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Demo 01: 3D CSI Phantom data

data download and setup

add paths and set up data paths. Download phantom data (1.82 GB "phantom-DMI.tar.gz") from zenodo.org (DOI: 10.5281/zenodo.14652737).

```
% add all dependencies
addpath(genpath('/ptmp/pvalsala/Packages/mapVBVD'))
addpath(genpath('/ptmp/pvalsala/Packages/DeuteMetCon'))
addpath(genpath('/ptmp/pvalsala/Packages/OXSA'))

% data path
sn='/ptmp/pvalsala/deuterium/dataForPublication/phantom-DMI';
dirst_csi=dir(fullfile(sn,"*rpcsi_fid*.dat"));
```

load metabolite structure

The chemical shifts, measured relaxation times and labels of all four metabolites in phantom is organised in a array of struct

```
% second argument is the frequency offset of water in Hz
metabolites=getMetaboliteStruct('phantom',0);
```

Inputs and flags for metabolite mapping

All functions and data required for all data processing steps like image reconstruciton, coil combination and spectral seperation were encapsualted in a single class `MetCon_CSI.m`. All inputs and flags except the raw data file is a name-value pair as described below.

```
% | name                       | description                                                    | default   | possible options                                                    |
% |----------------------------|----------------------------------------------------------------|-----------|---------------------------------------------------------------------|
% | 'metabolites'              | struct array with definition of metabolites                    | []        | see getMetaboliteStruct.m function                                  |
% | 'fm'                       | 1H fieldmap in rad/s                                           | []        | 3D numeric matrix or 'IDEAL'                                        |
% | 'csm'                      | coil maps                                                      | []        | 3D numeric matrix                                                   |
% | 'mask'                     | mask for spectral separation                                   | []        | 3D logical matrix                                                   |
% | 'doDenosing'               | SVD denoising                                                  | 0         | scalar No of components, -1 for debug                               |
% | 'Solver'                   | spectral separation method                                     | 'IDEAL'   | {'phaseonly','pinv','IDEAL','IDEAL-modes','AMARES','LorentzFit'}    |
% |                            |                                                                |           | 'phaseonly'- linear method with only phase evolution                |
% |                            |                                                                |           | 'pinv'- linear method with full signal model                        |
% |                            |                                                                |           | 'IDEAL'- iterative IDEAL algorithm                                  |
% |                            |                                                                |           | 'IDEAL-modes'-IDEAL algorithm for phase cycled data                 |
% |                            |                                                                |           | 'AMARES'- AMARES spectral fitting                                   |
% |                            |                                                                |           | 'LorentzFit'- lorentzian spectral fitting                           |
% | 'parfor'                   | flag to use parfor                                             | true      | boolean                                                             |
% | 'doZeroPad'                | zero pad factor                                                | [1 1 1 0] | positive scalar array [3 physical axis x 1 time]                    |
% | 'doSmoothFM','maxit'       | IDEAL flags: fieldmap smooth factor and maximum iterations     | 1,10      | scalar(+ve: gaussian, -ve: median),postive scalar                   |
% | 'doPhaseCorr'              | phase correction mode                                          | 'none'    | {'none','Manual','Burg'}                                            |
% | 'CoilSel','PCSel','EchoSel'| arrays to picks some of coils, time points and phasecyles.     | 1:max()   | positive integer array                                              |
% |'doNoiseDecorr'             | flag to perform noise decorrelation                            | true      | boolean                                                             |
% | 'doCoilCombine'            | coil combine mode                                              | 'adapt1'  | {'none','sos','adapt1','wsvd'}                                      |
```

```
CSI_setting={'metabolites',metabolites,'doPhaseCorr','none','parfor',true,...
    'doCoilCombine','adapt1','doZeropad',[0.5 0.5 0.5 0],'mask',[],'Solver','IDEAL','fm',[]};
```

