

Vendor-neutral pulse sequence prototyping with Pulseseq

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<http://pulseseq.github.io>

MRI Together

A global workshop on Open Science and Reproducibility
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Speaker name:

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Conflicts of interest regarding this presentation:

Nothing to disclose

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ESMRMB

European Society for Magnetic Resonance in Medicine and Biology

Overview

- *Pulseq* sequence definition and programming language overview
 - Pulseq philosophy
 - Pulseq file format
 - Development environments and other options
- Using Matlab *Pulseq* Toolbox on Siemens scanners
 - Sequences from scratch: from gradient echo to EPI in 20 minutes

Pulseseq Goals

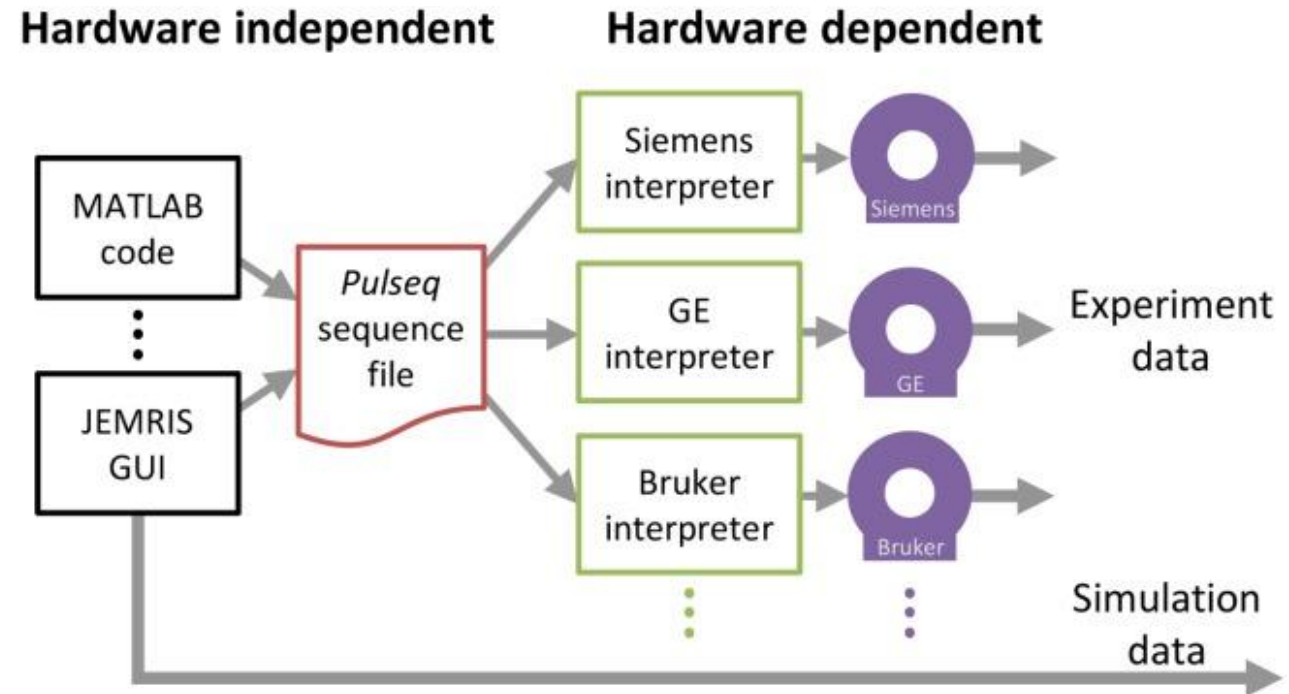


- Remove the initial threshold in sequence programming
 - Make simple things really simple
- Make researcher-oriented features accessible
 - Arbitrary gradients, arbitrary RF, flexible reordering, X-**Nuclei**, ...
- Prevent typical sources of (human) errors
 - Avoid timing errors with overlapping gradients
 - Make flag and counter setting optional/unnecessary
- Minimize effort for implementation and support on hardware
 - Lean sequence-to-hardware interface

Pulseq sequence programming

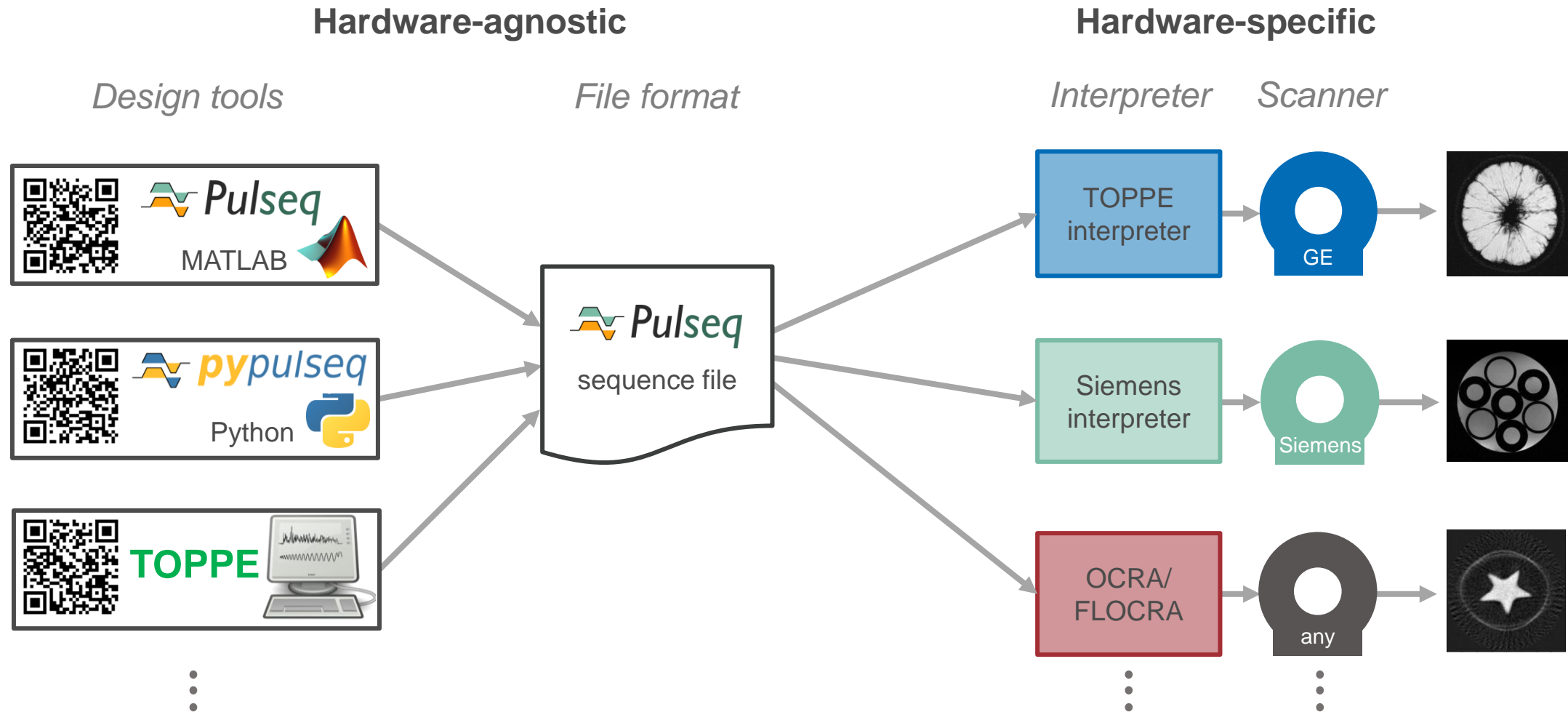
- Cross-platform MRI pulse programming framework
- Low level: *Pulseq* file
- High level: MATLAB¹ or Python² toolboxes
- Main goal: ease typical research tasks

