

# HD4630 Workshop I

## Preprocessing & Quality Control

Elizabeth DuPre

Human Neuroscience Institute  
Department of Human Development  
Cornell University

# 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 `tcs` script

# Plan for Today

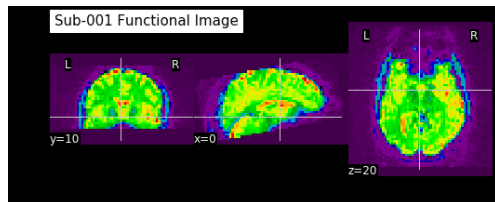
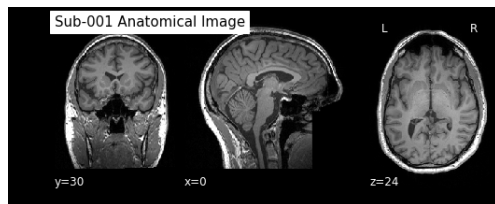
- ▶ Review, with examples, basic preprocessing
- ▶ Work along in AFNI using `uber_subject.py`
  - ▶ Preprocess a participant from OpenfMRI ds000102 (Flanker task)

# 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



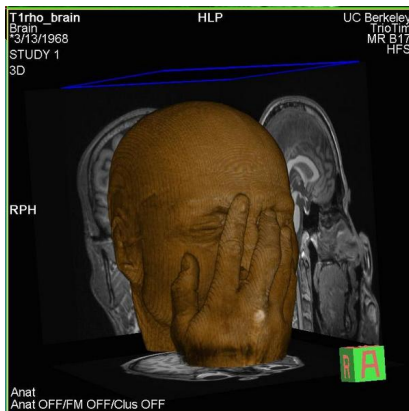
## To Do: Open Data in AFNI

- ▶ 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'. At the top, there are two text input fields: 'subject ID' and 'group ID'. Below these, the window is divided into three main sections, each with a checkbox and a title bar. The first section, 'analysis initialization', has an unchecked checkbox. The second section, 'anatomical dataset', has a checked checkbox and contains a 'browse anat' button, a 'clear anat' button, a '? help' button, a text input field, and an unchecked checkbox labeled 'include copy of anat+tlrc'. The third section, 'EPI datasets', has a checked checkbox and contains a 'browse EPI' button, a 'clear EPI' button, a '? help' button, a table with two columns 'scan index' and 'EPI dataset', an 'EPI directory' text input field, a 'wildcard form' text input field, a 'dataset count' text input field with the value '0', and an unchecked checkbox labeled 'use wildcard form'. Below the 'EPI datasets' section is a fourth section, 'stimulus timing files', which has a checked checkbox and contains a 'browse stim' button, a 'clear stim' button, a '? help' button, a table with four columns 'index', 'label', 'basis', and 'type', and a 'stim (timing) file' text input field. At the bottom, there are three more text input fields: 'stim directory', 'wildcard form', and 'stim file count' with the value '0'. Finally, there are two dropdown menus: 'init basis funcs:' with a 'choose' button and a text input field, and 'init file types:' with a 'choose' button and a text input field.

subject ID  group ID

input data and options

☐ analysis initialization

☒ anatomical dataset

browse anat clear anat ? help

☐ include copy of anat+tlrc

☒ EPI datasets

browse EPI clear EPI ? help

scan index	EPI dataset
<input type="text"/>	

EPI directory

wildcard form

dataset count

☐ use wildcard form

☒ stimulus timing files

browse stim clear stim ? help

index	label	basis	type	stim (timing) file
<input type="text"/>				

stim directory

wildcard form

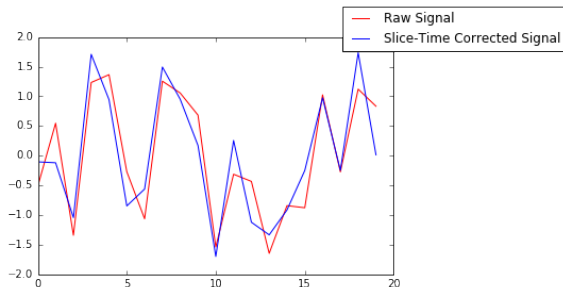
stim file count

init basis funcs: choose

init file types: choose

# 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

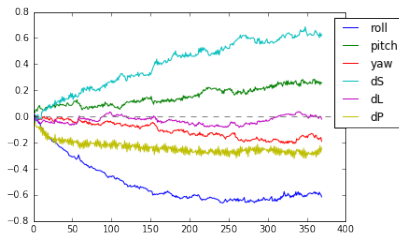
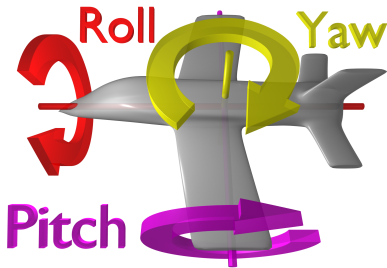


