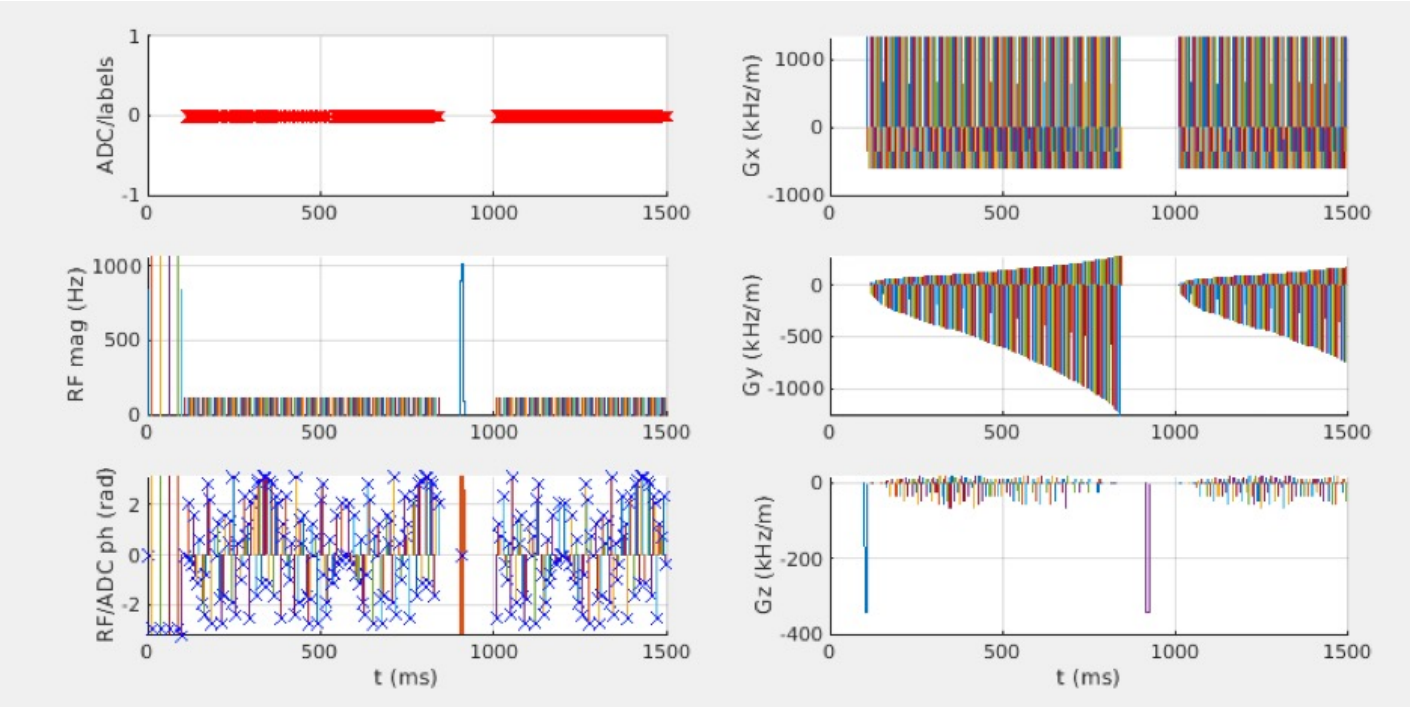
Sequence implementation on Pulseq: writeSeq.m

```
%--------------------------------------------------------------------------
% Build sequence
%--------------------------------------------------------------------------

for iZ = 1:nTR
    rf_phase=0;
    rf_inc=0;

    for iY = 1:nETL

        % Calculate index for ky-kz look up table
        index = iY + (iZ-1)*nETL;

        % RF spoiling
        rf.phaseOffset=rf_phase/180*pi;
        adc.phaseOffset=rf_phase/180*pi;
        rf_inc=mod(rf_inc+rfSpoilingInc, 360.0);
        rf_phase=mod(rf_phase+rf_inc, 360.0);       %increment RF phase

        % Excitation
        if iY == 1
            seq.addBlock(rf,mr.makeLabel('SET', 'LIN', segmentID)); % segment
        else
            seq.addBlock(rf);
        end

        % Encoding
        seq.addBlock(gxPre, ...
            mr.scaleGrad(gyPre,-stepsY(index)), ...
            mr.scaleGrad(gzPre,-stepsZ(index)));    % Gz, Gy blips, Gx pre-win
```

