**PROTOCOL: Processing R2\* maps**

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(Updated by: Corinne McGill; 08/06/18, 12/07/18)

**I. SAMPLE DATA INFO**

Path: (\\helperndatafs-v.mdc.musc.edu)\helpern\_share\Protocols\Sample\_Datasets\R2\_Star\_Dataset\_n18.zip

**II. SEQUENCE INFO**

Sequence name (3T Tim Trio): T2\_STAR

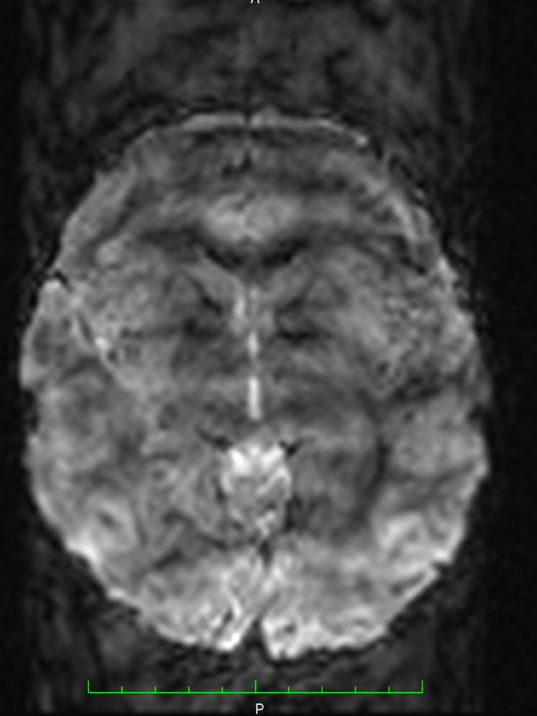
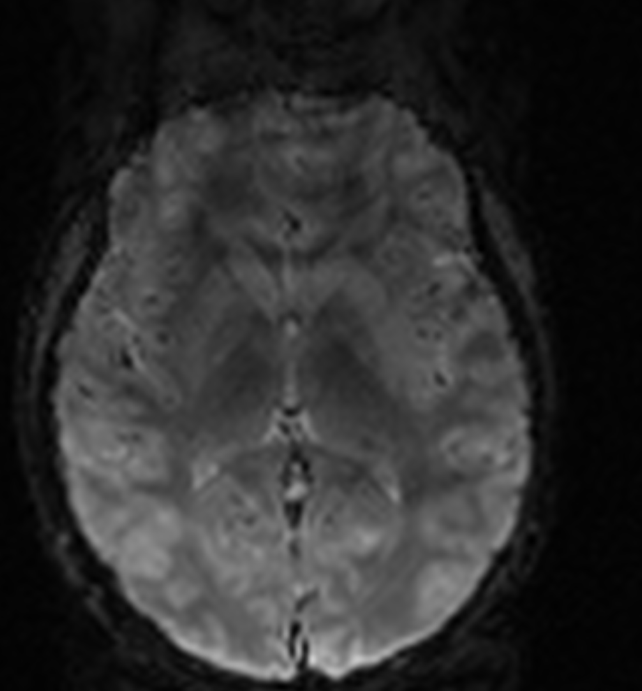
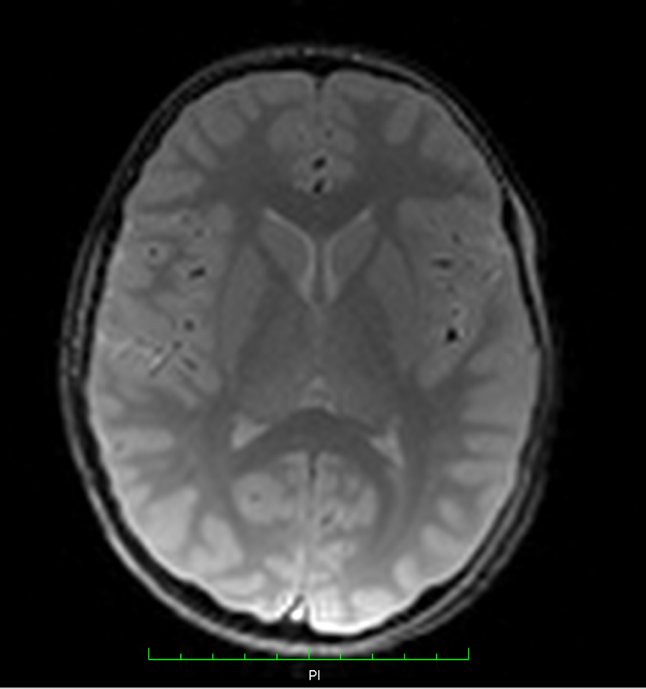
MRI protocol path: (\\helperndatafs-v.mdc.musc.edu)\users\adisetiyo\_v\Projects\KTGF\_Project\Protocols\

