Chemical Exchange Saturation Transfer Imaging

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4144273/

```
% MT list (set these based on experimental parameters chosen)
%MT is the magnetization transfer
mt power = ;
mt duration = ;
series list = ; %logarithmic frequencies
f ppm = ;
%% Read DICOM Directory
% Read frequency offset file
%% Analyze MT data
%Create intensity mask
threshold = 0.1;
mask = img(:,:,1,1,1);
mask = mask / max(abs(mask(:))) > threshold;
ix norm = ;
ix MT = ; %index
fid = fopen(filename, 'r');
C = textscan(fid, '%s', 1);
description = C{1};
C = textscan(fid, '%d', 1);
N = C\{1\};
C = textscan(fid, '%f', N);
offsets = cell2mat(C);
fclose(fid):
offsets MT = offsets(ix MT);
offsets_interp = 10.^[];
% Shift MT data by b0 map
[nx,ny,nz,nt,nr] = size(img);
img reshape = reshape(img, [nx*ny nt nr]);
img norm = mean(img reshape(:,ix norm,:),2);
img reshape = img reshape(:,ix_MT,:);
img reshape = bsxfun(@times, img reshape, 1./img norm);
nt interp = numel(offsets interp);
img b0 corrected = zeros(nx*ny,nt interp,nr);
for ix = 1:nx*ny
  if mask(ix)
    tmp = squeeze(img reshape(ix,:,:))
     tmp = interp1(offsets MT, tmp, offsets interp, 'pchip')
     img b0 corrected(ix,:,:) = tmp;
  end
```

```
end
img b0 corrected = reshape(img b0 corrected, [nx,ny,nt interp,nr]);
%% draw rois
if ~exist('masks.mat', 'file')
  figure();
  labels = {'phantom1', 'phantom2', 'phantom3, 'phantom4', 'phantom5'};
  r = draw rois(img b0 corrected(:,:,1,1), numel(labels), labels);
  for ix = 1:size(r, 3)
     r(:,:,ix) = and(r(:,:,ix), mask);
  end
  save masks mask r
end
load masks.mat
[nx,ny,nt_interp,nr] = size(img_b0_corrected);
img reshape = reshape(img b0 corrected, [nx*ny nt interp nr]);
n_{rois} = size(r,3);
signal = zeros(n rois, nt interp, nr);
for ix = 1:n rois
  signal(ix,:,:) = mean(img reshape(r(:,:,ix),:,:),1);
end
close all
```