Sequence implementation on Pulseq: timing check, PNS check

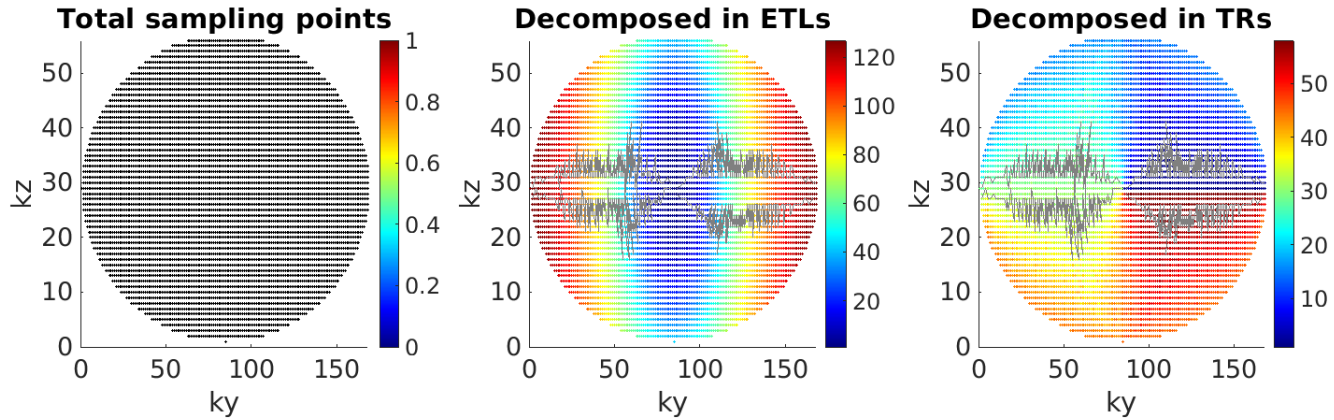
```
%--------------------------------------------------------------------------
% Check timing and write sequence
%--------------------------------------------------------------------------

% check whether the timing of the sequence is correct
[ok, error_report]=seq.checkTiming;

if (ok)
    fprintf('Timing check passed successfully\n');
else
    fprintf('Timing check failed! Error listing follows:\n');
    fprintf([error_report{:}]);
    fprintf('\n');
end

% PNS check
[pns_ok, pns_n, pns_c, tpns]=seq.calcPNS('/autofs/cluster/berkin/fujita/ma

if (pns_ok)
     fprintf('PNS check passed successfully\n');
else
     fprintf('PNS check failed! The sequence will probably be stopped by t
end

% Set definitions for recon
seq.setDefinition('FOV', fov);
seq.setDefinition('Matrix', N);
seq.setDefinition('nETL', nETL);
seq.setDefinition('nTR', nTR);
seq.setDefinition('traj_z', traj(:,1));
seq.setDefinition('traj_y', traj(:,2));

% plot
seq.plot('TimeRange',[0 1.5],'timeDisp','ms');

% Write to pulseq file
filename = strrep(mfilename, 'write', '');
seq.write([filename,'.seq']);
```

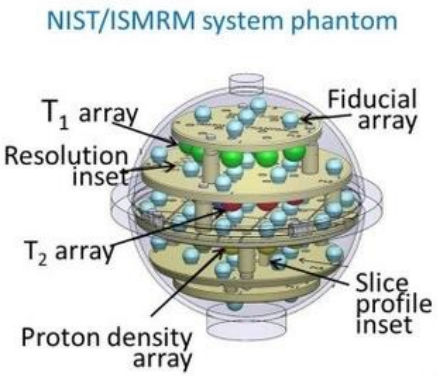
Sequence implementation on Pulseq



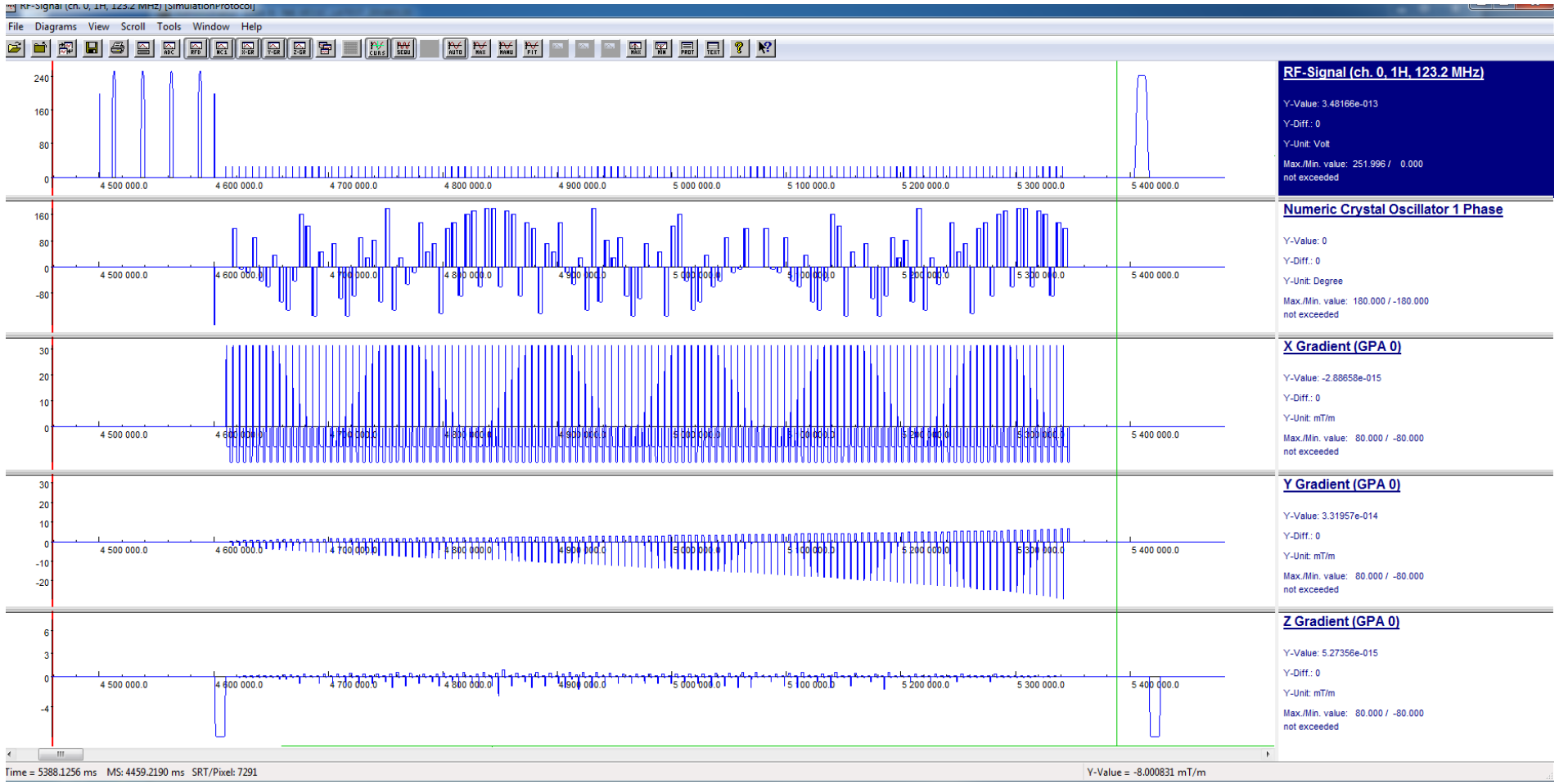
FOV: 192x168x168
Matrix: 192x168x56
TR: 4500ms
TE: 2.3ms
Echo spacing: 5.8ms
FA: 4°
ETL: 127
TA: 4:21

