fMRI Preprocessing Overview

Neal Morton

Preprocessing Pipelines

- setup_subject.py
    - Developed by Russ Poldrack
    - Runs basic BOLD preprocessing and QA, runs FreeSurfer
- FEAT
    - BOLD preprocessing, filtering and smoothing, registration to anatomical and standard space
- FAT
    - Includes elements of setup_subject.py and FEAT (some scripts are based on FEAT source code)
    - Bias field correction used before any registration
    - Most registration uses ANTS instead of FSL tools like flirt
    - Nonlinear registration used in some cases to deal with distortion

Preprocessing Pipelines

- Wiki page: https://github.com/prestonlab/fat/wiki/fMRI-Preprocessing

- Anyone with write access to the FAT project can edit (full history is saved, so can always revert if needed)

- Basic formatting is easy (use toolbar, or write text in Markdown format)

FAT Pipeline

- The FAT pipeline is available on GitHub
    - Setup GitHub (see FAT page for details)
    - Run: git clone git@github.com:prestonlab/fat.git
    - Anyone can test the code and report or fix bugs, or add features they need, and push those changes to GitHub
    - FAT is for general analysis scripts only (e.g. there should be no hard-coded paths to data like /corral-repl/utexas/prestonlab/bender)
    - Can make a separate project to manage code for individual experiments

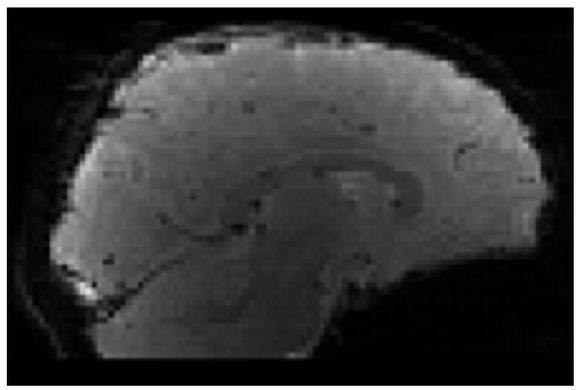
Steps

- Preparing image files
- Basic BOLD preprocessing and quality assurance
- Basic anatomical preprocessing
- FreeSurfer
- EPI unwarping
- EPI co-registration
- Smoothing and filtering

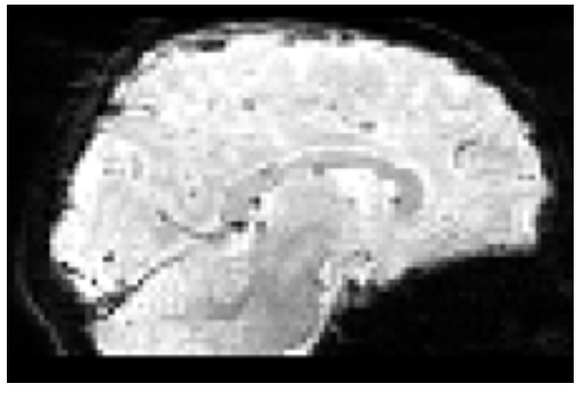
Preparing Image Files

- Put DICOM files on TACC (WORK directory is usually best)
- Run DICOM to NIfTI conversion using dcm2nii
- Rename files to have desired functional run names
- See wiki for standard directory structure