1. <http://pulseq.github.io>
2. <http://github.com/imr-framework/pypulseq>

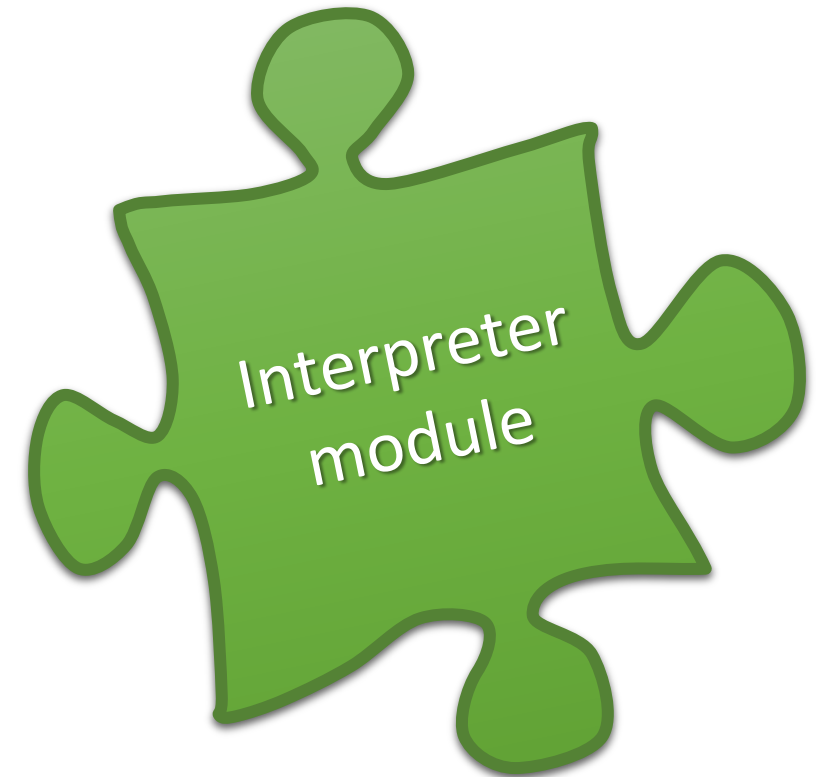


Source: Layton, et al., “Pulseq: A rapid and hardware-independent pulse sequence prototyping framework”, MRM 2017

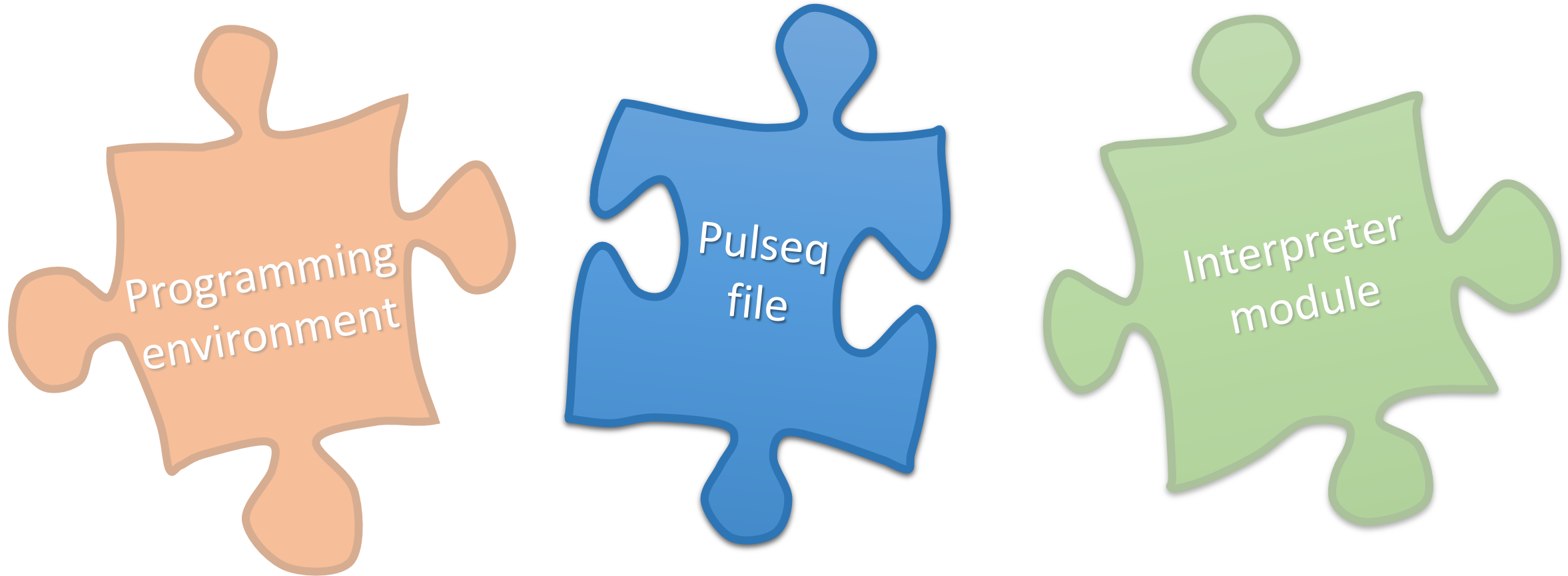
Pulseseq framework overview



Pulseq : pieces of the puzzle

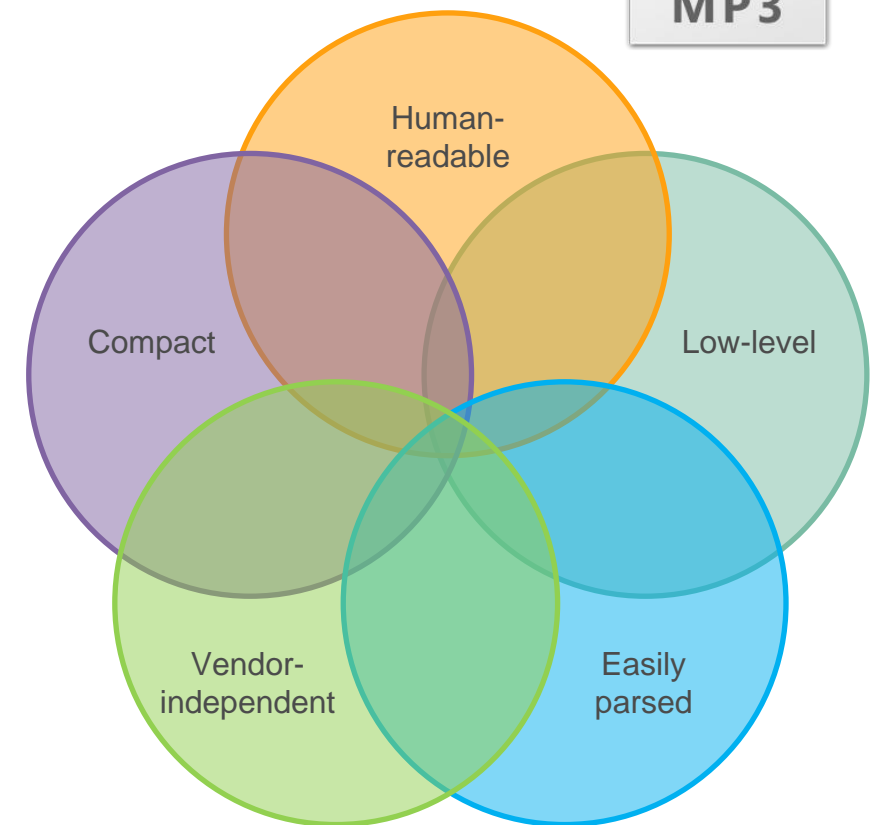


Pulseq : pieces of the puzzle



Pulseseq file

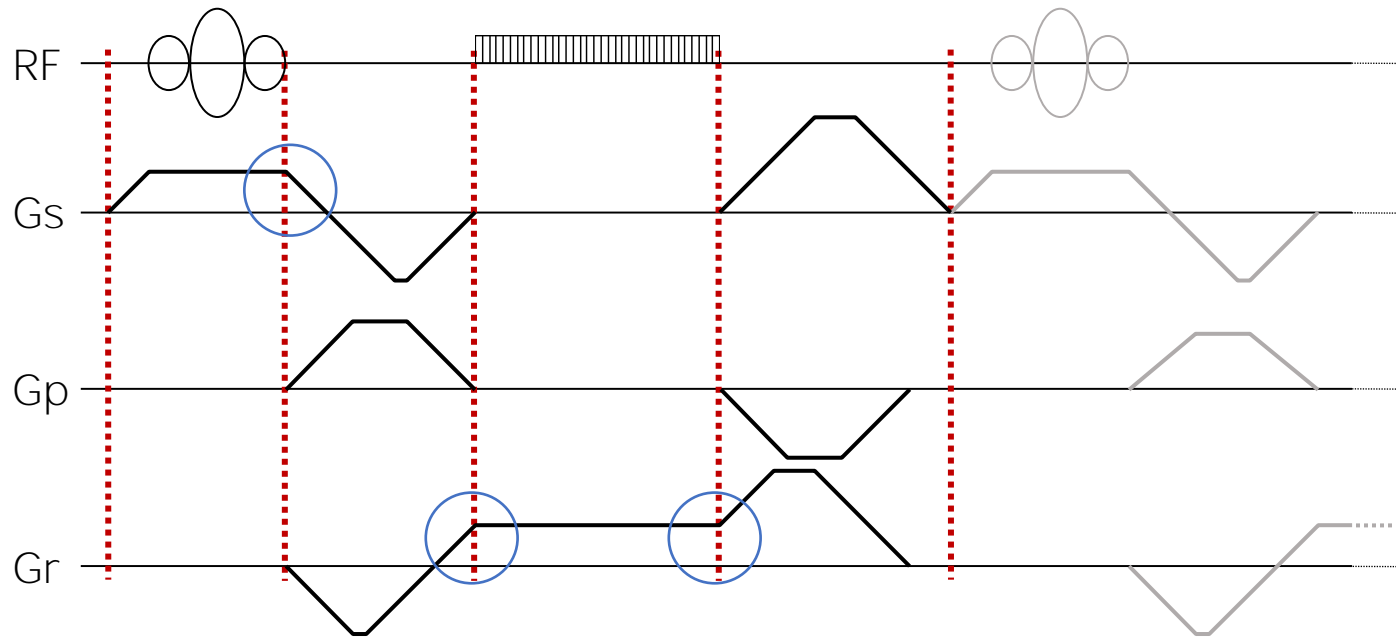
- Explicit (low level) specification of the pulse sequence
 - Think of an MP3 file (or more precisely lossless FLAC)
- No loops, no parameters, no dependencies, no fuss!
- Text file (human-readable)
 - Simple hierarchy (RF pulses, gradients, shapes)
 - Event table keeps it together
 - See <http://pulseseq.github.io/specification.pdf> for more details