Process data

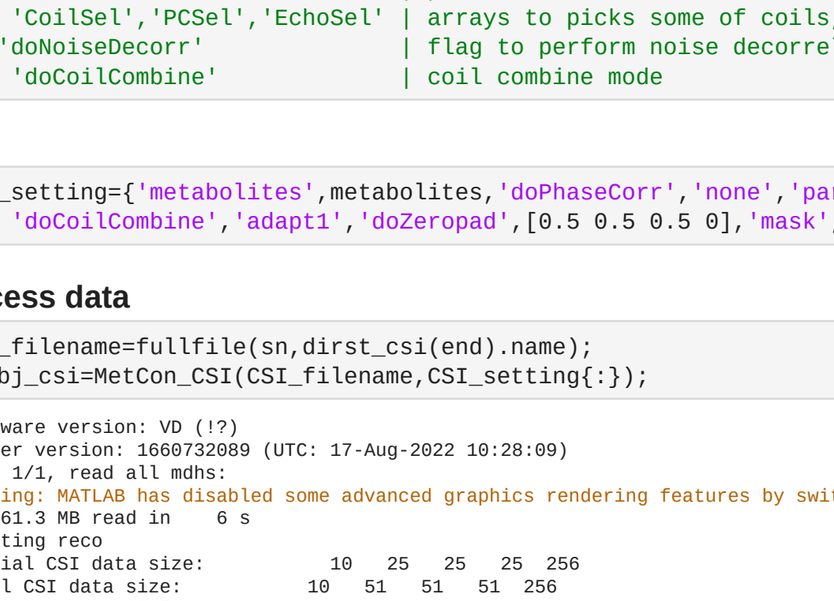
```
CSI_filename=fullfile(sn,dirst_csi(end).name);
mcobj_csi=MetCon_CSI(CSI_filename,CSI_setting{:});
```

```
Software version: VD (!?)
Reader version: 1660732089 (UTC: 17-Aug-2022 10:28:09)
Scan 1/1, read all mdhs:
Warning: MATLAB has disabled some advanced graphics rendering features by switching to software OpenGL. For more information, click here.
   661.3 MB read in    6 s
starting reco
initial CSI data size:          10   25   25   25  256
final CSI data size:          10   51   51   51  256
reco  time =   18.5 s
estimating field map(1/2)
estimating metabolities(2/2)
Metabolite mapping time =   27.6 s
```

Plotting

After image reconstruciton and spectral seperation, metbolite amplitudes are store in mcobj_csi.Metcon. The 4D Metcon matrix and 2H field map estimated by IDEAL algorithm can be quickly visualized with `PlotResults` method.

```
mcobj_csi.PlotResults()
```



Data structure of Metcon_CSI object

1x1 MetCon_CSI

Property	Value
time	*[ ]*
FieldMap	*[ ]*
mask	*51x51x51 logical*
twix	*1x1 struct*
DMIPara	*1x1 struct*
flags	*1x1 struct*
filename	'/ptmp/pvalsala/deuterium/dataForPublication/phantom/MID01423...
metabolites	*1x4 struct*
sig	*5-D complex single*
img	*5-D complex single*
coilSens	*4-D complex single*
coilNormMat	*51x51x51 single*
SolverObj	*1x1 IDEAL*
Metcon	*4-D complex double*
Experimental	*1x1 struct*
D	*10x10 complex single*

Where

- DMIPara are the important sequence parameters parsed from twix with `getDMIPara.m` fucntion
- flags contains all the processing flags
- sig - averaged signal [CHAx LIN xSEG x PAR x COL (time) x REP(PhaseCylces)]
- img - reconstructed image [CHA x 3 physical dimension x time]
- Metcon - Metabolite amplitudes [CHA x 3 physical dimension x time]
- Experimental- contains all experimental outputs of processing (fieldmap, residue, other fit parameters, fit quality)
- D- noise decorrelation matrix.

Processing CSI-bSSFP data

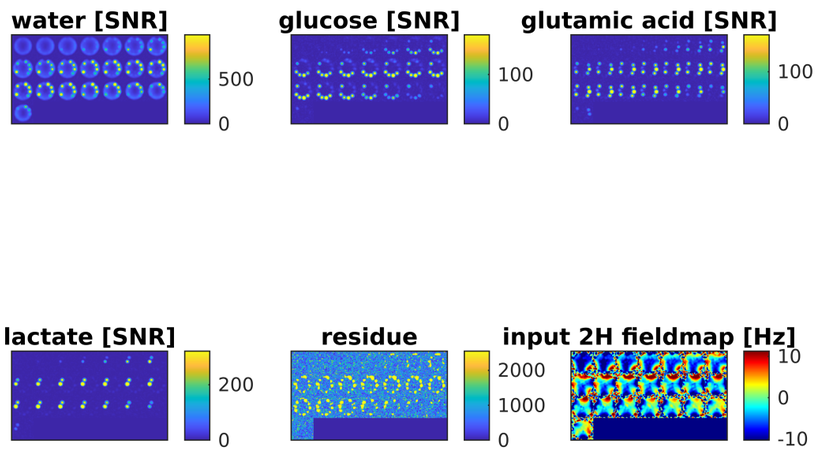
We use `IDEAL-modes` for phase-cycled data for SNR optimallity. Other Solver flags use averaged phase-cyles volumes

```
CSI_setting_ssfp={'metabolites',metabolites,'doPhaseCorr','none','parfor',true,...
     'doCoilCombine','adapt1','doZeropad',[0.5 0.5 0.5 0],'mask',[],'Solver','IDEAL-modes','fm','IDEAL'};
dirst_csi_ssfp=dir(fullfile(sn,"*rpcsi_ssfp*.dat"));
CSI_filename=fullfile(sn,dirst_csi_ssfp(end).name);
mcobj_ssfp=MetCon_CSI(CSI_filename,CSI_setting_ssfp{:});
```

```
Software version: VD (!?)
Reader version: 1660732089 (UTC: 17-Aug-2022 10:28:09)
Scan 1/1, read all mdhs:
   335.9 MB read in    6 s
starting reco
initial CSI data size:          10  25  25  25  64   4
final CSI data size:          10  51  51  51  64   4
reco  time =   17.0 s
estimating field map(1/2)
estimating metabolities(2/2)
Metabolite mapping time =   24.4 s
```

```
mcobj_ssfp.PlotResults()
```

