

Table of Contents	
FISP CSI dataset with acquision weighting.....	1
Plot FISP noise characteristics.....	1
CSI-bSSFP dataset with acquision weighting.....	1
Plot CSI-bSSFP noise characteristics.....	1
multiecho-bSSFP dataset with acquision weighting.....	2
assemble inputs and processing flags.....	2
Plot ME-bSSFP noise characteristics.....	2

Demo 05: noise test

A demo script to check the noise statistics. Not all spectral separation modes and processing steps gives a proper SNR metric. This script is to verify the standard normal distribution of data, image and metabolite amplitudes after every processing step. Download noise data (800 MB "phantom-DMI-noise.tar.gz") from [zenodo.org](https://zenodo.org/record/14652737) (DOI: 10.5281/zenodo.14652737) to follow this excercise.

FISP CSI dataset with acquision weighting

```
% 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-Noise';

fn=fullfile(sn,'meas_MID00750_FID11717_rpcsi_fid_Stan_res15_6_TR36_5min_0FA.dat');
metabolites=getMetaboliteStruct('phantom',0);
CSI_setting={'metabolites',metabolites,'parfor',true,...
    'doCoilCombine','adapt1','doZeropad',[0.5 0.5 0.5 0]*0,'mask',[],'Solver','IDEAL'};
mcobj_fisp=MetCon_CSI(fn,CSI_setting{:});
```

Software version: VD (!?)
Reader version: 1660732089 (UTC: 17-Aug-2022 10:28:09)
Scan 1/1, read all mdhs:
 324.1 MB read in 7 s
starting reco
initial CSI data size: 10 25 25 25 256
final CSI data size: 10 25 25 25 256
reco time = 4.3 s
estimating field map(1/2)
estimating metabolities(2/2)
Metabolite mapping time = 5.8 s