Center-out elliptical ordering
Cartesian sampling

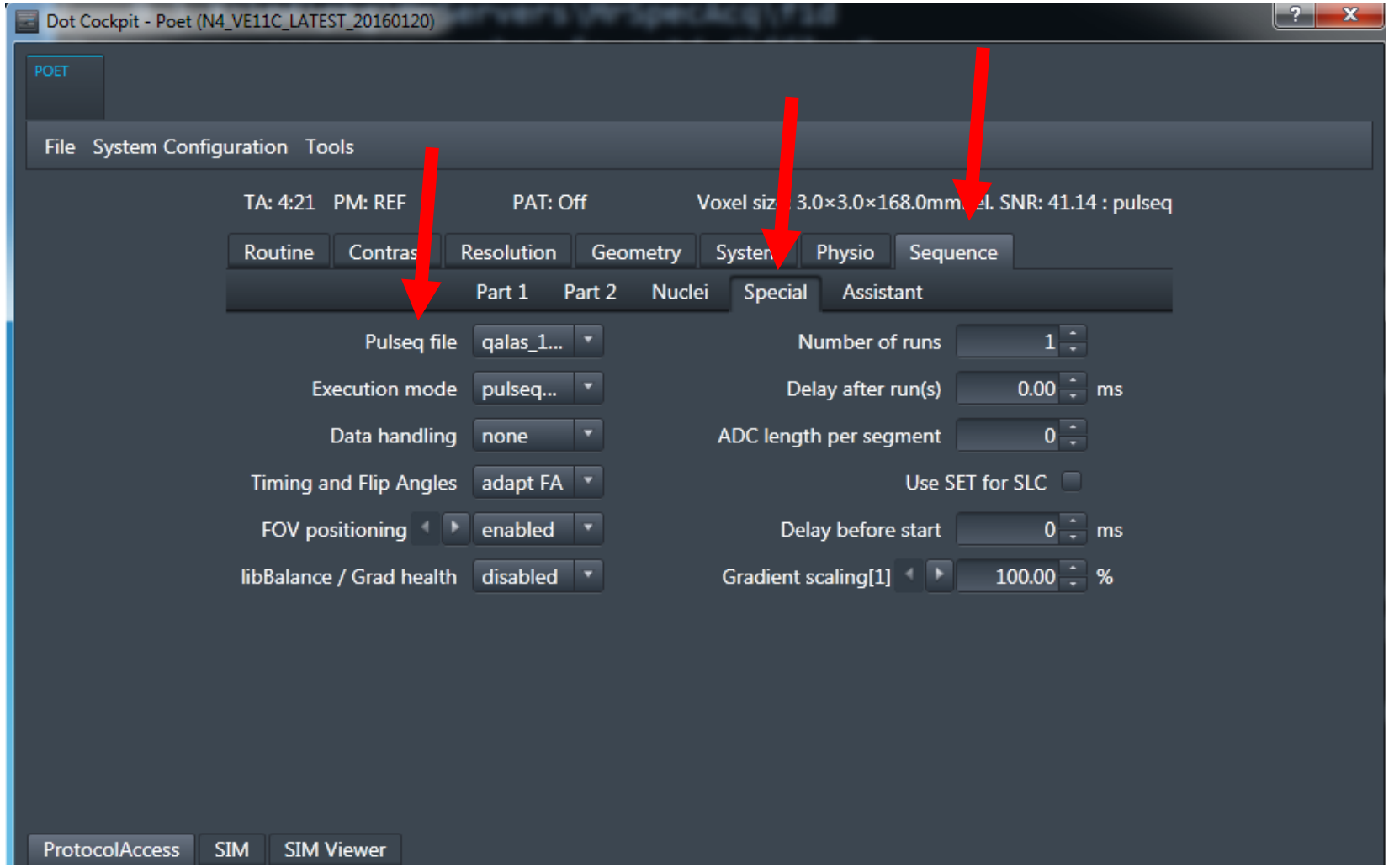




Before going to the scanner… simulating the .seq file in POET



Running your sequence on the scanner

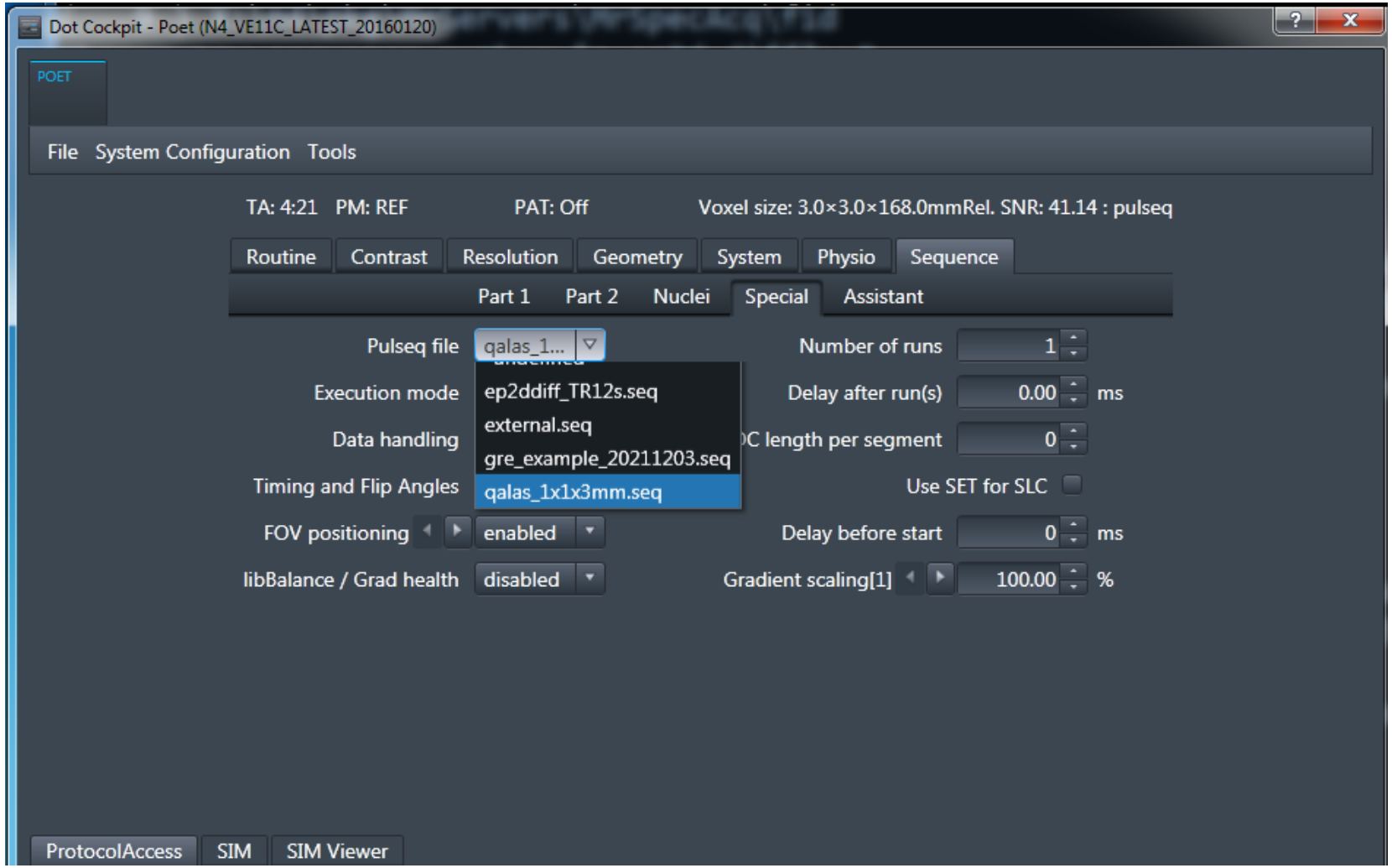


%CustomerSeq%\pulseq\myseq

Name

- QALAS_1x1x3mm_4ge.seq
- qalas_1x1x3mm.seq
- external.seq
- ep2ddiff_TR12s.seq
- gre_example - Copy.seq.txt
- gre_example_20211203.seq

Running your sequence on the scanner



%CustomerSeq%\pulseq\myseq

Name

- QALAS_1x1x3mm_4ge.seq
- qalas_1x1x3mm.seq
- external.seq
- ep2ddiff_TR12s.seq
- gre_example - Copy.seq.txt
- gre_example_20211203.seq

