

# HD4630 Workshop I

## Preprocessing & First-Level Analysis

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# Why Preprocess?

- ▶ fMRI data is acquired with physical, biological constraints
  - ▶ MRI machines aren't magic!
  - ▶ Sampling neural activity in living, breathing human beings
- ▶ We need to compare data across participants to draw (statistically) meaningful conclusions

# Basic Preprocessing

- ▶ Discard pre-steady state TRs
- ▶ Slice-timing correction
- ▶ Rigid-body motion correction
- ▶ Coregistration of functional & anatomical
- ▶ Normalization to standard template
- ▶ Spatial filtering (Smoothing)

# Preprocessing in AFNI

- ▶ AFNI allows you to see as little (or as much) detail as you want when preprocessing
- ▶ In this class, we'll be using `uber_subject.py`, a preprocessing GUI that hides many technical details
  - ▶ To see what's happening, we'll have to look at the generated `tcsch` script

# First-level Analysis

- ▶ `uber_subject.py` also includes first-level analysis
- ▶ First-level analysis involves estimating the  $\beta$ -matrix in

$$Y = X\beta + \epsilon$$

by constructing the contrast matrix  $X$

- ▶ A great review of the math underlying this is available from [Mumford Brain Stats](#)

# Plan for Today

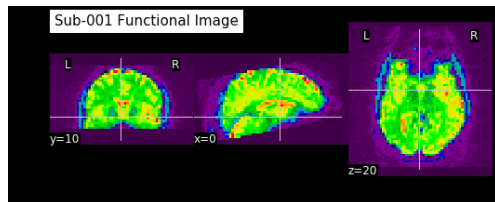
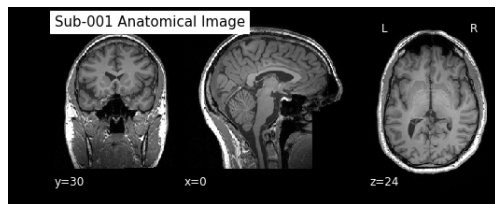
- ▶ Review, with examples, basic preprocessing
- ▶ Discuss first-level analysis in a traditional general linear model (GLM) framework
- ▶ Work along in AFNI using `uber_subject.py`
  - ▶ Preprocess a participant from OpenfMRI ds000102 (Flanker task)
  - ▶ Perform a first-level analysis for incongruent vs. congruent Flanker trials

# Launching the Docker Container

- ▶ We want you to run this locally, so you'll need to launch the docker image you downloaded
- ▶ The full instructions to do so are on the [course website](#), but as a quick reminder:
  - ▶ For Mac: execute `mac_launch.sh` in a terminal with Docker running
  - ▶ For Windows: execute `windows_ip.cmd` in a command prompt. Then, supply that IP to `windows_launch.sh` in a Docker Quickstart Terminal

# First Steps: Looking at the Data

- ▶ No matter what you're doing, this is the first step!
- ▶ Here, we'll need to look at both our anatomical and functional images



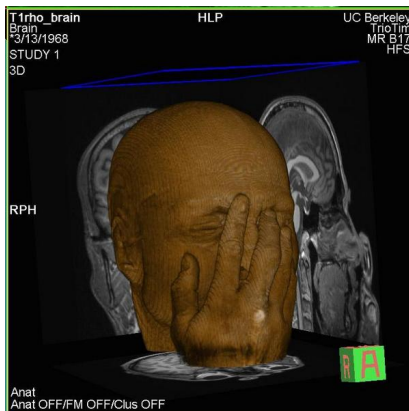


## To Do: Open Data in AFNI

- ▶ Type `afni` into the terminal window to open a new session
- ▶ For sub-01 of the Flanker task:
  - ▶ Read in the `anat` directory
  - ▶ Read in the `func` directory and scroll through the time series of one run
  - ▶ Close `afni`

# What Happened to My Anatomical Image?

- ▶ Defacing is a common step in publicly available MRI data
- ▶ Intended to reduce the risk of participant identification



# Discard Pre-Steady State TRs

- ▶ Pre-steady state or unsaturated volumes show vastly different properties from the rest of an EPI series
- ▶ Because of this, some scanners do not reconstruct these "dummy scans" by default
  - ▶ Both of our OpenfMRI datasets exclude pre-steady state volumes, so we will not discard any TRs

*To Do: Open uber\_subject.py*

The screenshot shows a software window titled "input data and options" with a sidebar on the left containing icons for a folder, a document, and a disk. The main area is divided into three sections, each with a header and a "help" button.