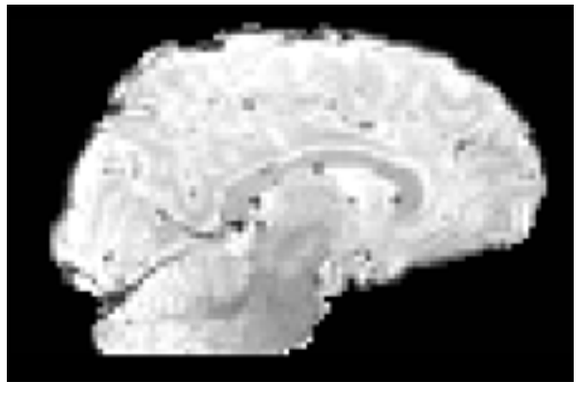
Basic BOLD Preprocessing



Raw

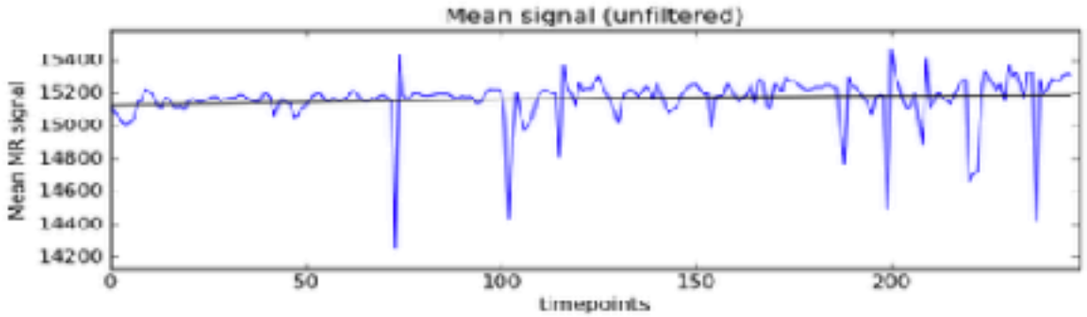


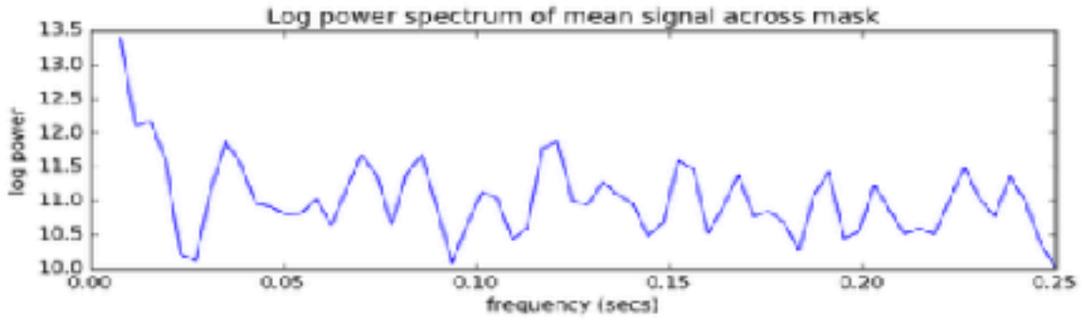
Bias field corrected

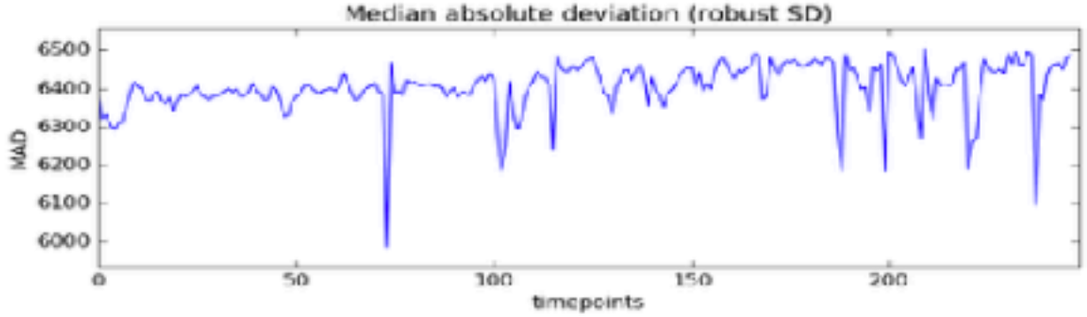


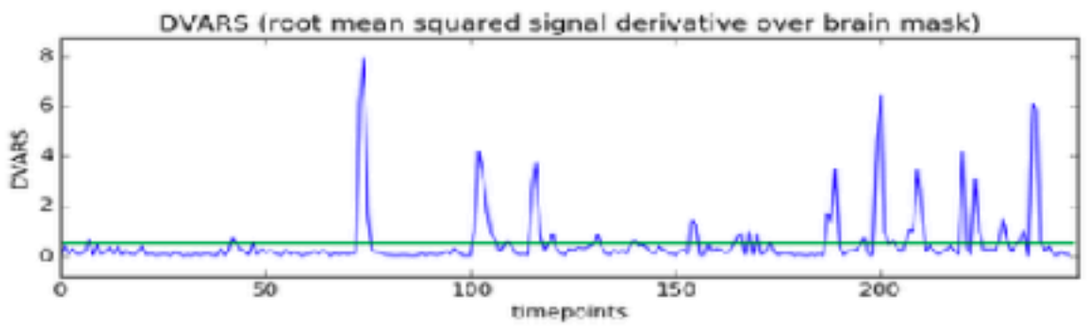
Brain extracted (for QA; more precise mask used for later steps)