## *To Do: Slice Timing*

- ▶ 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!*

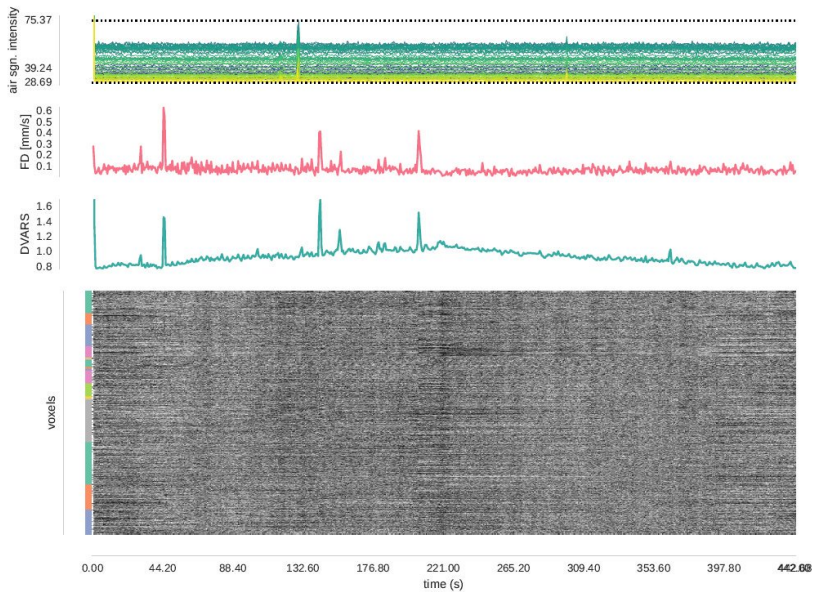
## *To Do: Set Volume Registration Base*

- ▶ 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





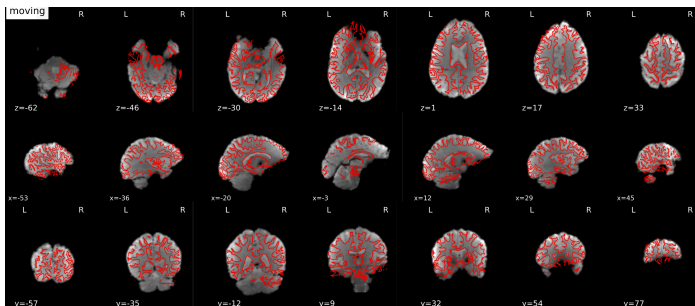
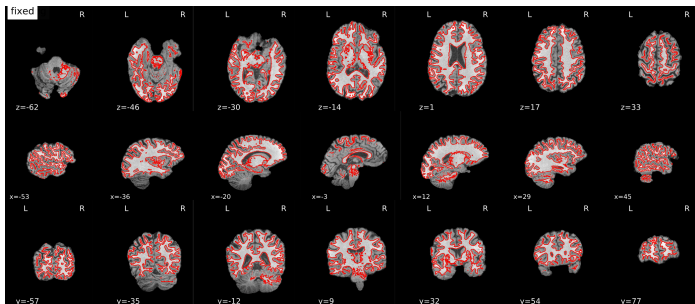
Visualization from **MRIQC**

## *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



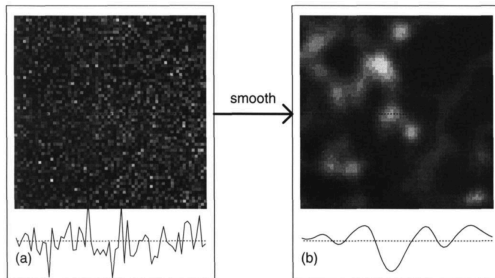
6:37 PM - 27 Feb 2017 from Pittsburgh, PA

## *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

