AFNI\_proc.py Overview

Defining the subject (and it’s imaging data)

• set subject ID

• mark anatomical(anat) image

• mark functional (EPI) images

Setting the blocks used (processing steps performed in the script)

• Automatic Blocks: Don’t need to be defined. These are always done

• tcat - set the amount of initial TRs to remove “tcat\_remove\_first\_trs”  
The default option for this block is 0

• setup - copying files, defining subject, creating output directory

• Default Blocks: Steps whose order can be reorganized or set to be skipped

• tshift - slice timing alignment for the volumes (default 0)

• volreg - 3D volume registration

• mask - create brain mask from EPI data

• Scale - scale each EPI run mean to 100, for all voxels (max set to 200)

• regress - 3dDeconvlve regression analysis

• blur - blur each volume (default is 4mm fwhm)

• Optional Block: Off

• align - align EPI to anat

• tlrc - warp anat to standard space

• empty - vacant block where users can set their own commands

Options within each Block

• align

• done with align\_epi\_anat.py, recommended to be done before using afni\_proc.py

• -deoblique [on]/off : deoblique datasets before alignment

• deoblique\_opts : The script will try to determine if either EPI or anat data is oblique and do the initial transformation to align anat to epi data using

• -Allineate\_opts : calls for 3dAllineate for anat to epi

• \*\*Optional: 3dskullstrip can be performed with ‘-skullstrip\_opts’ option

• epi2anat: align EPI dataset to anat dataset

• -child\_epi: Names of epi datasets that are being aligned

• ‘-epi\_base 0’ set the epi base sub-brick

• -tshift [on]/off : do time shifting of EPI dataset before alignment

• -tshift\_opts: options to use with 3dTshift

The script will determine if slice timing correction is necessary unless tshift is set to off.

• tcat

• tcat\_remove\_first\_trs: removes ***x*** amount of TRs from beginning of run

• setup

• subj\_id: set subject ID name

• copy\_anat: define anatomical data for copying

• script: set the name of the output completed script

• -outlier\_count yes/no: counting outliers (command:3dToutcount) [default:yes]

• -outlier\_legendre yes/no: use Legendre polynomials in 3dToutcount? [default:yes]

• -outlier\_polort NUMBER: Set polynomial baseline with 3dToutcount for detrending each voxel time series[default same as the number set in 3dDeconvolve]

• -automask -fraction : Output the fraction of automasked values

• based on ~ regress\_censor\_outliers : censor TRs with excessive outliers

• Both these options are off by default

• \*\* If no polynomial is set then the outliers are based on the median values for each TR

• tshift

• -tshift\_align\_to: specify 3dTshift alignment option [default: -tzero 0] the default aligns each slice to the first

• -tshift\_interp: specify interpolation method(slice time correction ) for 3dTshift [default: -quintic]

• volreg

• -volreg\_interp METHOD(-quintic, -Fourier, etc) : specify the interpolation method for volreg [default: -cubic]

• -volreg\_zpad N\_SLICES : zeropad around the edges by 'n' voxels [default: -volreg\_zpad 1]

• -volreg\_tlrc\_warp : warp EPI to +tlrc space at volreg step [default: stay in +orig space]

• -volreg\_align\_e2a : aligning the EPI to the original anat [default: no, only if standardizing EPI during volreg block]

• \*\*\* afni\_proc.py [by default] aligns each run to the base TR with the smallest outlier percentage

• -volreg\_align\_to POSN : specify the base position for volume reg [default: align to the 3rd volume of the 1st run]

• mask

• -mask\_dilate NUM\_VOXELS : specify the automask dilation [default: -mask\_dilate 1]

• -mask\_type TYPE : specify 'union' or 'intersection' mask type [default: -mask\_type union

• -mask\_epi\_anat yes/no : apply epi\_anat mask in place of EPI mask [default: yes]

• scale

• -scale\_max\_val MAX : specify the maximum value for scaled data [default: -scale\_max\_val 200]