KTGF\_MRI\_Protocol\_rfMRI\_PE.pdf

**III. QC Guidelines**

Most applicable in high iron regions, so focus on those. (i.e. basal ganglia)

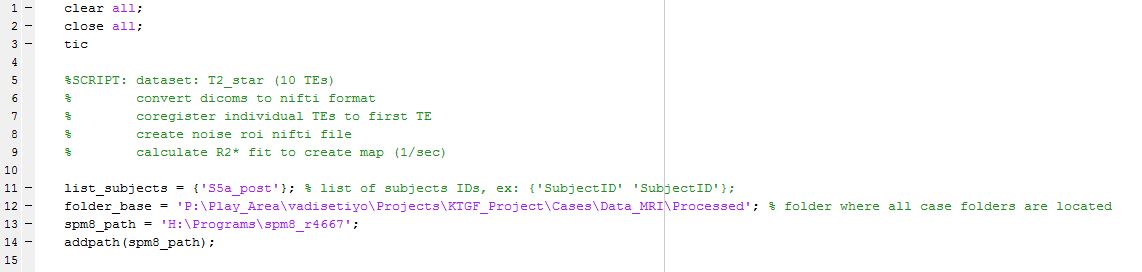
**BAD – DO NOT USE USABLE GOOD - USE**

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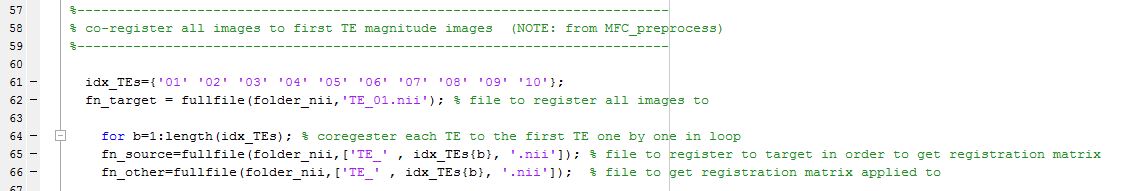
**III. SCRIPT INFO**

Master script path: (\\helperndatafs-v.mdc.musc.edu)\helpern\_data\Protocols\BatchScript\_Templates

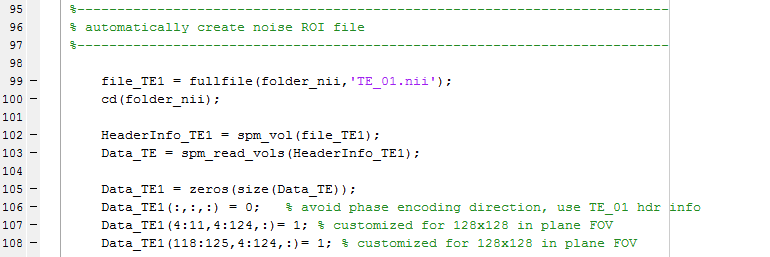
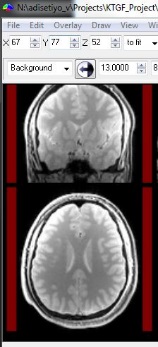
* R2star\_nonlinear.m (batch script with functions; NOTE: ensure TE’s in script match sequence protocol)
* Copy template into owns study folder & customize following variables in script:
  + list\_subjects
  + paths: folder\_base, spm8\_path



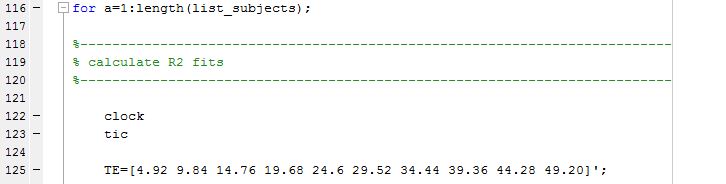
* + indx\_TEs (specify number of TEs used in T2\* protocol)



* + Data\_TE1 (customize X & Y indices for inplane FOV of T2\* protocol; confirm not overlap w/brain)

* + TE (specify TE values used in T2\* protocol)



Processing requires:

* MATLAB R2009b (Curve\_Fitting\_Toolbox21 needed to calc map; registration can run on any version: 2015a, 2009b)
* SPM8

**IV. PROCESSING INFO**

Input structure:

* Case\_ID\dicom\T2\_star\
  + TE\_all (820 dicoms from all 10 TEs in this folder; no subfolders)

Output structure:

* Case\_ID\T2\_star\
  + SPM\_nifti
  + R2star\_map\_nlin (maps in this folder; R2star map: by\_voxel\_R2s.nii)

Processing time/case:

* ~4 hours (on my desktop, Matlab R2009b, helpern\_data\Programs\spm8\_r4667)