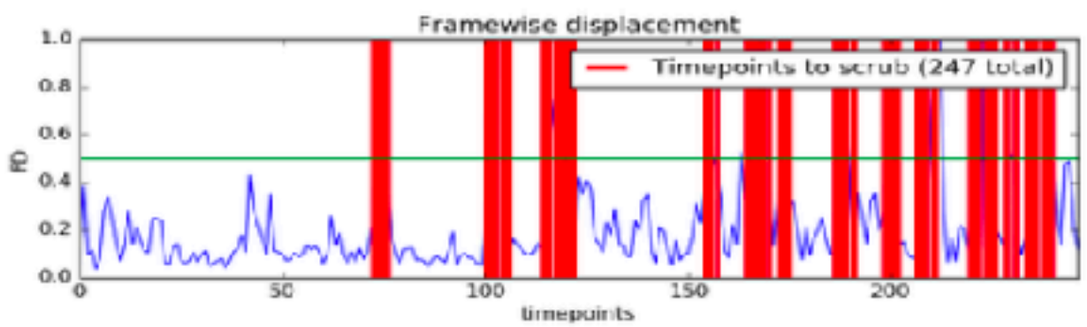
QA Report: November 16, 2017: 16:09:04
infile: /work/03206/mortonne/lonestar/moshigo/moshigo_204/3OLD/task_1/bold_mcf.nii.gz
Mean SNR: 11.556758
Mean SFNR (in brain mask): 31.721397
Drift term: 0.415887 (p=0.403489)
potential spikes: 0
timepoints exceeding FD threshold: 73