• regress

• -regress\_compute\_tsnr yes/no: compute temporal signal to noise ratio (tSNR) from errts output

• -regress\_local\_times : specify -stim\_times as local times within each run rather than global times (every timing based from the start of run 1) [default: 3dDeconvolve determines this automatically]

• -regress\_polort NUM : specify the polynomial degree of baseline [default: 1 + floor(longest\_run\_length / 150.0) which is the Automatic (A) ]

• -regress\_stim\_types TYPE1 TYPE2 ... : specify list of stim types [default: times]

• times: a standard stimulus timing file [ex: -stim\_times]

• AM1: timing files have one or more married parameters [ex: -stim\_times\_AM1]

• AM2: have one or more married parameters [ex: -stim\_times\_AM2]

• IM: No married parameters, but get beta for each stim [ex: -stim\_times\_IM]

• file: a 1D regressor, not a stimulus timing file [ex: -stim\_file]

• -demean : same as dfile\_rall.1D motion parameters but the mean per run has been removed

• -jobs NUM : computing resources ( NUM out of 32) used to complete command

• -basis\_normall NUM : Normalize all basis functions for '-stim\_times' to have amplitude ‘NUM’

• -float : format of output datasets (instead of scaled shorts) [ now the default method]

• -num\_stimts NUM : NUM = number of input stimulus time series

• \*\*use of AM1 or AM2 requires dmBlock(1)

• blur

• -blur\_size SIZE\_MM : specify the size, in millimeters [default: -blur\_size 4]

• tlrc

• -allineate : Align the -source dataset to the -base

• \*\*Default option in auto\_warp.py is to perform automated skullstrip of the anatomical before standardizing

• empty ( relevant preprocessing commands that would need to be added)

• 3dwarp: Warp (spatially transforms) a dataset

• oblique2card: deoblique the EPI data

• 3dFourier: Program to lowpass and/or highpass each voxel time series in data

• -highpass .01 (high pass filter .01 hz | 100 sec)

• 3dSkullStrip: Remove the skull

• \*\*AFNI\_proc.py by default performs skullstriping in the tlrc block during auto\_warp.py. It can also perform the skullstripping in the align block.

**AFNI Command Glossary:**

**3dcopy:** Converts anatomy .nii file into AFNI-readable anatomy .BRIK/.HEAD file

**3dTshift**: Shifts voxel time series from the input dataset so that the separate

slices are aligned to the same origin.

**3dWarp**: Warp (spatially transforms) a dataset.

**3dTcat**: Concatenates input sub-bricks from into one 3D+time dataset.

**3dToutcount**: Calculates number of outliers in a (3D+time)functional dataset at each timepoint and writes them to a text file.

**3dTstat**: Performs voxel-wise statistics for a functional data set. Specifies type of statistic in options.

**3dvolreg**: Registers each 3D sub-brick from the input dataset to the base brick.

**cat**: concatenates datasets or .1D files.

**1d\_tool**.**py**: Used to set motion parameters onto .1D motion file.

**3dAutomask**: Automatically creates a brain-only mask.

**3dMean**: Takes the voxel-by-voxel mean of all input datasets.

**3dcalc**: Performs voxel-by-voxel arithmetic on datasets.

**3dFourier**: can perform low/high pass filter for each voxel in time series.

**3dDetrend**: Removes components from voxel time series using linear least squares. Used to create empty (brain-less) pb05 files.

**Gen\_epi\_review**.**py**: generate an AFNI processing script that can be used to review functional data. Script called @epi\_review$subj .

**3dSkullStrip**: Extract brain from anatomical image. Output is in native space. ‘-ld’ option allows for a more denser mesh which would ideally require less manual skullstripping.

**SSwarper**: Extract brain from anatomical image. Output is in native space. The ‘SS’ in the command script **S**kull**S**trips the anatomical. The warper options creates an MNI standardized version of the anatomical. This tool greatly improves on 3dSkullStrip.

**3dresample**: change the orientation or grid spacing of a dataset to match master dataset. Typically done to match anatomical data with functional data.