Plot FISP noise characteristics

verify noise is uniformly distributed

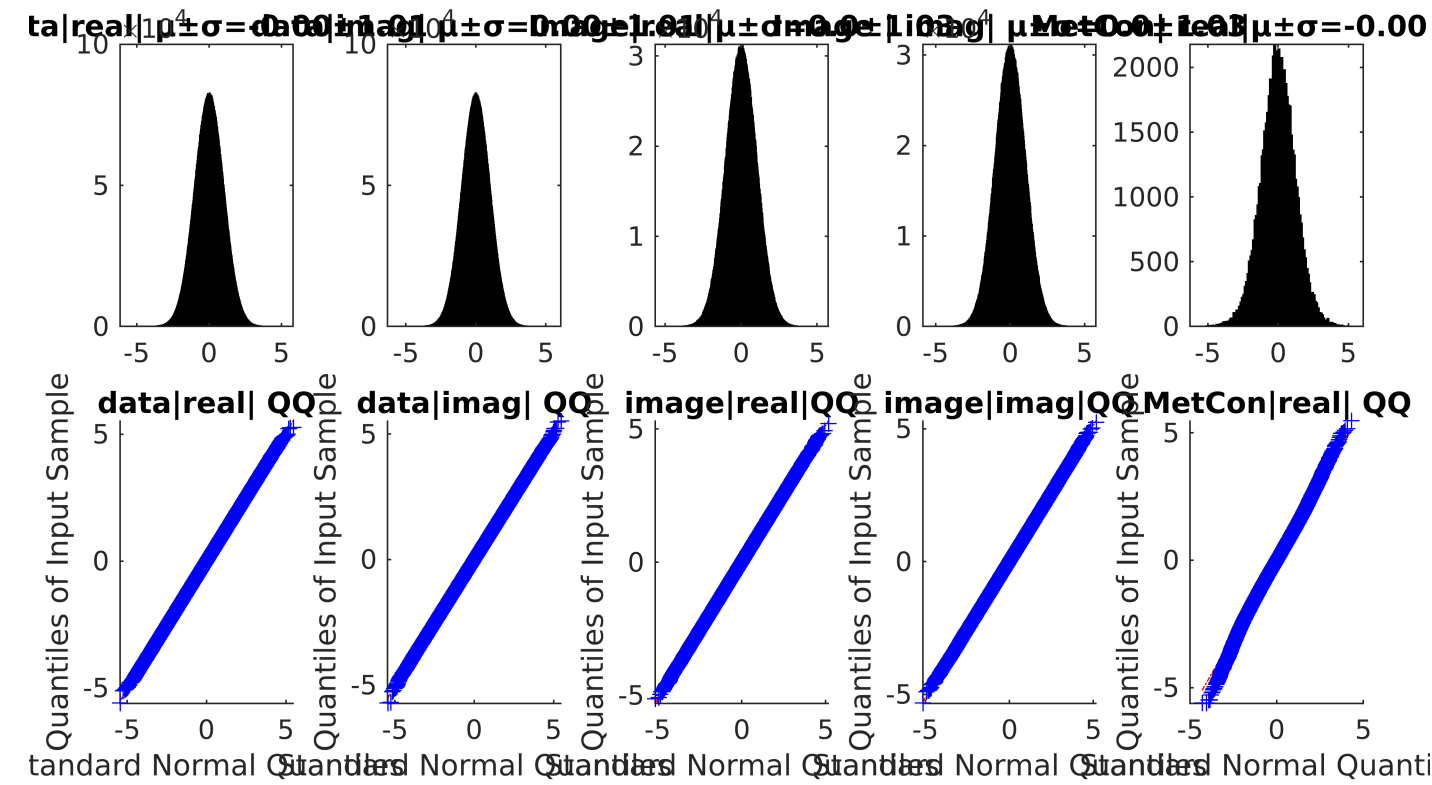
```
figure,
set(gcf,'Position',[0,0,1400,800])
tiledlayout(2,5,'TileSpacing','compact','Padding','compact')

%raw data
sig=permute(mcobj_fisp.twix.image{''},[2 1 3:8]);
sig=mcobj_fisp.D*sig(:,:); % noise decorrelation
sig=sig(:,abs(sum(sig,1))>0);%take all samples without zeropadding

nexttile(1),histogram(real(sig(:))),title(sprintf('data|real| \mu\pm%.2f\pm%.2f',mean(real(sig(:))),std(real(sig(:)))));
nexttile(1+5),qqplot(real(sig(:))),title('data|real| QQ');
nexttile(2),histogram(imag(sig(:))),title(sprintf('data|imag| \mu\pm%.2f\pm%.2f',mean(imag(sig(:))),std(imag(sig(:)))));
nexttile(2+5),qqplot(imag(sig(:))),title('data|imag| QQ');

% reconstructed images
nexttile(3),histogram(real(mcobj_fisp.img(:))),title(sprintf('Image|real|\mu\pm%.1f\pm%.2f',mean(real(mcobj_fisp.img(:))),std(real(mcobj_fisp.img(:)))));
nexttile(3+5),qqplot(real(mcobj_fisp.img(:))),title('image|real|QQ');
nexttile(4),histogram(imag(mcobj_fisp.img(:))),title(sprintf('Image | imag| \mu\pm%.1f\pm%.2f',mean(real(mcobj_fisp.img(:))),std(real(mcobj_fisp.img(:)))));
nexttile(4+5),qqplot(imag(mcobj_fisp.img(:))),title('image|imag|QQ')

%Metabolite maps
[~,scl_fac]=mcobj_fisp.getNormalized();
% scl_fac is the eucledian norm of complex weights used during spectral
% seperation is used for normalization to SNR units.
Metcon_SNR=real(reshape(mcobj_fisp.Metcon,[],4)./scl_fac)/sqrt(2);
nexttile(5),histogram(Metcon_SNR(:)),title(sprintf('MetCon| real|\mu\pm%.2f\pm%.2f',mean(Metcon_SNR(:)),std(Metcon_SNR(:)))));
nexttile(5+5),qqplot(Metcon_SNR(:)),title('MetCon|real| QQ');
```