Exporting and reconstructing your pulseq data

Siemens

Twix

meas_MID*.dat

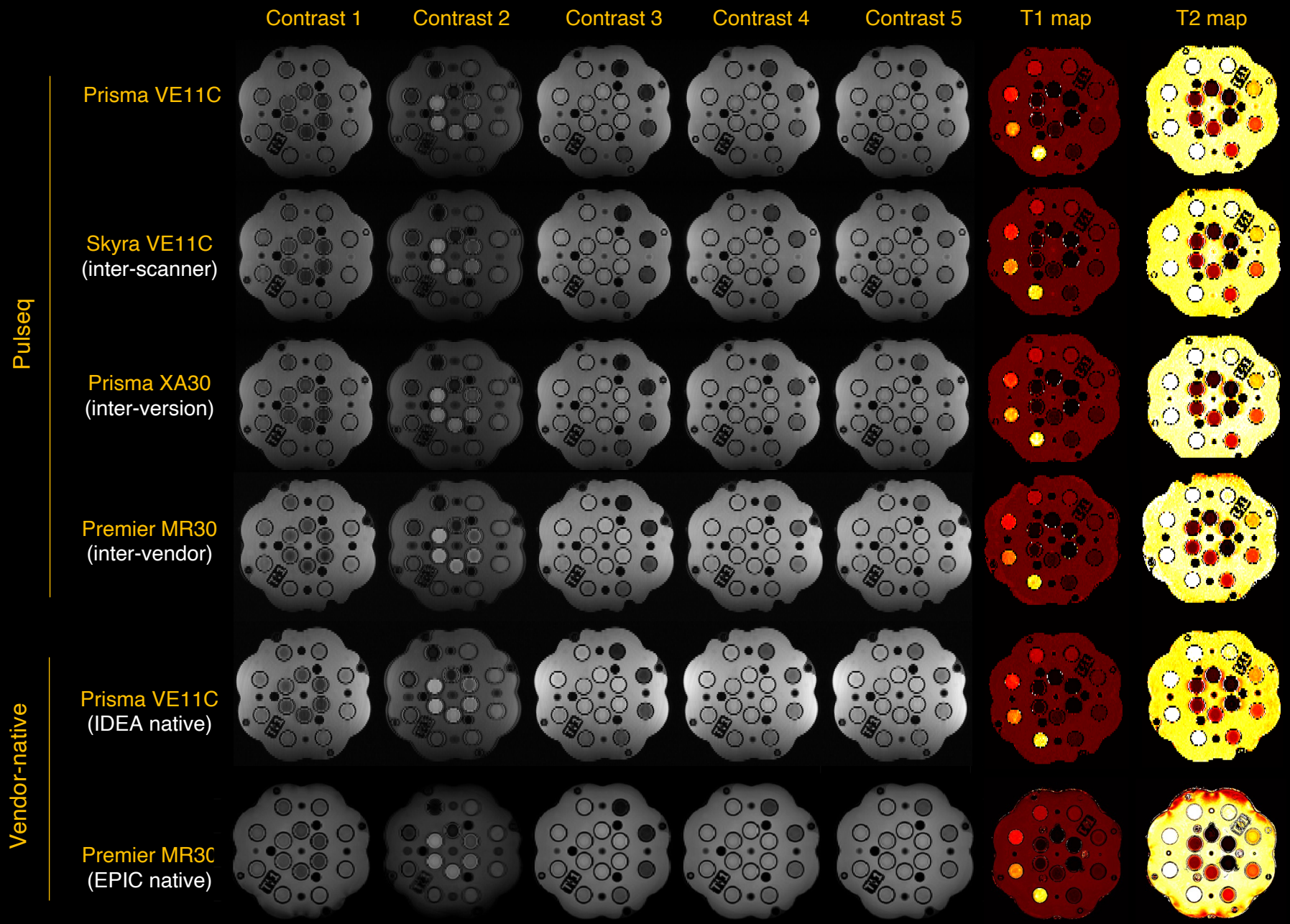
```
data_file_path =
'/autofs/cluster/berkin/fujita/testscan/archive/meas
_MID00465_FID38558_pulseq_qalas.dat';

twix_obj = mapVBVD2(data_file_path);
data_unsorted = twix_obj{end}.image.unsorted();

% size(data_unsorted): adc_len, ncoil, readouts
```

GE

```
pfile = 'P06144.7';

data_unsorted =
toppe.utils.loadpfile(pfile, [], [], [], 'acqOrder', true);

% size(data_unsorted): adc_len, ncoil, readouts
```

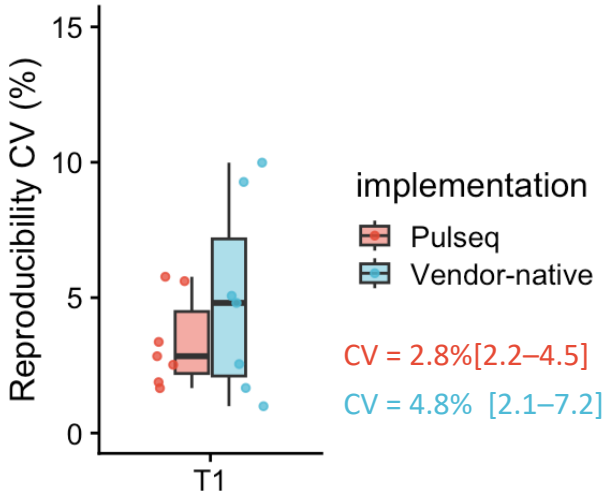
Data sorted in the order it was acquired
Sort using your seq file

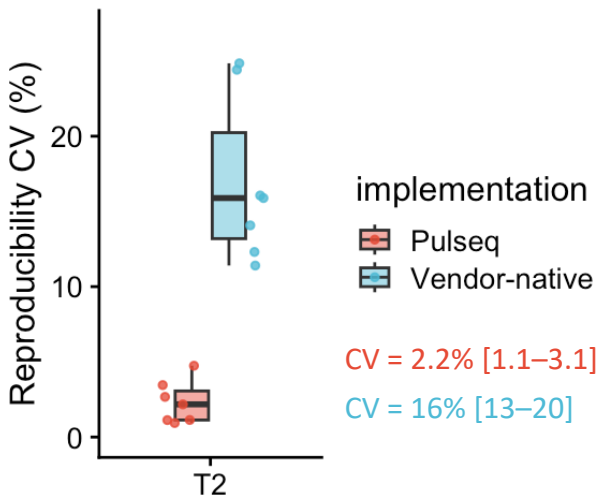
Cross-platform multiparametric mapping



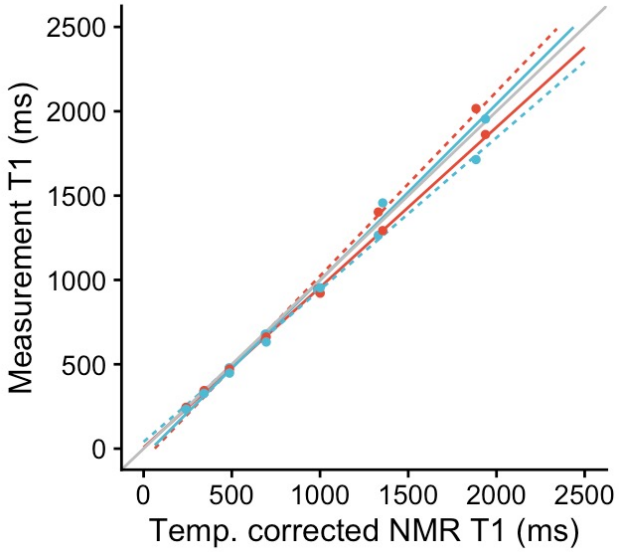
Identical implementation and reconstruction pipeline improves cross-vendor reproducibility