M1425|TR 19 ms| 48 deg | 8.32 mm | 4 rep | 64 echoes|IDEAL-mo



Other miscallaneous methods which can be useful

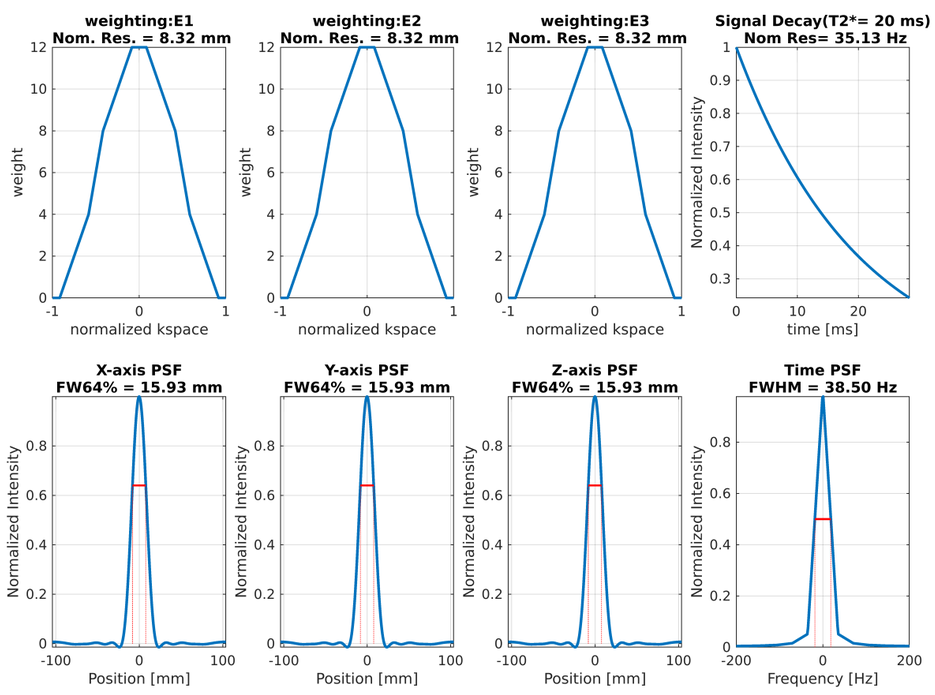
```
% The metabolite amplitudes can be normalized into SNR
metcon_SNR= mcobj_csi.getNormalized();

% method and quantified into mM with 10 mM water reference using `getmM`
% fucntion. (Doesn't work in phantom as 10mM water reference is not there!)
metcon_mM= mcobj_csi.getmM();

% export NIFTI volumes of all outputs (average image, metabolite amplitude in SNR unit and mM)
pn=fullfile(sn,'proc',sprintf('CSI_%s',datetime('today','Format','yyyyMMMdd')));
mkdir(pn);cd(pn);
niiFileName=mcobj_csi.WriteImages(pn);

% it is non-sense for phantom scans but still!
Intake_time_mins=mcobj_csi.getMinutesAfterIntake('08:00');

%plot the k-space weighting and PSF to get realistic voxel size (FW64%)
voxel_size_mm= getPSF_CSI(mcobj_csi.twix,true);
```



Debug (only for AMARES and Lorentzian solver so far)

Useful for checking data at a particular voxel index. [15,14,25] is the voxel with all metabolites.

```
mcobj_csi.demoFit([15,14,25])
```

```
Iterations = 36.
Norm of residual = 770.811
Norm of the data = 62474.292
resNormSq / dataNormSq = 0.012
zeroOrderPhaseRad = 2.222
```



```
chemShift: [0.0474 -1.0161 -2.4680 -3.4884]
linewidth: [2.0000 11.2813 4.7048 2.2230]
amplitude: [34.5440 11.3873 8.7223 14.5698]
```

```
phase: [127.3026 127.3026 127.3026 127.3026]
sigma: [0 0 0 0]
```