Pulse sequence definition



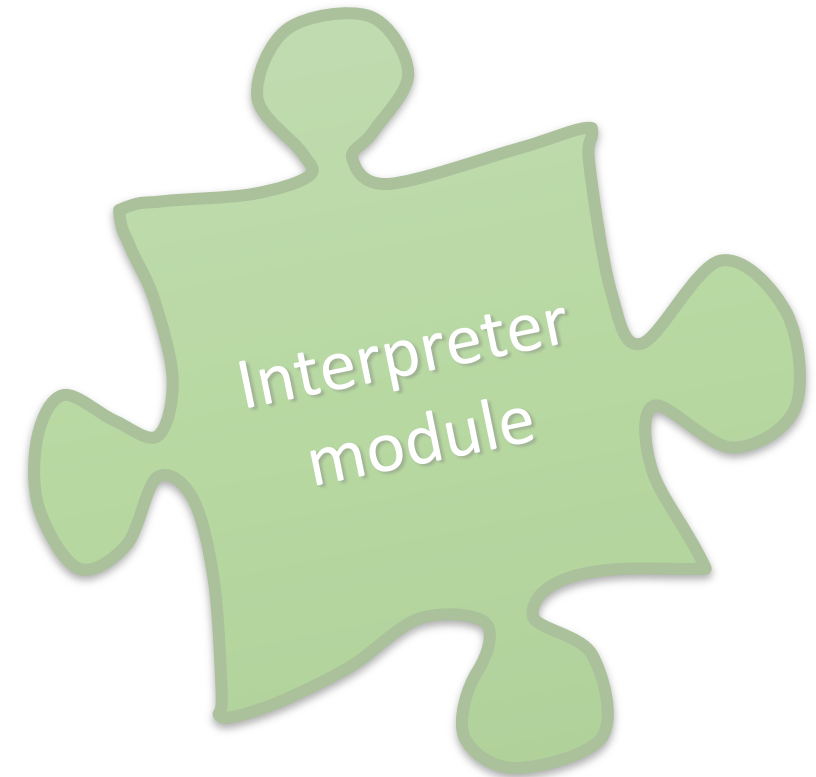
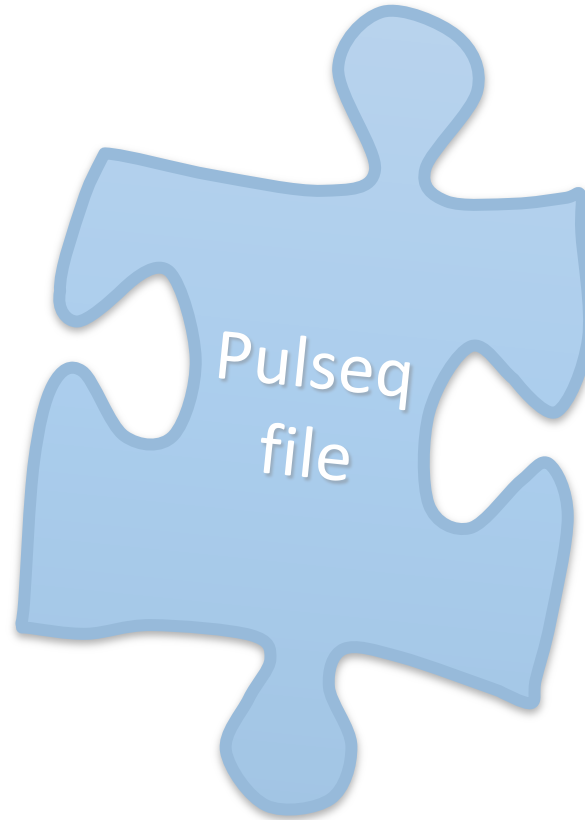
Concatenation of non-overlapping blocks



- Block 1:
gradient and RF
- Block 2:
only gradients
- Block 3:
gradient and ADC
- Block 4:
only gradients
- Block 5:
gradient and RF ...

Gradients do not have to start or end at 0 at the block boundaries

Pulseq : pieces of the puzzle



High-level programming environments

- Matlab *Pulseq* toolbox
- Python *pypulseq* toolbox

(see presentation by K. S, Ravi in Session C1 in Caribbean time zone today)



- Further options
 - TOPPE is primarily targeted at GE but can import and export *pulseq* files
(see hands-on by J.-F. Nielsen in Session C1 in Caribbean time zone today)
 - GammaStar can export *pulseq* files
 - JEMRIS Bloch simulator can export *pulseq* files
 - CoreMRI Bloch simulator can export *pulseq* files
 - ...