CSI-bSSFP dataset with acquision weighting

```
%data path
sn='/ptmp/pvalsala/deuterium/dataForPublication/phantom-DMI-Noise';

fn=fullfile(sn,'meas_MID00749_FID11716_rpcsi_ssfp_Stan25_15_6mm_5mins_0FA.dat');
metabolites=getMetaboliteStruct('phantom',0);
CSI_setting={'metabolites',metabolites,'parfor',true,...
    'doCoilCombine','adapt1','doZeropad',[0.5 0.5 0.5 0]*0,'mask',[],'Solver','IDEAL-modes'};
mcobj_ssfp=MetCon_CSI(fn,CSI_setting{:});
```

Software version: VD (!?)
Reader version: 1660732089 (UTC: 17-Aug-2022 10:28:09)
Scan 1/1, read all mdhs:
 163.8 MB read in 7 s
starting reco
initial CSI data size: 10 25 25 25 64 4
final CSI data size: 10 25 25 25 64 4
reco time = 3.1 s
estimating field map(1/2)
estimating metabolities(2/2)
Metabolite mapping time = 4.8 s

Plot CSI-bSSFP noise characteristics

verify noise is uniformly distributed

```
figure,
set(gcf,'Position',[0,0,1400,800])
tiledlayout(2,5,'TileSpacing','compact','Padding','compact')

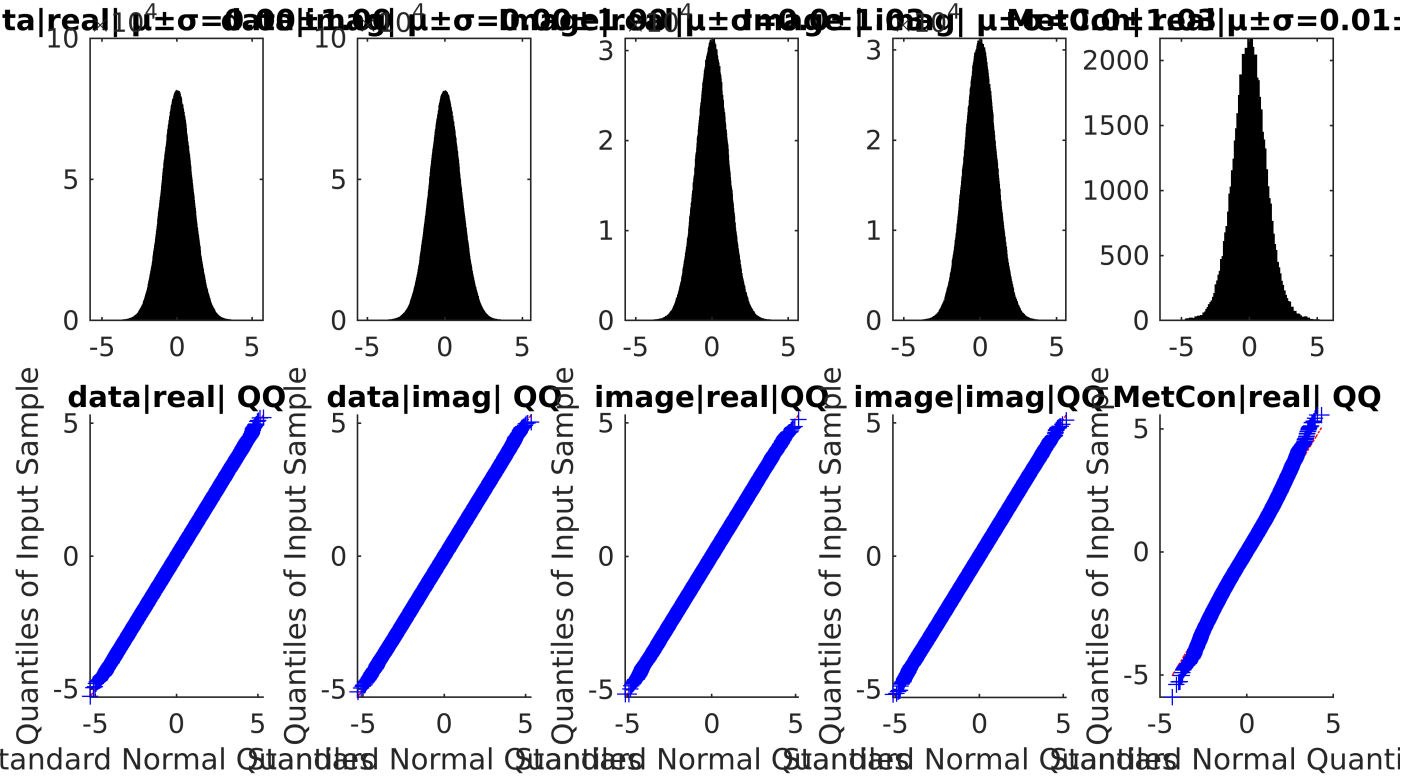
%raw data
sig=permute(mcobj_ssfp.twix.image{''},[2 1 3:8]);
sig=mcobj_ssfp.D*sig(:,:); % noise decorrelation
sig=sig(:,abs(sum(sig,1))>0);%take all samples without zeropadding

nexttile(1),histogram(real(sig(:))),title(sprintf('data|real| \mu\pm%.2f\pm%.2f',mean(real(sig(:))),std(real(sig(:)))));
nexttile(1+5),qqplot(real(sig(:))),title('data|real| QQ');
nexttile(2),histogram(imag(sig(:))),title(sprintf('data|imag| \mu\pm%.2f\pm%.2f',mean(imag(sig(:))),std(imag(sig(:)))));