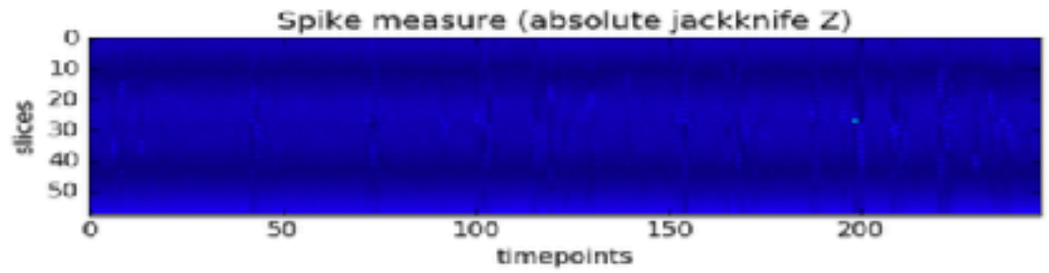


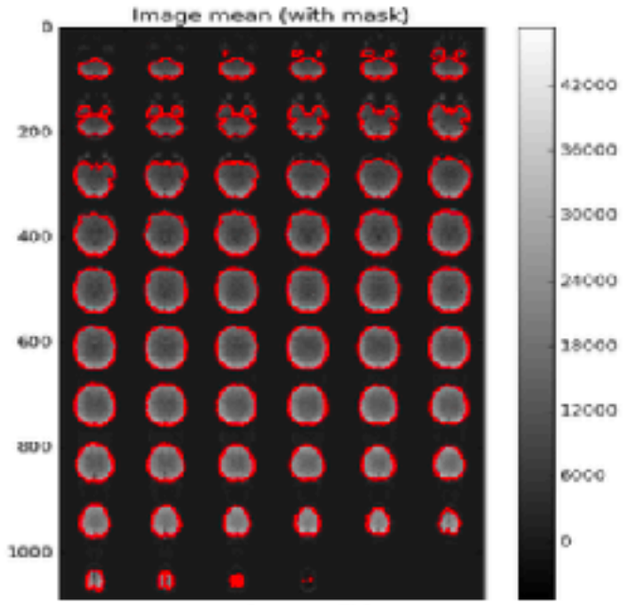


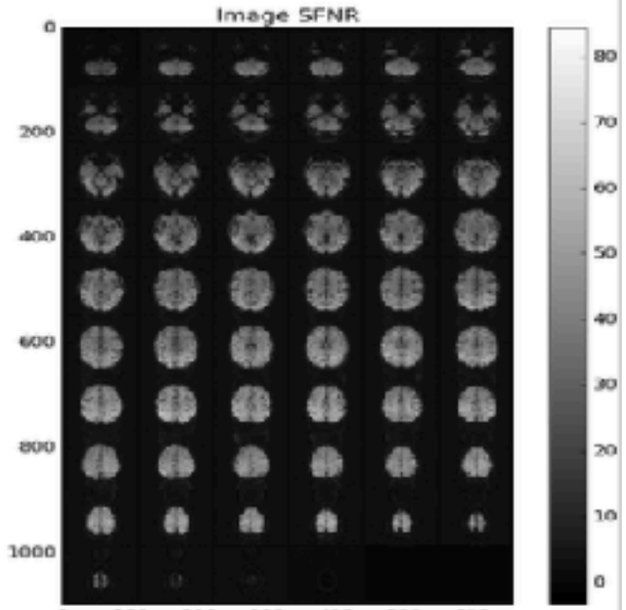


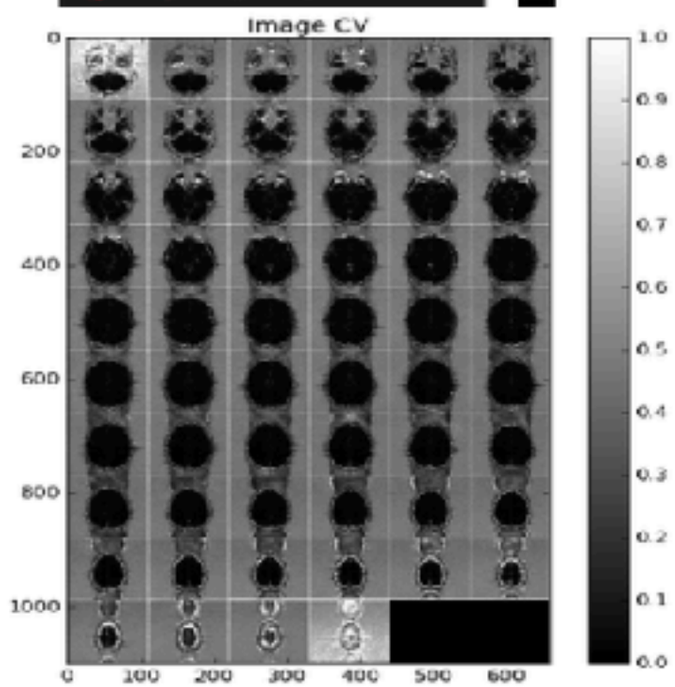


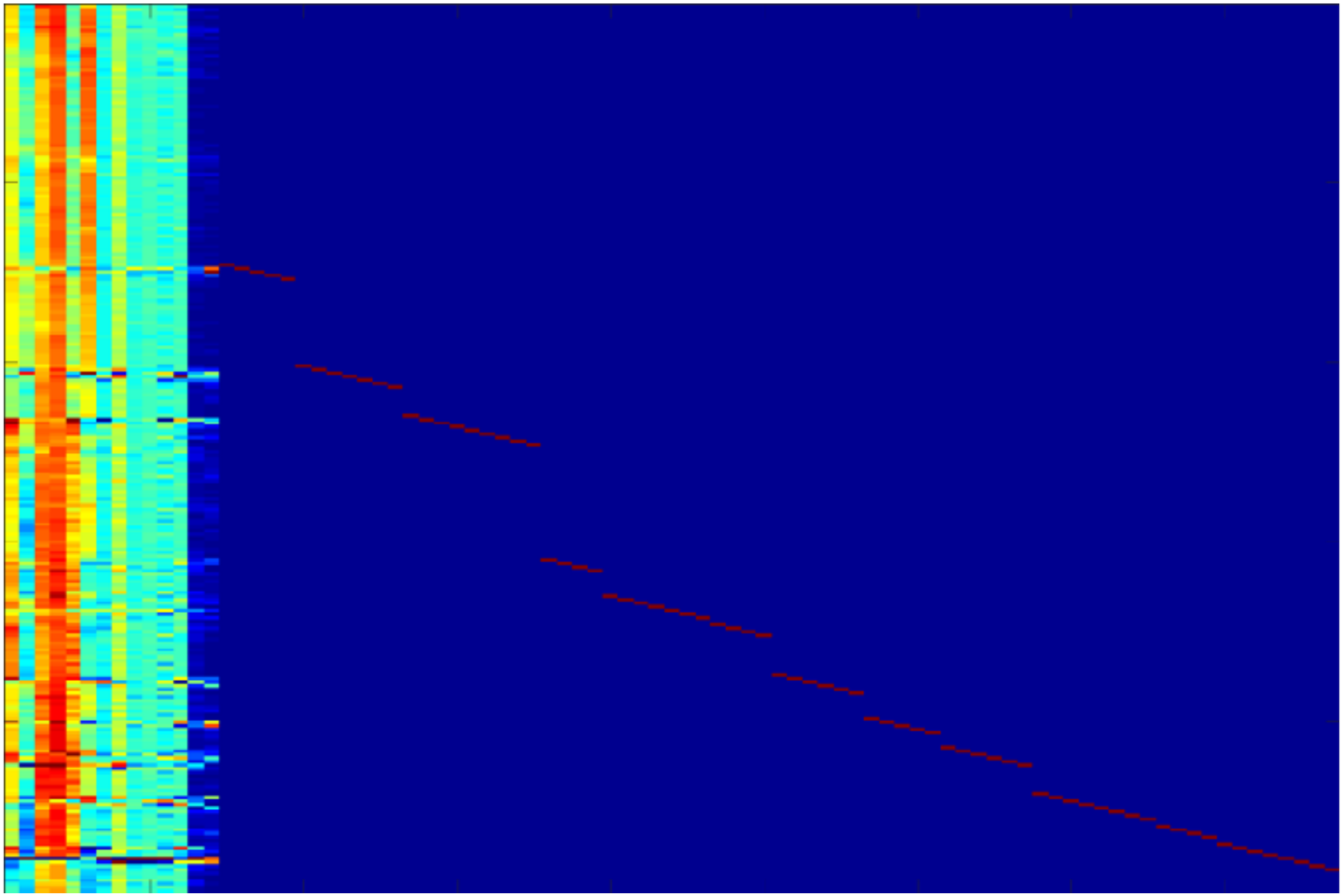






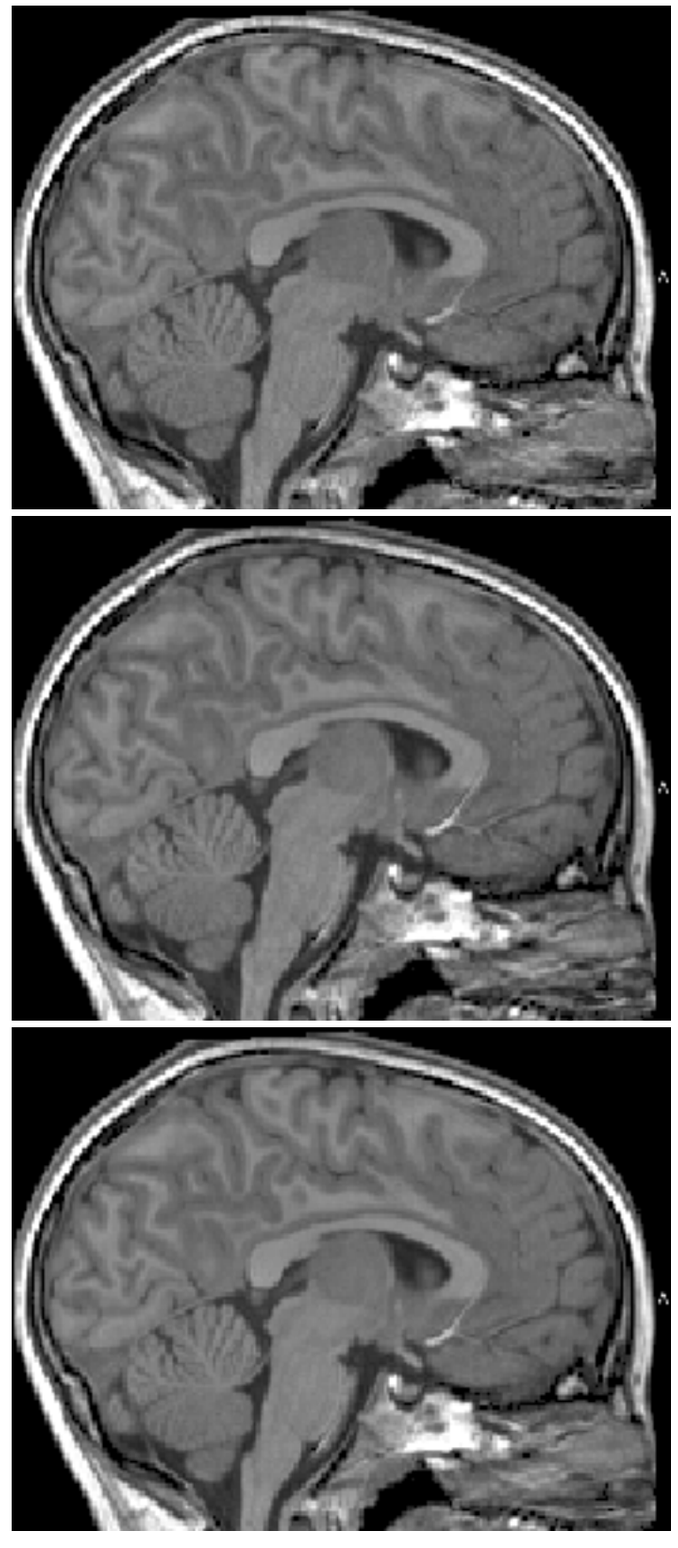






- 6 motion parameters
- 6 motion parameter derivatives
- framewise displacement
- DVARS (root mean squared signal derivative)
- scrubbed time points

Preparing Anatomical Images



- If multiple images of a type of anatomical scan, need to register them and create an average
  - If acquired near in time to one another, can use rigid registration
  - Otherwise, may need nonlinear registration to deal with differences in distortion
- merge_anat.sh will register, scale, and average anatomical images