Matlab Pulseseq workflow



- Define the system properties
- Define high-level parameters (convenience)
- Define pulses used in the sequence
- Calculate the delays and reordering tables
- Loop and define sequence blocks
 - Duration of each block is defined by the duration of the longest event
- **Copy 'gre.seq' to the scanner and run it!**
- *Screenshot shows an entire runnable gradient echo sequence code (similar to Siemens' example miniFlash)*

```
system = mr.opts('MaxGrad',30,'GradUnit','mT/m',...
    'MaxSlew',170,'SlewUnit','T/m/s');
seq=mr.Sequence(system);

fov = 220e-3; Nx=64; Ny=64; TE = 10e-3; TR = 20e-3;

[rf, gz] = mr.makeSincPulse(15*pi/180,system,'Duration',4e-3,...
    'SliceThickness',5e-3,'apodization',0.5,'timeBwProduct',4);

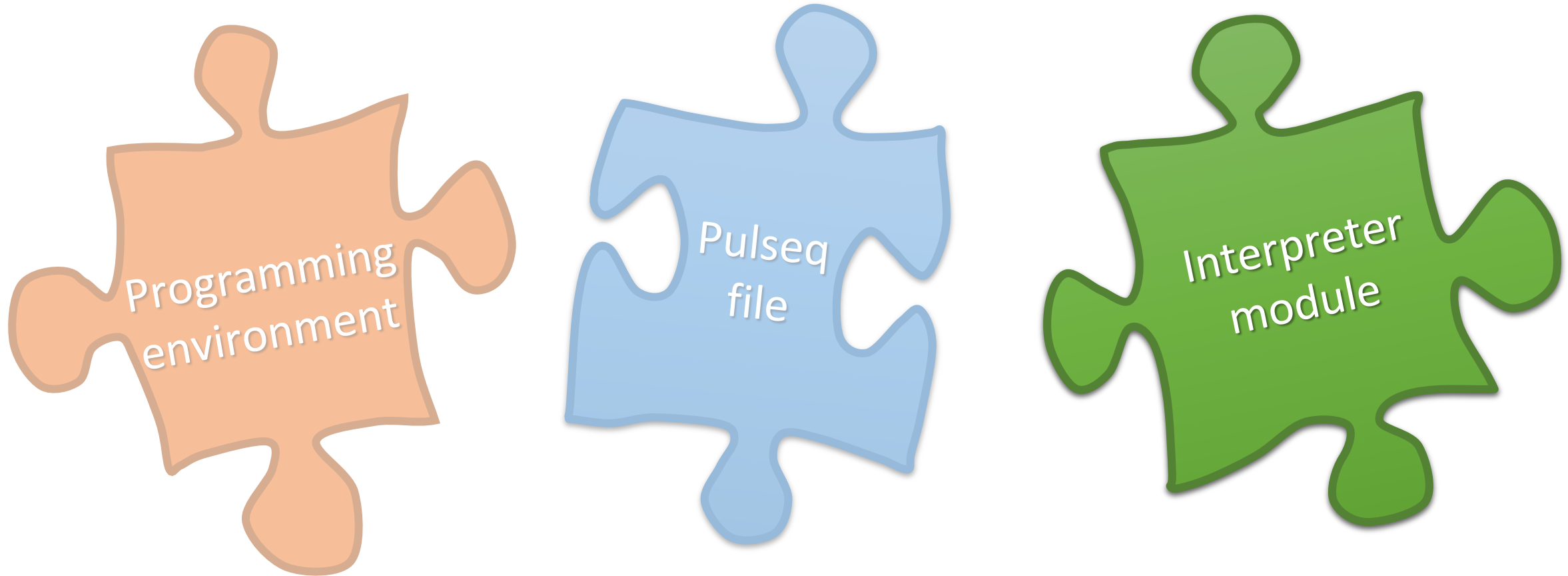
gx = mr.makeTrapezoid('x',system,'FlatArea',Nx/fov,'FlatTime',6.4e-3);
adc = mr.makeAdc(Nx,'Duration',gx.flatTime,'Delay',gx.riseTime);
gxPre = mr.makeTrapezoid('x',system,'Area',-gx.area/2,'Duration',2e-3);
gzReph = mr.makeTrapezoid('z',system,'Area',-gz.area/2,'Duration',2e-3);
phaseAreas = ((0:Ny-1)-Ny/2)*1/fov;

delayTE = TE - mr.calcDuration(gxPre) - mr.calcDuration(rf)/2 ...
    - mr.calcDuration(gx)/2;
delayTR = TR - mr.calcDuration(gxPre) - mr.calcDuration(rf) ...
    - mr.calcDuration(gx) - delayTE;
delay1 = mr.makeDelay(delayTE);
delay2 = mr.makeDelay(delayTR);

for i=1:Ny
    seq.addBlock(rf,gz);
    gyPre = mr.makeTrapezoid('y',system,'Area',phaseAreas(i),...
        'Duration',2e-3);
    seq.addBlock(gxPre,gyPre,gzReph);
    seq.addBlock(delay1);
    seq.addBlock(gx,adc);
    seq.addBlock(delay2)
end

seq.write('gre.seq')
```

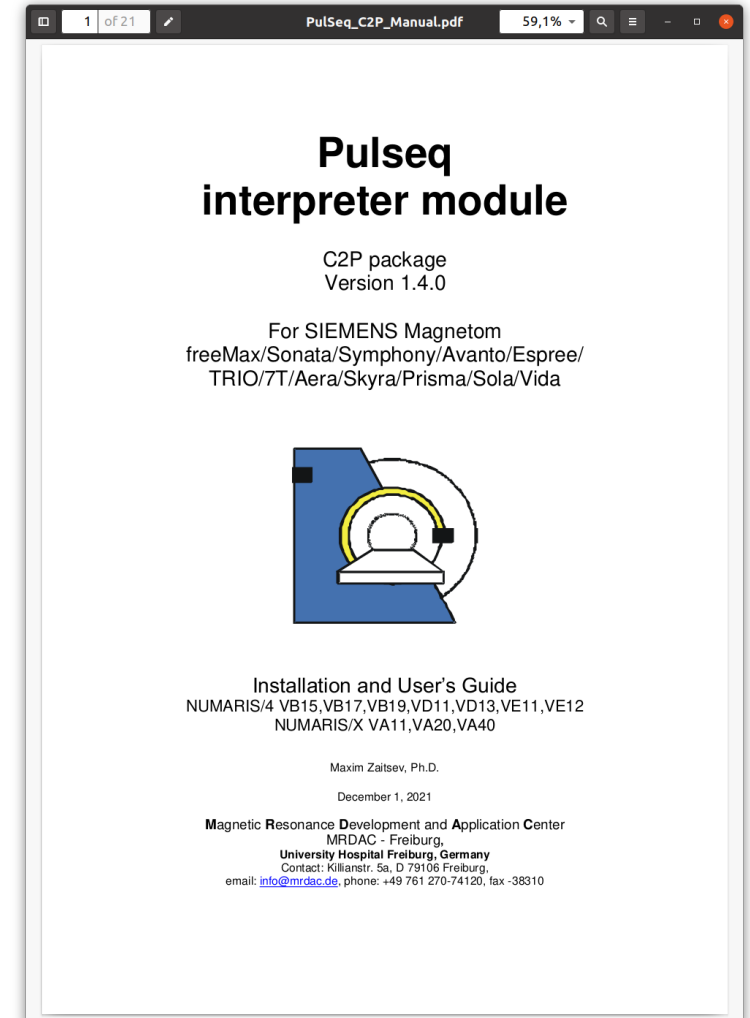
Pulseq : pieces of the puzzle



Pulseseq Siemens interpreter

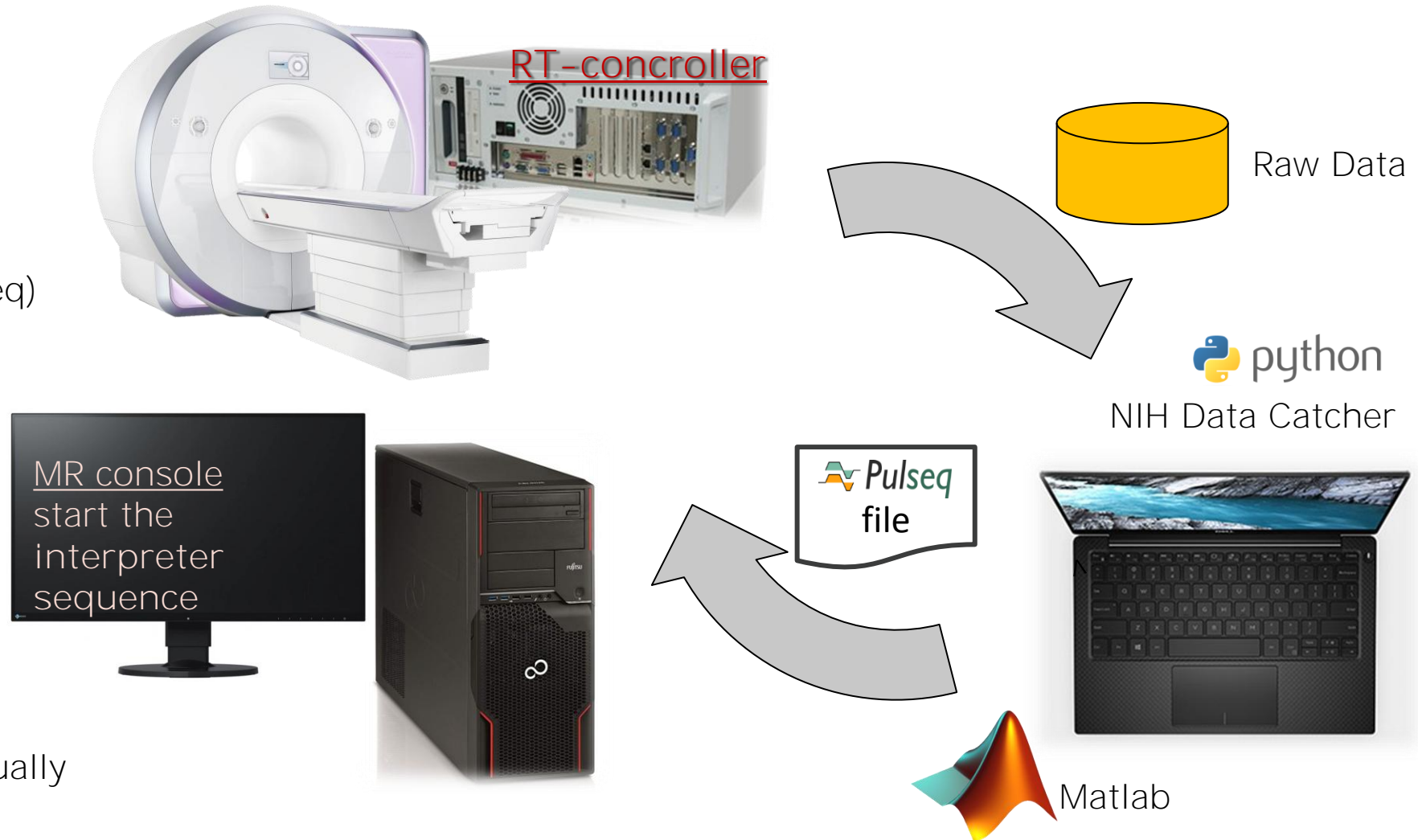


- Just a “normal” sequence
 - Loads its “content” from a Pulseseq file
 - All aspects of the sequence are pre-defined
 - FOV positioning and scaling possible
- Based on miniFlash
 - No product code
 - No hacks, no backdoors
- Distributed as a C2P package in source form
- Standard SAR calculation
- Since 1.3.1: libBalance applicable to all sequences
- Safety equal or higher than a typical IDEA sequence