nexttile(2+5),qqplot(imag(sig(:))),title('data|imag| QQ');

% reconstructed images
nexttile(3),histogram(real(mcobj_ssfp.img(:))),title(sprintf('Image|real|\mu\pm%.1f\pm%.2f',mean(real(mcobj_ssfp.img(:))),std(real(mcobj_ssfp.img(:)))));
nexttile(3+5),qqplot(real(mcobj_ssfp.img(:))),title('image|real|QQ');
nexttile(4),histogram(imag(mcobj_ssfp.img(:))),title(sprintf('Image | imag| \mu\pm%.1f\pm%.2f',mean(real(mcobj_ssfp.img(:))),std(real(mcobj_ssfp.img(:)))));
nexttile(4+5),qqplot(imag(mcobj_ssfp.img(:))),title('image|imag|QQ');
```

```
nexttile(4+5),qqplot(imag(mcobj_ssfp.img(:)),title('image|imag|QQ'))

%Metabolite maps
[~,scl_fac]=mcobj_ssfp.getNormalized();
% scl_fac is the eucledian norm of complex weights used during spectral
% seperation is used for normalization to SNR units.
Metcon_SNR=real(reshape(mcobj_ssfp.Metcon,[],4)./scl_fac)/sqrt(2);
nexttile(5),histogram(Metcon_SNR(:)),title(sprintf('MetCon| real|μ±σ=% .2f±%.2f',mean(Metcon_SNR(:)),std(Metcon_SNR(:))));
nexttile(5+5),qqplot(Metcon_SNR(:)),title('MetCon|real| QQ');
```



multiecho-bSSFP dataset with acquisition weighting

```
%data path
sn='/ptmp/pvalsala/deuterium/dataForPublication/phantom-DMI-Noise';
% trufi sequence acquire noise data only when parallel imaging is enabled. Therefore, we acquire noise scan with 0 flip angle seperately.
twix_noise=mapVBVD(fullfile(sn,'meas_MID00735_FID11702_pvrh_trufi_5E_noise_12P5mm.dat'),'rmos');
```

