Codes location:

* [\\129.128.117.89\hongfu\Documents\MATLAB\qsm\_testing](file:///\\129.128.117.89\hongfu\Documents\MATLAB\qsm_testing)

This is a testing repository, the codes will get frequent bug fixes and updates, after tested the changes will be merged into the stable branch below:

* [\\129.128.117.89\hongfu\Documents\MATLAB\qsm\_stable](file:///\\129.128.117.89\hongfu\Documents\MATLAB\qsm_stable)

Directory structure:

* 15 -- recon codes for 1.5T sequences, e.g. EPI (fMRI) and SWI
  + qsm\_epi15.m
  + qsm\_swi15.m
* 47 -- recon codes for 4.7T sequences, e.g. EPI (fMRI), SWI and R2\*
  + qsm\_epi47.m
  + qsm\_swi47.m
  + qsm\_r2s47.m
* PRISMA -- recon codes for 3T PRISMA sequences, e.g. EPI (fMRI), SWI and R2\*
  + qsm\_epi\_prisma.m
  + qsm\_swi\_prisma.m
  + qsm\_r2s\_prisma.m
* arr\_cmb -- coils combination related codes
  + adaptive\_cmb.m -- adaptive filter method for single-echo, e.g. EPI, SWI
  + geme\_cmb.m -- dual echo approach for multi-echo, e.g. R2\*
* bkg\_rm -- background field removal, including RESHARP/SHARP/ESHARP/PDF/LBV
  + sharp.m -- SHARP
  + resharp.m -- RESHARP
  + projectionontodipolefields.m -- PDF
  + extendharmonicfield.m -- ESHARP
  + LBV.m -- LBV
  + poly2d.m -- 2nd order 2D polynomial fit
  + poly3d.m -- 2nd order 3D polynomial fit
* dip\_inv -- dipole inversion with TV regularization
  + tvdi.m -- total variation dipole inversion
* Misc -- other functions including NIFTI and Ryan's small functions

Usage:

* Call the main QSM function corresponding to the sequence, e.g. "qsm\_r2s47" is the function for QSM recon of R2\* at 4.7T.
* Function inputs are
  + Directory of the raw data for 1.5T/4.7T or directories of both magnitude and unfiltered phase DICOMs for PRISMA 3T)
  + User defined directory for QSM output results
  + User specified parameters "options"
* Examples:

options.bkg\_rm='resharp';

options.ph\_unwrap='laplacian'

qsm\_swi47('FID\_DIR','OUTPUT\_DIR',options);

* For other advanced usage, see help, e.g. "help qsm\_swi\_prisma"

* Some of the commonly user-changed options:
  + bet\_thr -- threshold level for BET extracting the brain mask, by default is 0.3-0.5 depending on the sequence, smaller threshold keeps more region of the brain
  + ph\_unwrap -- phase unwrapping methods, can be 'prelude', 'laplacian' or 'bestpath'
  + bkg\_rm -- background field removal methods, can be 'sharp', 'pdf','resharp','esharp' or 'lbv', can pick multiple methods to compare, e.g. options.bkg\_rm={'resharp','lbv'}
  + smv\_rad -- radius in mm of SHARP/RESHARP/ESHARP kernel (erosion size, ESHARP recovers some)
  + tik\_reg -- tikhonov regularization for RESHARP, by default 1e-3, bigger value more regularization
  + tv\_reg -- total variation regularization, by default 5e-4, bigger value gives smoother result
  + For more options, seek "help" of the specific function

Recon flow:

Extract complex img --> combine coils --> extract brain mask --> unwrap phase maps --> linearly fit unwrapped phase with TE if multiple echo --> background field removal --> dipole inversion