Running FreeSurfer

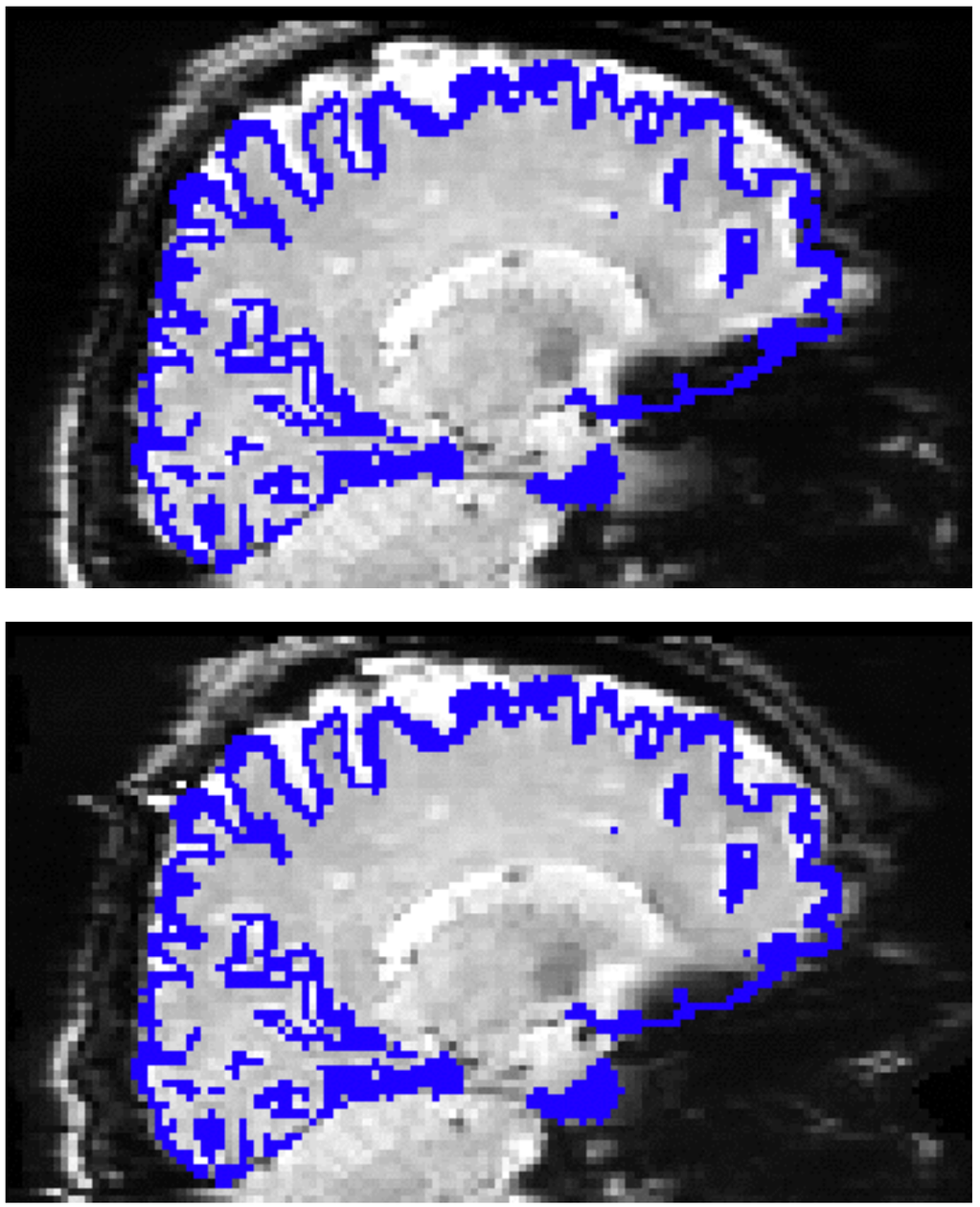
- run_freesurfer.sh will run standard reconstruction using multiple cores
    - Pass in just one MPRAGE (assumes registration and averaging of multiple images has already been done)
    - Can use a FLAIR image also to refine the surface reconstruction
- convert_freesurfer.py will put the FS output in NIfTI format and in the same space as the MPRAGE

Distortion Correction

- Prepare fieldmap images using fsl_prepare_fieldmap
- Run distortion correction using epi_reg_ants
    - Fieldmap provides an estimate of how shifted each voxel in the EPI scan should be
    - But need to register the EPI to the fieldmap to know how much each voxel in the EPI has shifted
    - FSL simultaneously unwarps and registers EPIs to solve this problem
- To limit influence of anatomical distortion, use same-day MPRAGE

Distortion Correction

- Fit is not always perfect
- Registration is based on the edge of white matter mask
- Sometimes slips the EPI to match the incorrect boundary to the white matter
- epi_reg_ants: runs the standard FSL registration, followed by refinement using ANTS