Software version: VD (!?)
Reader version: 1660732089 (UTC: 17-Aug-2022 10:28:09)
Scan 1/1, read all mdhs:
40.4 MB read in 6 s

```
[D_noise,D_image,noise_info]=CalcNoiseDecorrMat(twix_noise);
%D_image is the noise correlation from image data measured with 0 FA
```

assemble inputs and processing flags

```
ME_setting={ 'NoiseDecorr',D_image,'mask',[],'metabolites',metabolites,...
             'doPhaseCorr',true,'doZeropad',[1 1 1]*0.5,'parfor',true,'fm','IDEAL','Solver','IDEAL-modes'};
fn=fullfile(sn,'meas_MID00752_FID11719_pvrh_trufi_5E_18PC_12P5mm_FA50_s4_r180_0FA.dat');
metabolites=getMetaboliteStruct('phantom',0);
mcobj_me=MetCon_ME(fn,ME_setting{:});
```

Software version: VD (!?)
Reader version: 1660732089 (UTC: 17-Aug-2022 10:28:09)
Scan 1/1, read all mdhs:
428.6 MB read in 7 s
Warning: applied Phase cycle correction for data before 20.Sep.24
starting reco
reco time = 17.9 s
estimating field map(1/2)
estimating metabolities(2/2)
Performed pixel shift along read: (0.0,-2.2,-5.2 ,-7.2) mm
Metabolite mapping time = 24.4 s

Plot ME-bSSFP noise characteristics

verify whether noise is uniformly distributed. The zeros added by the translation to compensate chemical shifts along read is visible in the metcon histogram

```
figure,
set(gcf,'Position',[0,0,1400,800])
tiledlayout(2,5,'TileSpacing','compact','Padding','compact')

%raw data
sig=permute(mcobj_ssfp.twix.image{''},[2 1 3:8]);
sig=mcobj_ssfp.D*sig(:,:); % noise decorrelation
sig=sig(:,abs(sum(sig,1))>0);%take all samples without zeropadding

nexttile(1),histogram(real(sig(:))),title(sprintf('data|real| μ±σ=% .2f±%.2f',mean(real(sig(:))),std(real(sig(:)))));
nexttile(1+5),qqplot(real(sig(:))),title('data|real| QQ');
nexttile(2),histogram(imag(sig(:))),title(sprintf('data|imag| μ±σ=% .2f±%.2f',mean(imag(sig(:))),std(imag(sig(:)))));
nexttile(2+5),qqplot(imag(sig(:))),title('data|imag| QQ');

% reconstructed images
nexttile(3),histogram(real(mcobj_ssfp.img(:))),title(sprintf('Image|real|μ±σ=% .1f±%.2f',mean(real(mcobj_ssfp.img(:))),std(real(mcobj_ssfp.img(:)))));
nexttile(3+5),qqplot(real(mcobj_ssfp.img(:))),title('image|real|QQ');
nexttile(4),histogram(imag(mcobj_ssfp.img(:))),title(sprintf('Image | imag| μ±σ=% .1f±%.2f',mean(real(mcobj_ssfp.img(:))),std(real(mcobj_ssfp.img(:)))));
nexttile(4+5),qqplot(imag(mcobj_ssfp.img(:))),title('image|imag|QQ')

%Metabolite maps
[~,scl_fac]=mcobj_ssfp.getNormalized();
% scl_fac is the eucledian norm of complex weights used during spectral
% seperation is used for normalization to SNR units.
Metcon_SNR=real(reshape(mcobj_ssfp.Metcon,[],4)./scl_fac)/sqrt(2);
nexttile(5),histogram(Metcon_SNR(:)),title(sprintf('MetCon| real|μ±σ=% .2f±%.2f',mean(Metcon_SNR(:)),std(Metcon_SNR(:))));
nexttile(5+5),qqplot(Metcon_SNR(:)),title('MetCon|real| QQ');
```