**subject ID**  **group ID**

**input data and options**

☐ analysis initialization

☒ anatomical dataset

☐ include copy of anat+tlrc

☒ EPI datasets

scan index  EPI dataset

EPI directory

wildcard form

dataset count

☐ use wildcard form

☒ stimulus timing files

index label basis type  stim (timing) file

stim directory

wildcard form

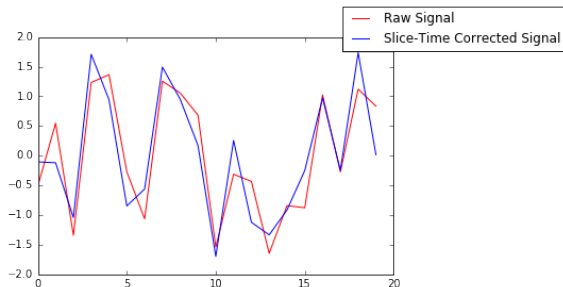
stim file count

init basis funcs:

init file types:

# Slice Timing Correction

- ▶ In single-shot EPI, each slice in a volume is acquired at a different time
- ▶ In our Flanker task, slices were acquired over a 2000ms TR in an interleaved fashion

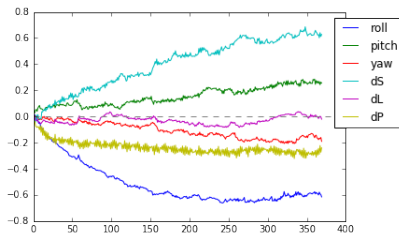
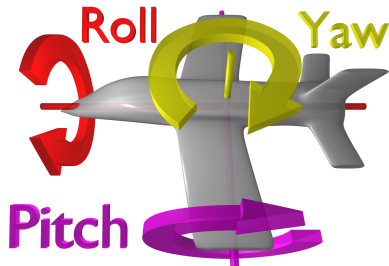


## *To Do: Slice Timing*

- ▶ By default, AFNI will check the image header for slice timing information
- ▶ You can change the default interpolation used, but we won't address that in this workshop

# Rigid-Body Motion Correction

- ▶ AFNI will estimate and correct for movement across the entire scan



*This is a well-behaved participant!*

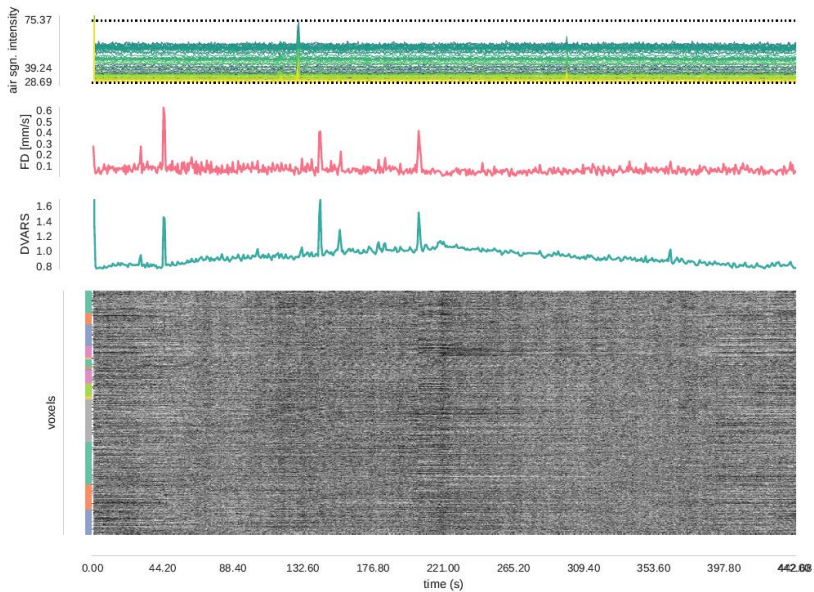
## *To Do: Set Volume Registration Base*

- ▶ To perform rigid body motion correction, we need to select a volume to which to register all other volumes
- ▶ Since we did not remove any pre-steady state TRs, we can set this option to 'first'



# The Limits of Motion Correction

- ▶ Movement is a *major* concern in fMRI analysis
- ▶ Participants who show high levels of movement may not be usable
  - ▶ Even when correcting for motion, subtle differences may remain