Pulseq on Siemens scanners

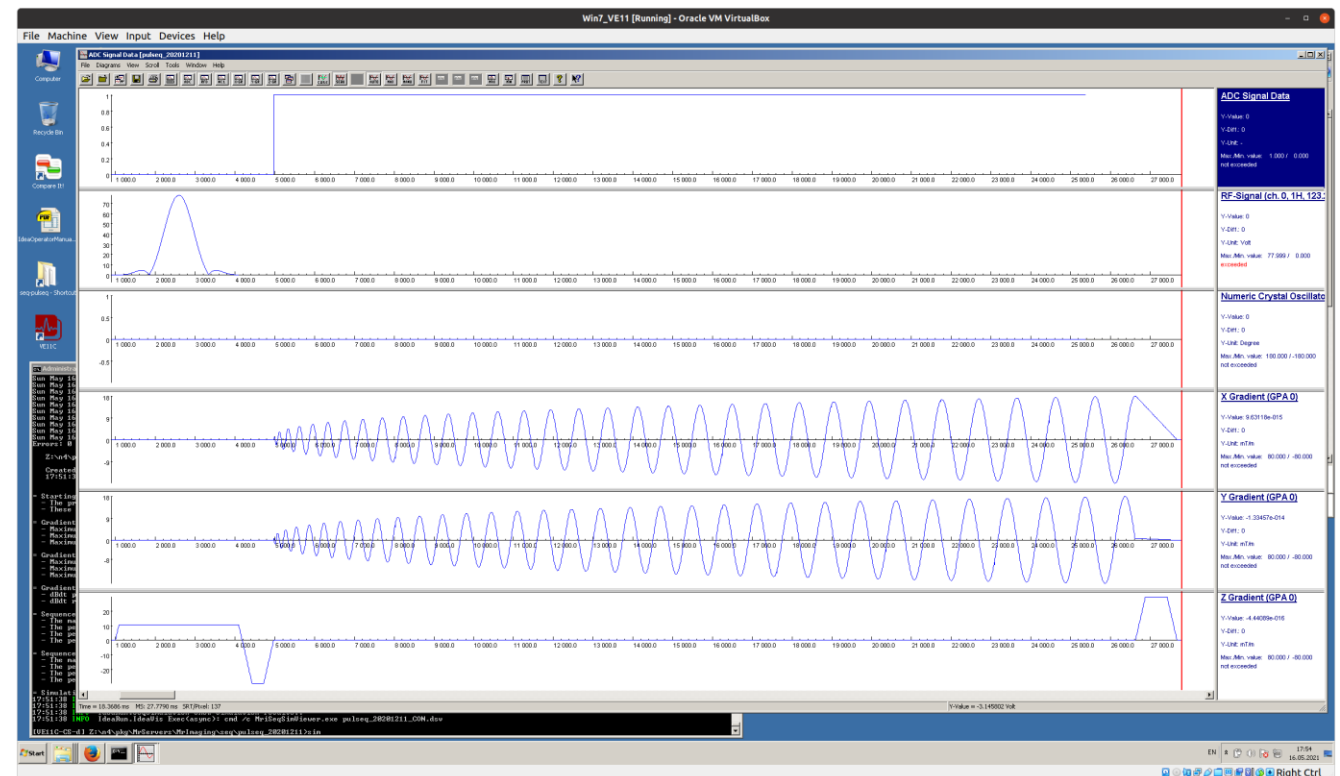
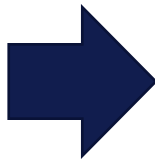
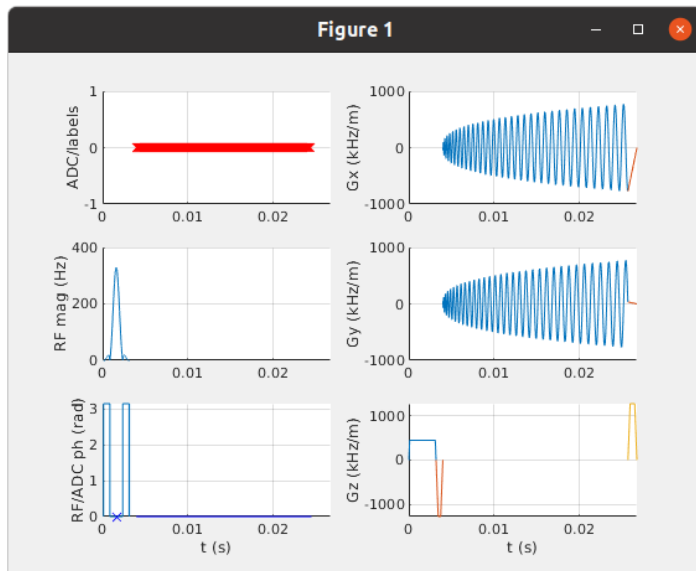
- *Optional initial step:*
connect your PC to the scanner
- Save the .seq file on the scanner (e.g. external.seq)
- Run the
interpreter_sequence
on the scanner
- *Optional step:*
*stream raw data to your
with NIH_DataCatcher*
- or export raw data manually



IDEA simulation with *Pulseq*

Pulseseq interpreter sequence can also be used with the Siemens' IDEA

1. Save your .seq file as %CustomerSeq%/Pulseseq/external.seq
2. In the IDEA command run
sim



Pulseseq on Siemens platforms

- Over 40 C2P sites
- Works on all Numaris4 platforms (tested on vb15...ve12u) and numerous hardware platforms (Symphony, Trio, 7T, Connectom, Skyra, Prisma,...)
- Tested on selected NumarisX versions (xa11, xa20, **xa30**, **xa40** ...)
- Confirmed to work on Sola and Vida and 0.55T free.Max