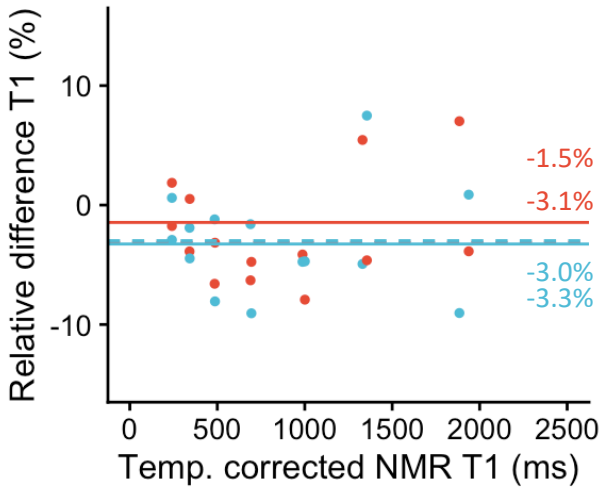
(A) Cross-vendor reproducibility

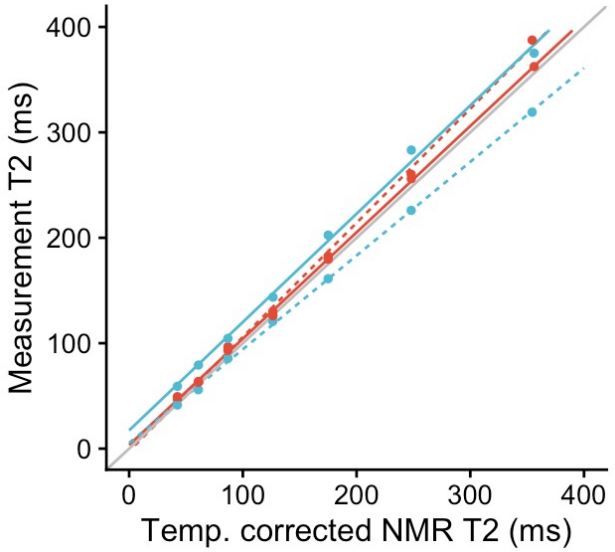


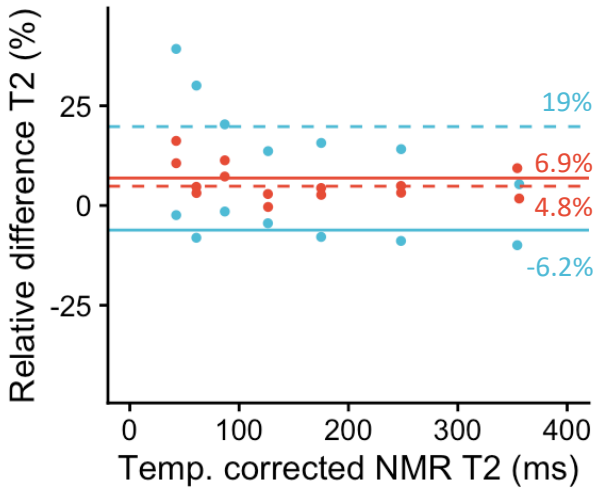


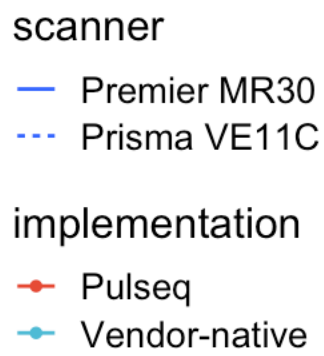
(B) Comparison of Pulseq- and vendor-native implementation