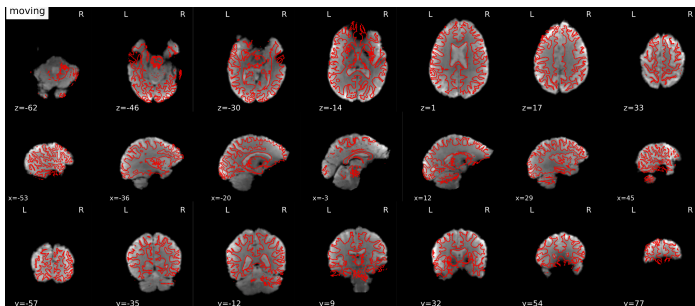
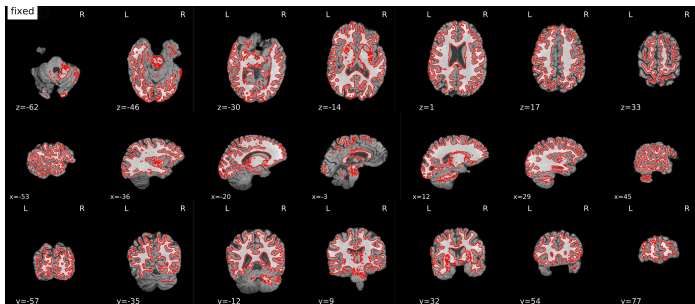
Visualization from MRIQC

## *To Do:* Set Motion Censoring

- ▶ 'Motion censor limit' sets the maximum amount of motion allowed in any one TR
- ▶ TRs showing motion higher than this limit are 'scrubbed' from the time series

# Coregistration

- ▶ We need to get the functional and anatomical images into the same space
- ▶ By default, these are likely to be out of alignment as participants move between scans
  - ▶ After motion correction, all of our functional images should be aligned to one another
  - ▶ Aligning these to the anatomical image should therefore be a one step correction



Visualization from **fMRIPrep**

## *To Do: Extra Alignment Options*

- ▶ 'Local Pearson Correlation' is the default coregistration option
  - ▶ This is appropriate for T1 to EPI registration, but may need to be changed for other modalities
- ▶ Select 'use giant\_move' to allow AFNI to align anatomical and functional images where participants have moved substantially

# Normalization

- ▶ Standard templates currently in use include Talarach and MNI
  - ▶ MNI based on many living subjects rather than one post-mortem
  - ▶ Several different versions of the MNI are in use!



Jamie Hanson  
@JamieLarsH

Following

@AFNlman @laurenatlas I nominate you, Bob...



LIKES  
3



6:37 PM - 27 Feb 2017 from Pittsburgh, PA

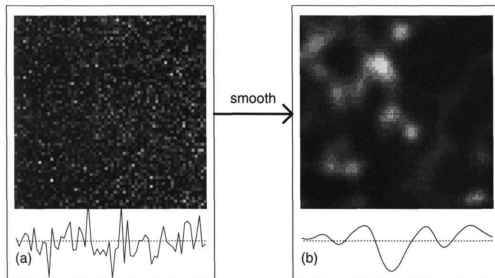
## *To Do:* Extra TLRC Options

- ▶ 'TLRC' is short for Talaraich, the default normalization space in AFNI
- ▶ Change this to MNI\_avg152T1 to align our subject to MNI space
  - ▶ This corresponds to the MNI 2009c nonlinear template



# Spatial Filtering (Smoothing)

1. Increases signal-to-noise ratio
2. Helps to ameliorate residual anatomical variability
3. Allows data to meet assumptions of Gaussian Random Field theory
  - ▶ A fun introduction to this is provided in [Worsley, 1996](#)

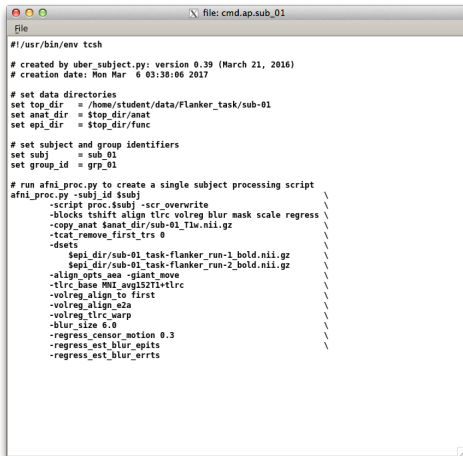
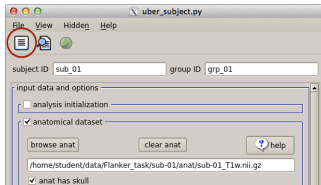


## *To Do: Set Blur Size*

- ▶ We need to specify the FWHM (Full-Width at Half-Maximum) of our Gaussian kernel
- ▶ 4mm is the default, but we'll increase this to 6mm (FWHM  $\geq$  2x voxel size)

# Inspecting our Script

- Now that we have preprocessing set up, we can look at the parameters for our example subject



# First-Level Analysis

- ▶ `uber_subject.py` also incorporates first-level analysis
- ▶ For this, we'll need to know the stimulus timing for each of the conditions in the Flanker task
  - ▶ We'll collapse the two 'congruent' and 'incongruent' conditions, ignoring participant accuracy