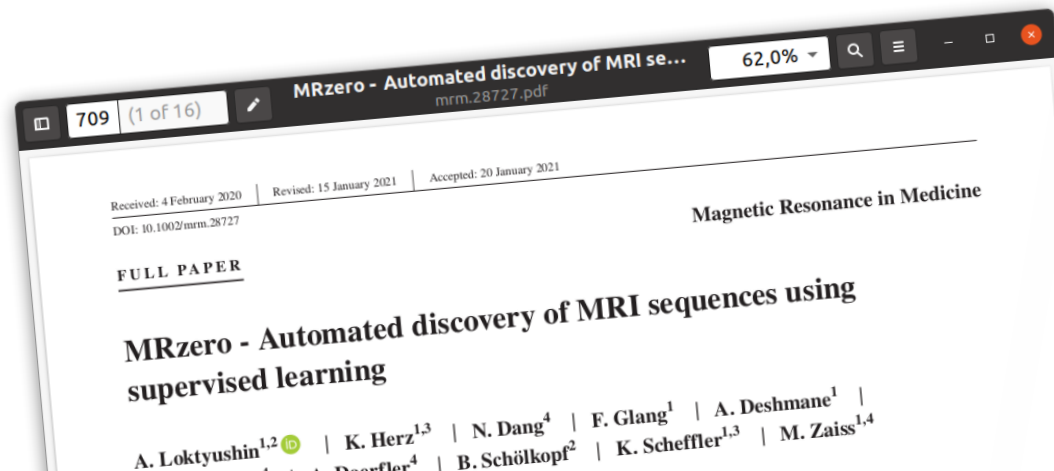


Pulseseq on the Internet

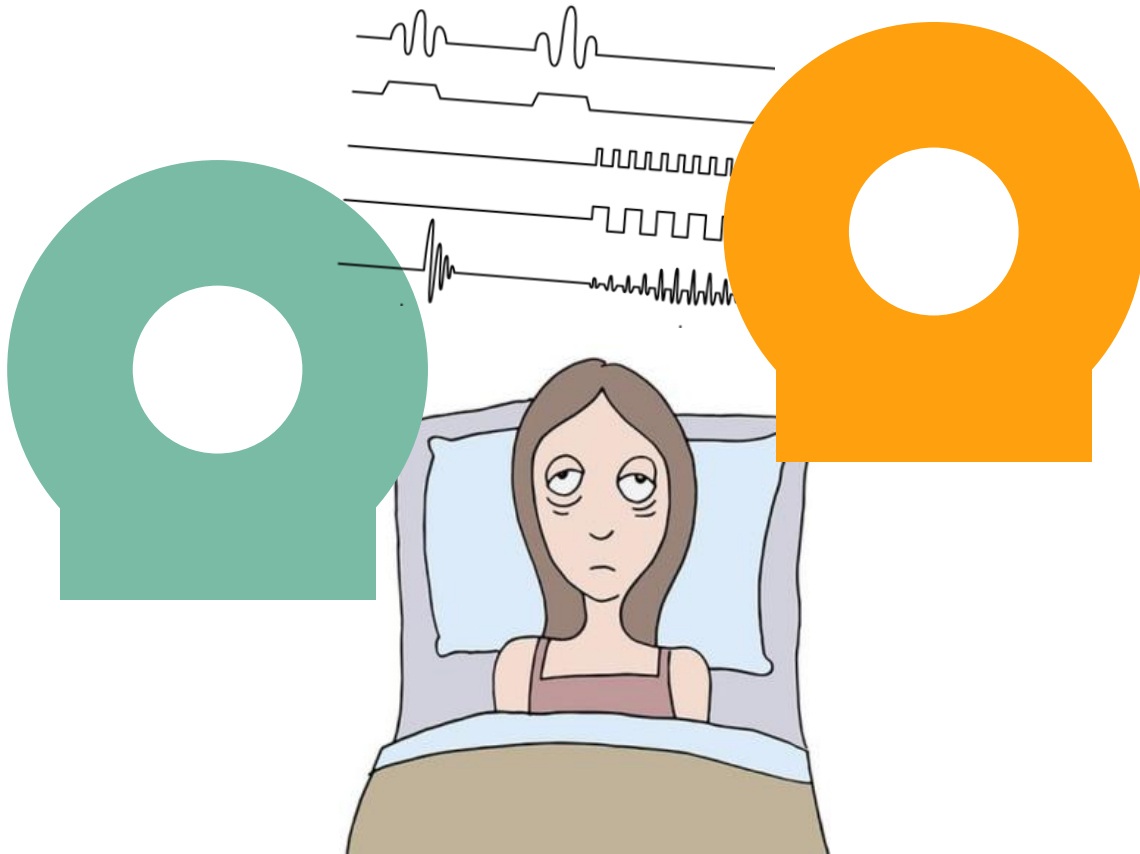
- Main Pulseseq site & Matlab Toolbox:
<https://pulseseq.github.io>
- Python Pulseseq Toolbox:
<https://github.com/imr-framework/pypulseseq>
- MRI Together live demo page on GitHub:
https://github.com/pulseseq/pulseseqMRI_Together/
- Live raw data and results of the MRI Together demo on Dropbox:
https://www.dropbox.com/sh/i7f1gpwyigdugps/AACd2jQJg_WjoTY2nqh7O8IHa?dl=0

Pulseseq in the press

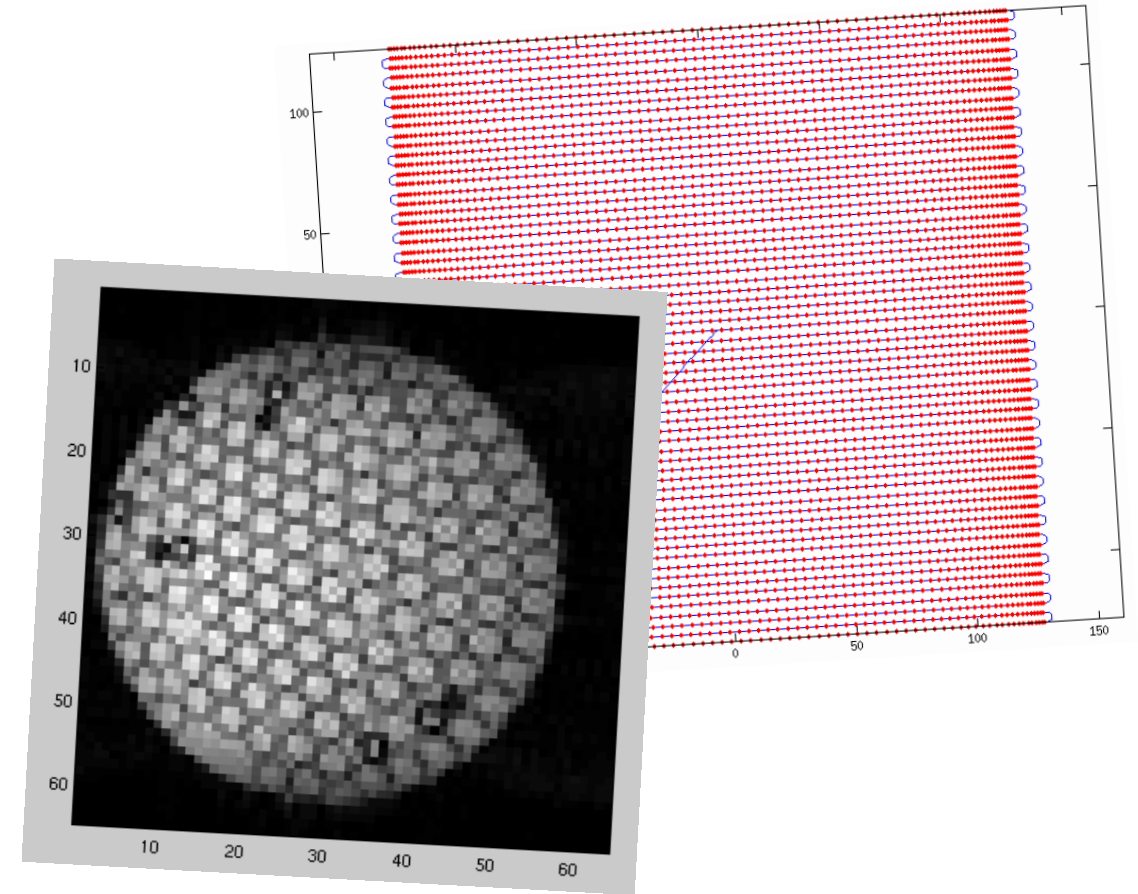
- De-facto standard for CEST collaboration
- Several MRM papers rely entirely on Pulseseq
- Numerous ISMRM abstracts



Pulseseq – that's the way you do it!



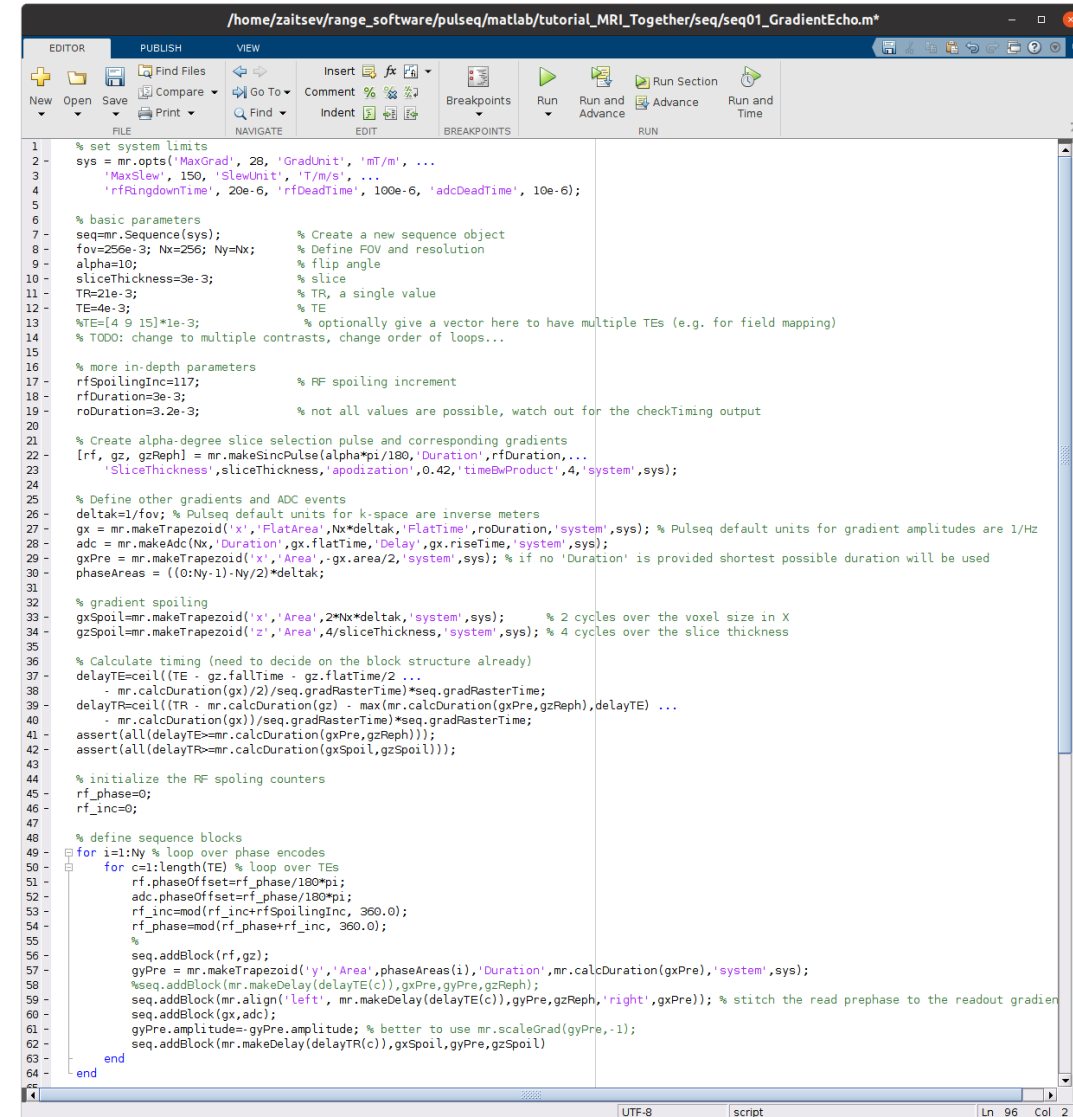
...dream of a sequence in the morning...