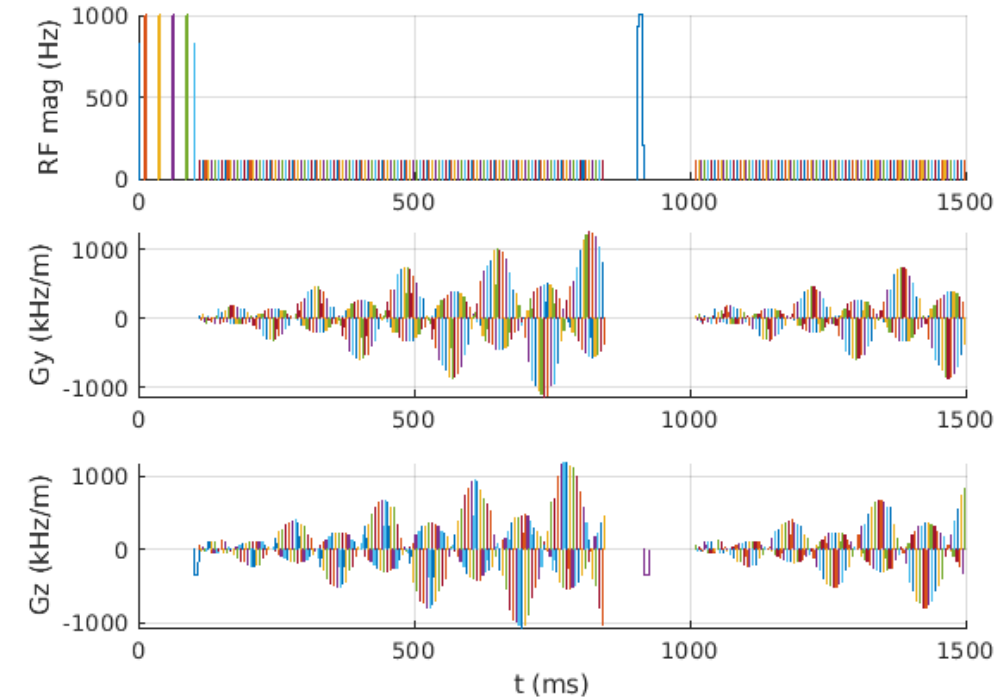




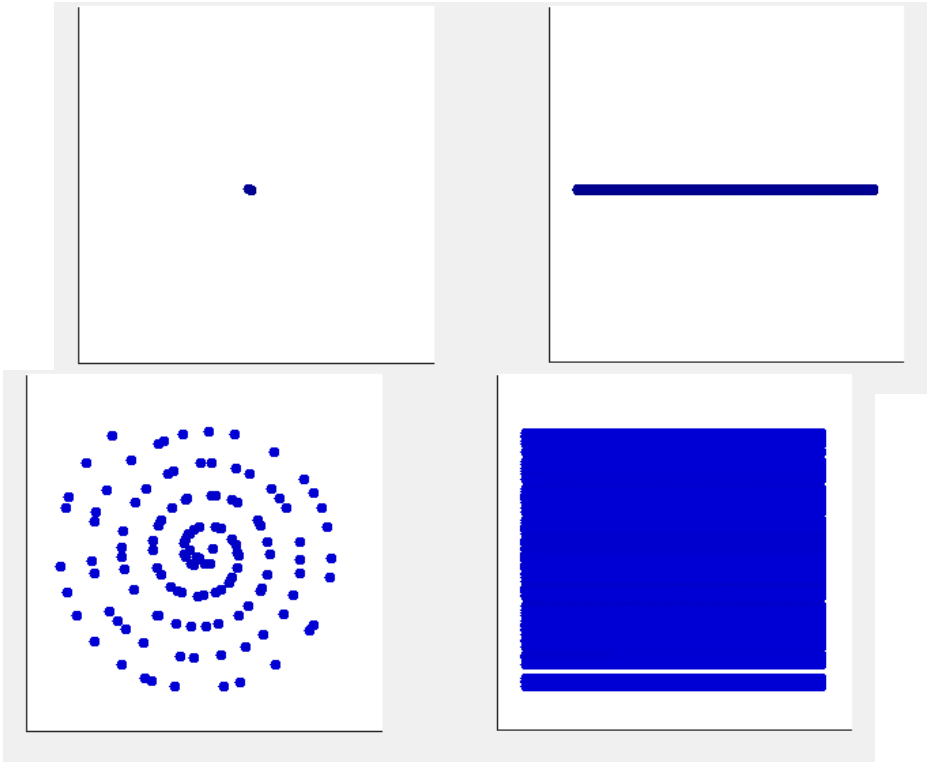




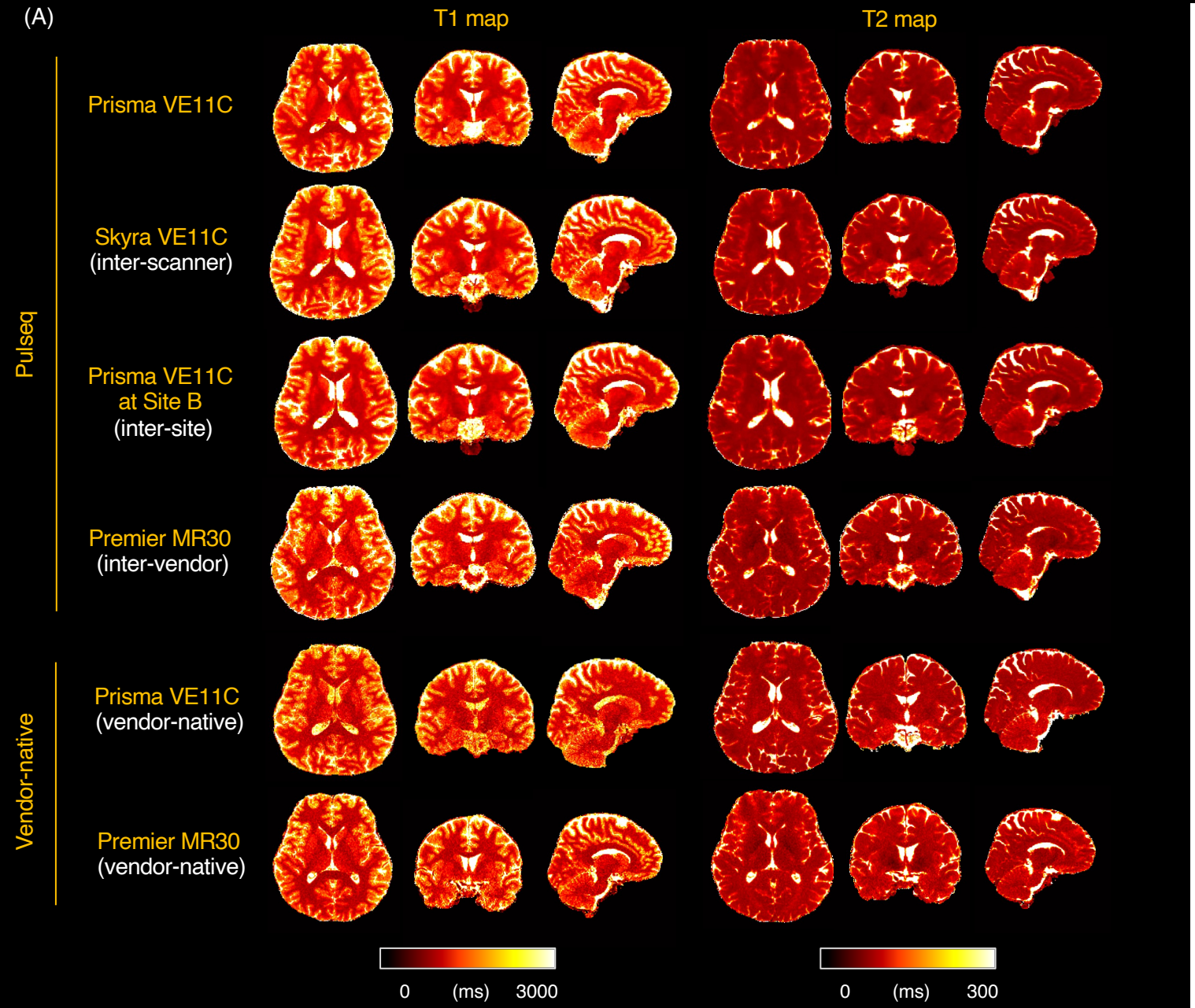
Implementation for in vivo acquisition

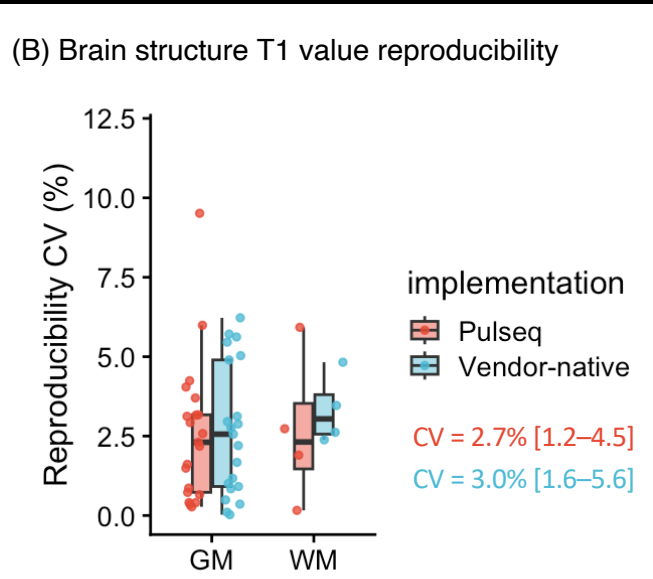


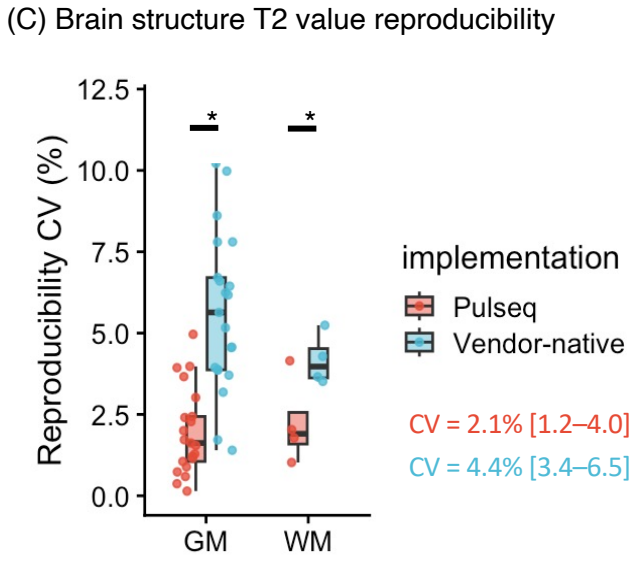
FOV: 256x240x208 (ADNI-compliant)
Matrix: 256x240x208
TR: 4500ms
TE: 2.3ms
Echo spacing: 5.8ms



Vendor-agnostic implementation improves reproducibility

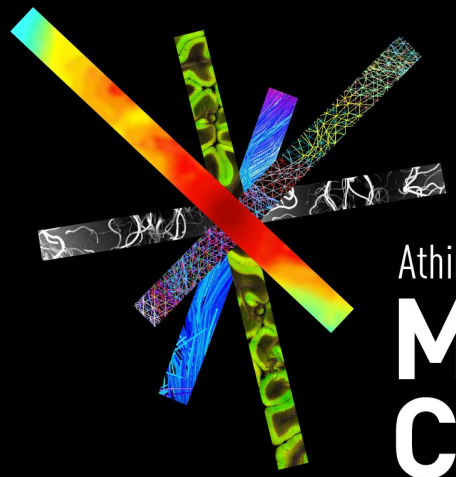






Summary

- Workflow for using custom sequences implemented in Pulseq was demonstrated
- An application of multiparametric mapping using Pulseq was demonstrated
- Pulseq implementation exhibited:
  - Higher reproducibility than vendor-native implementations
  - ADNI-compliant field-of-view sizes with 1mm isotropic resolution within 5 minutes, while maintaining a cross-platform coefficient of variation below 4%.



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Massachusetts
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Technology

Thank you!

Shohei Fujita

BRAIN (Bilgic Reconstruction Acquisition for Imaging Neuroscience) Lab