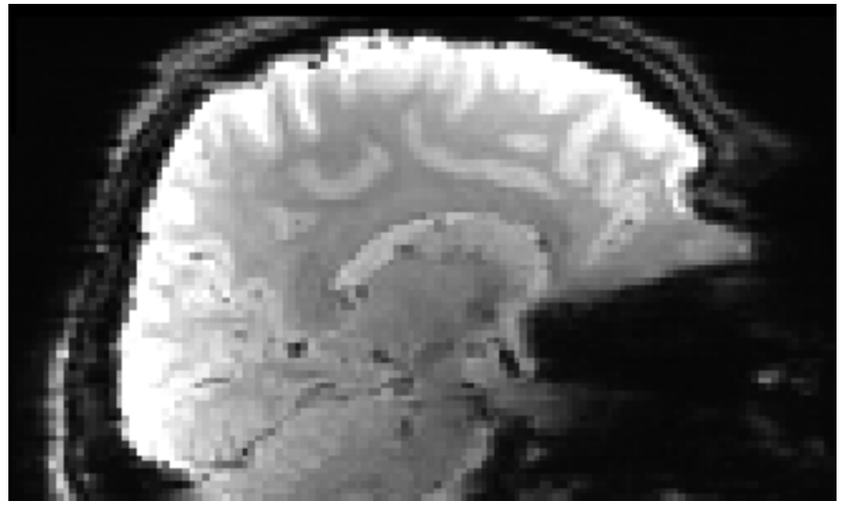


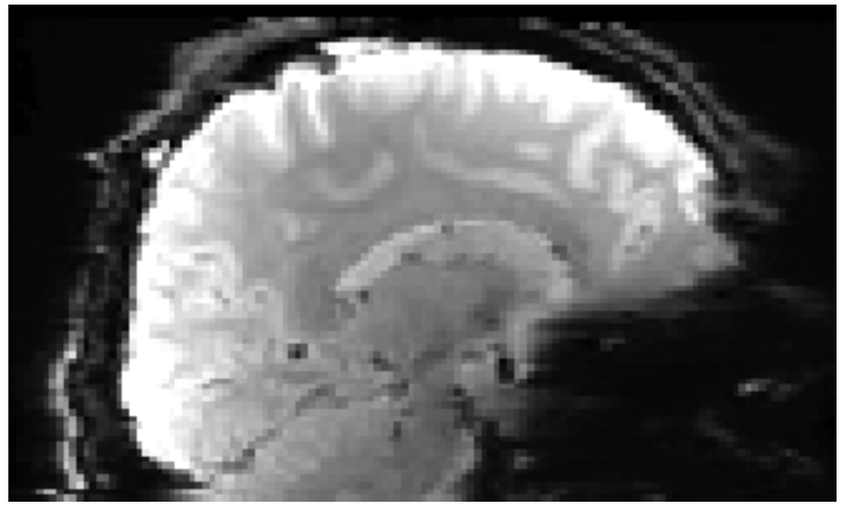
Final Transformation

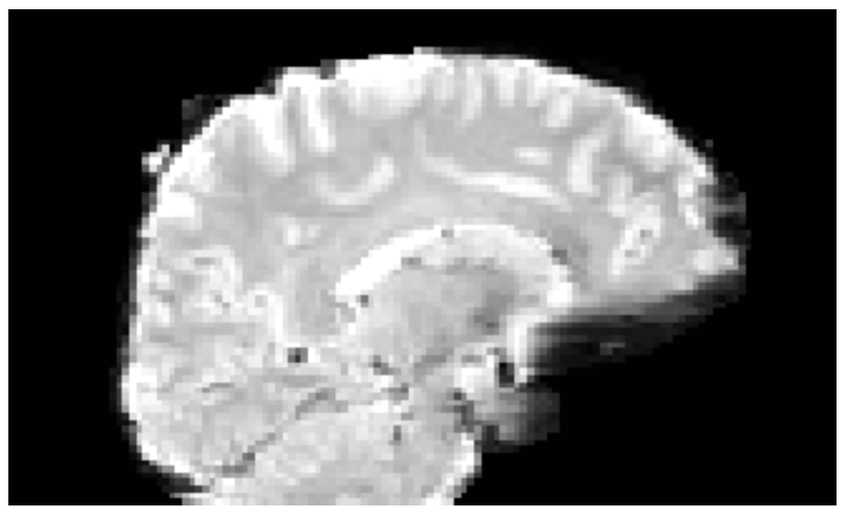
- Functional scans are nonlinearly registered to a reference scan using ANTS

- Motion correction, unwarping, and co-registration are applied in two steps to limit interpolation

- Finally, correct for average bias field and apply anatomical brain mask







Future Directions

- Develop FAT wiki page with more information
- More detailed step-by-step instructions
- Implementation examples for cases that vary by experiment
- Tutorial in the future, and/or clinic

Thanks

- Alison Preston
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