...check the images in the afternoon!

Gradient Echo from Scratch™ with *Pulseseq*

- Fully-operational GRE sequence
 - Gradient spoiling
 - RF spoiling
 - PE refocusing
 - Multiple contrasts
 - ...
- 64 lines of code including comments
- “zoom into” respective code sections in the following slides



```
% /home/zaitsev/range_software/pulseseq/matlab/tutorial_MRI_Together/seq/seq01_GradientEcho.m
1 % set system limits
2 sys = mr.opts('MaxGrad', 28, 'GradUnit', 'mT/m', ...
3 'MaxSlew', 150, 'SlewUnit', 'T/m/s', ...
4 'rfRingdownTime', 20e-6, 'rfDeadTime', 100e-6, 'adcDeadTime', 10e-6);
5
6 % basic parameters
7 seq = mr.Sequence(sys); % Create a new sequence object
8 fov=256e-3; Nx=256; Ny=Nx; % Define FOV and resolution
9 alpha=10; % flip angle
10 sliceThickness=3e-3; % slice
11 TR=21e-3; % TR, a single value
12 TE=4e-3; % TE
13 % TE=[4 9 15]*1e-3; % optionally give a vector here to have multiple TEs (e.g. for field mapping)
14 % TODO: change to multiple contrasts, change order of loops...
15
16 % more in-depth parameters
17 rfSpoilingInc=117; % RF spoiling increment
18 rfDuration=3e-3;
19 roDuration=3.2e-3; % not all values are possible, watch out for the checkTiming output
20
21 % Create alpha-degree slice selection pulse and corresponding gradients
22 [rf, gzReph] = mr.makeSincPulse(alpha*pi/180, 'Duration', rfDuration, ...
23 'SliceThickness', sliceThickness, 'apodization', 0.42, 'timeBwProduct', 4, 'system', sys);
24
25 % Define other gradients and ADC events
26 deltak=1/fov; % Pulseseq default units for k-space are inverse meters
27 gx = mr.makeTrapezoid('x', 'FlatArea', Nx*deltak, 'FlatTime', roDuration, 'system', sys); % Pulseseq default units for gradient amplitudes are 1/Hz
28 adc = mr.makeADC(Nx, 'Duration', gx.flatTime, 'Delay', gx.riseTime, 'system', sys);
29 gxPre = mr.makeTrapezoid('x', 'Area', -gx.area/2, 'system', sys); % if no 'Duration' is provided shortest possible duration will be used
30 phaseAreas = ((0:Ny-1)-Ny/2)*deltak;
31
32 % gradient spoiling
33 gxSpoil=mr.makeTrapezoid('x', 'Area', 2*Nx*deltak, 'system', sys); % 2 cycles over the voxel size in X
34 gzSpoil=mr.makeTrapezoid('z', 'Area', 4/sliceThickness, 'system', sys); % 4 cycles over the slice thickness
35
36 % Calculate timing (need to decide on the block structure already)
37 delayTE=ceil((TE - gz.flatTime - gx.flatTime)/2 ...
38 mr.calcDuration(gx)/2)/seq.gradRasterTime)*seq.gradRasterTime;
39 delayTR=ceil((TR - mr.calcDuration(gz) - max(mr.calcDuration(gxPre, gzReph), delayTE) ...
40 - mr.calcDuration(gx))/seq.gradRasterTime)*seq.gradRasterTime;
41 assert(all(delayTE>mr.calcDuration(gxPre, gzReph)));
42 assert(all(delayTR>mr.calcDuration(gxSpoil, gzSpoil)));
43
44 % initialize the RF spoiling counters
45 rf_phase=0;
46 rf_inc=0;
47
48 % define sequence blocks
49 for i=1:Ny % loop over phase encodes
50 for c=1:length(TE) % loop over TEs
51 rf_phaseOffset=rf_phase/180*pi;
52 adc_phaseOffset=rf_phase/180*pi;
53 rf_inc=mod(rf_inc+rfSpoilingInc, 360.0);
54 rf_phase=mod(rf_phase+rf_inc, 360.0);
55 %
56 seq.addBlock(rf, gz);
57 gyPre = mr.makeTrapezoid('y', 'Area', phaseAreas(i), 'Duration', mr.calcDuration(gxPre), 'system', sys);
58 %seq.addBlock(mr.makeDelay(delayTE(c)), gxPre, gyPre, gzReph);
59 seq.addBlock(mr.align('left', mr.makeDelay(delayTE(c)), gyPre, gzReph, 'right', gxPre)); % stitch the read prephase to the readout gradient
60 seq.addBlock(gx, adc);
61 gyPre.amplitude=gyPre.amplitude; % better to use mr.scaleGrad(gyPre, -1);
62 seq.addBlock(mr.makeDelay(delayTR(c)), gxSpoil, gyPre, gzSpoil);
63
64 end
65 end
```

seq01_GradientEcho.m : part 1

1. Start by defining system limits

- Do not be too greedy
 - Reduce maximum amplitude if you plan to apply FOV rotations
 - Reduce slew rate to avoid peripheral nerve stimulation (PNS) or reduce sound pressure

```
1 % set system limits
2 - sys = mr.opts('MaxGrad', 28, 'GradUnit', 'mT/m', ...
3   'MaxSlew', 150, 'SlewUnit', 'T/m/s', ...
4   'rfRingdownTime', 20e-6, 'rfDeadTime', 100e-6, 'adcDeadTime', 10e-6);
5
6 % basic parameters
7 - seq=mr.Sequence(sys);           % Create a new sequence object
8 - fov=256e-3; Nx=256; Ny=Nx;     % Define FOV and resolution
9 - alpha=10;                      % flip angle
10 - sliceThickness=3e-3;           % slice
11 - TR=21e-3;                      % TR, a single value
12 - TE=4e-3;                       % TE
13 - %TE=[4 9 15]*1e-3;             % optionally give a vector here to have multiple TEs (e.g. for field mapping)
14 - % TODO: change to multiple contrasts, change order of loops...
15
16 % more in-depth parameters
17 - rfSpoilingInc=117;              % RF spoiling increment
18 - rfDuration=3e-3;
19 - roDuration=3.2e-3;             % not all values are possible, watch out for the checkTiming output
20
```

2. Define the Sequence object

3. Define convenience high-level parameters

- Remember: there will be no UI to define or modify them later

seq01_GradientEcho.m : part 2

4. Define RF and gradient pulses

- Define objects on-by-one
- Some functions return sets of objects that work together well
- *Remember to provide 'system'*
- Pulseq units make life simple
 - Gradients are defined in Hz/m
 - K-space unit is 1/m

5. Plan your block structure

6. Calculate timing

- Some consistency/validity checks do not hurt

```
21 % Create alpha-degree slice selection pulse and corresponding gradients
22 [rf, gz, gzReph] = mr.makeSincPulse(alpha*pi/180,'Duration',rfDuration,...
23     'SliceThickness',sliceThickness,'apodization',0.42,'timeBwProduct',4,'system',sys);
24
25 % Define other gradients and ADC events
26 deltak=1/fov; % Pulseq default units for k-space are inverse meters
27 gx = mr.makeTrapezoid('x','FlatArea',Nx*deltak,'FlatTime',roDuration,'system',sys); % Pulseq default units for
28 adc = mr.makeAdc(Nx,'Duration',gx.flatTime,'Delay',gx.riseTime,'system',sys);
29 gxPre = mr.makeTrapezoid('x','Area',-gx.area/2,'system',sys); % if no 'Duration' is provided shortest possible
30 phaseAreas = ((0:Ny-1)-Ny/2)*deltak;
31
32 % gradient spoiling
33 gxSpoil=mr.makeTrapezoid('x','Area',2*Nx*deltak,'system',sys); % 2 cycles over the voxel size in x
34 gzSpoil=mr.makeTrapezoid('z','Area',4/sliceThickness,'system',sys); % 4 cycles over the slice thickness
35
36 % Calculate timing (need to decide on the block structure already)
37 delayTE=ceil((TE - gz.fallTime - gz.flatTime/2 ...
38     - mr.calcDuration(gx)/2)/seq.gradRasterTime)*seq.gradRasterTime;
39 delayTR=ceil((TR - mr.calcDuration(gz) - max(mr.calcDuration(gxPre,gzReph),delayTE) ...
40     - mr.calcDuration(gx))/seq.gradRasterTime)*seq.gradRasterTime;
41 assert(all(delayTE>=mr.calcDuration(gxPre,gzReph)));
42 assert(all(delayTR>=mr.calcDuration(gxSpoil,gzSpoil)));
```


seq01_GradientEcho.m : part 3

7. Loop to populate the sequence

- Use seq.addBlock()
- Update or create new objects as needed
 - For 3D sequences “constant” objects with fixed IDs improve calculation speed
- No limitations
 - Mind calculation time in Matlab
 - Size of the .seq file may become a problem (after 60MB scanner may become unstable)

```
48 % define sequence blocks
49 for i=1:Ny % loop over phase encodes
50     for c=1:length(TE) % loop over TEs
51         rf.phaseOffset=rf_phase/180*pi;
52         adc.phaseOffset=rf_phase/180*pi;
53         rf_inc=mod(rf_inc+rfSpoilingInc, 360.0);
54         rf_phase=mod(rf_phase+rf_inc, 360.0);
55         %
56         seq.addBlock(rf,gz);
57         gyPre = mr.makeTrapezoid('y','Area',phaseAreas(i),'Duration',mr.calcDuration(gxPre),'system',sys);
58         %seq.addBlock(mr.makeDelay(delayTE(c)),gxPre,gyPre,gzReph);
59         seq.addBlock(mr.align('left', mr.makeDelay(delayTE(c)),gyPre,gzReph,'right',gxPre)); % stitch the read
60         seq.addBlock(gx,adc);
61         gyPre.amplitude=-gyPre.amplitude; % better to use mr.scaleGrad(gyPre,-1);
62         seq.addBlock(mr.makeDelay(delayTR(c)),gxSpoil,gyPre,gzSpoil)
63     end
64 end
```

8. Recommended: seq.checkTiming()

9. Optional: visualization and further checks

Structure of the tutorial

Seq01: basic Gradient Echo

Seq02: multi-echo gradient echo (monopolar readout with a fly-back rewinder)

Seq03: bipolar multi-echo gradient echo

Seq04: segmented gradient echo (variants a,b,c gradually increase in complexity; for Seq04c $n_{\text{Seg}}=n_{\text{PE}}$ is possible – initial echo-planar (EPI) implementation)

Seq05: fairly time-optimal EPI sequence

Seq06: **a step from EPI towards arbitrary trajectories, such as spirals, etc...**

All sequences are derived from each other

use text compare tool (e.g. MELD) to see point-wise changes e.g. seq01 to seq02...

Recon scripts

Recon01: fairly universal 2D FFT with automatic reordering detection
(see next slide)

Recon02: basic EPI reconstruction for ramp-sampling
contains some correction and compensation approaches

Recon03: basic 2D gridding followed by FFT

Pulseq – recon scripts

- All recon scripts are similar
- General logic
 - Expect data to be stored in a directory of choice (line 14 in this example points to data)
 - Raw data MUST always be accompanied with a Pulseq file with the identical name
 - By default load the most recent data
 - To load the second last data set replace 'end-0' with 'end-1' (line 21)
 - All data counters, data sorting and similar parameters are calculated from the Pulseq file
- 2D FFT can detect *almost* any reordering (will be used intensively)

file number
selector

data path

load raw
data

load sequence

k-space
trajectory

calculate
reordering

```
/home/zaitsev/range_software/pulseq/matlab/tutorial_MRI_Together/recon/recon01_2DFFT.m
EDITOR PUBLISH VIEW
New Open Save Find Files Compare Go To Insert Comment % fx Breakpoints Run Run and Advance Run Section Advance Run and Time
FILE NAVIGATE EDIT BREAKPOINTS RUN
11 % Load the latest file from the specified directory
12 %path='../IceNIH_RawSend/'; % directory to be scanned for data files
13 %path='/data/Dropbox/mriTogether_Pulseq_liveDemo/dataPrerecorded';
14 path='/data/Dropbox/mriTogether_Pulseq_liveDemo/dataLive';
15
16 if path(end)~=filesep, path=[path filesep]; end
17
18 pattern='*.seq';
19 D=dir([path pattern]);
20 [~,I]=sort([D(:).datenum]);
21 seq_file_path=[path D(I(end-0)).name]; % use end-1 to reconstruct the second-last data set, etc...
22                                     | % or replace I(end-0) with I(1) to process the first dataset, I(2) for the second, etc...
23 % keep basic filename without the extension
24 [p,n,e] = fileparts(seq_file_path);
25 basic_file_path=fullfile(p,n);
26
27 % Load raw data
28 % try loading Matlab data
29 data_file_path=[basic_file_path '.mat'];
30 if isfile(data_file_path)
31     fprintf(['loading ' data_file_path ' ... \n']);
32     data_unsorted = load(data_file_path);
33     if isstruct(data_unsorted)
34         fn=fieldnames(data_unsorted);
35         assert(length(fn)==1); % we only expect a single variable
36         data_unsorted=data_unsorted.(fn{1});
37     end
38 else
39     % revert to Siemens .dat file
40     data_file_path=[basic_file_path '.dat'];
41     fprintf(['loading ' data_file_path ' ... \n']);
42     twix_obj = mapVBVD(data_file_path);
43     if iscell(twix_obj)
44         data_unsorted = twix_obj{end}.image.unsorted();
45     else
46         data_unsorted = twix_obj.image.unsorted();
47     end
48     seqHash_twix=twix_obj.hdr.Dicom.tSequenceVariant;
49     if length(seqHash_twix)==32
50         fprintf(['raw data contain pulseq-file signature ' seqHash_twix ' \n']);
51     end
52 end
53 [adc_len,channels,readouts]=size(data_unsorted);
54
55 % Load sequence from file
56 fprintf(['loading ' seq_file_path ' ... \n']);
57 seq = mr.Sequence(); % Create a new sequence object
58 seq.read(seq_file_path,'detectRFuse');
59 [ktraj_adc, t_adc, ktraj, t_ktraj, t_excitation, t_refocusing] = seq.calculateKspacePP();
60 figure; plot(ktraj(1,:),ktraj(2,:), 'b',...
61             ktraj_adc(1,:),ktraj_adc(2,:), 'r'); % a 2D plot
62 axis('equal'); title('2D k-space trajectory');
63
64 % Analyze the trajectory data (ktraj_adc)
65 fprintf(['analyzing the k-space trajectory ... \n']);
66 k_extent=max(abs(ktraj_adc),[],2);
67 k_scale=max(k_extent);
68 k_threshold=k_scale/5000;
69
70 % detect unused dimensions and delete them
71 if any(k_extent<k_threshold)
72     ktraj_adc(k_extent<k_threshold,:)=[]; % delete rows
73     k_extent(k_extent<k_threshold)=[];
74 end
75
76 % detect dk, k-space reordering and repetitions (or slices, etc)
77 kt_sorted=sort(ktraj_adc,2);
78 dk_all=kt_sorted(:,2:end)-kt_sorted(:,1:(end-1));
79 dk_all(dk_all<k_threshold)=NaN;
80 dk_min=min(dk_all,[],2);
```

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Speaker name:

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Nothing to disclose

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