FMRI processing with AFNI: Some comments and corrections on "Exploring the Impact of Analysis Software on Task fMRI Results"

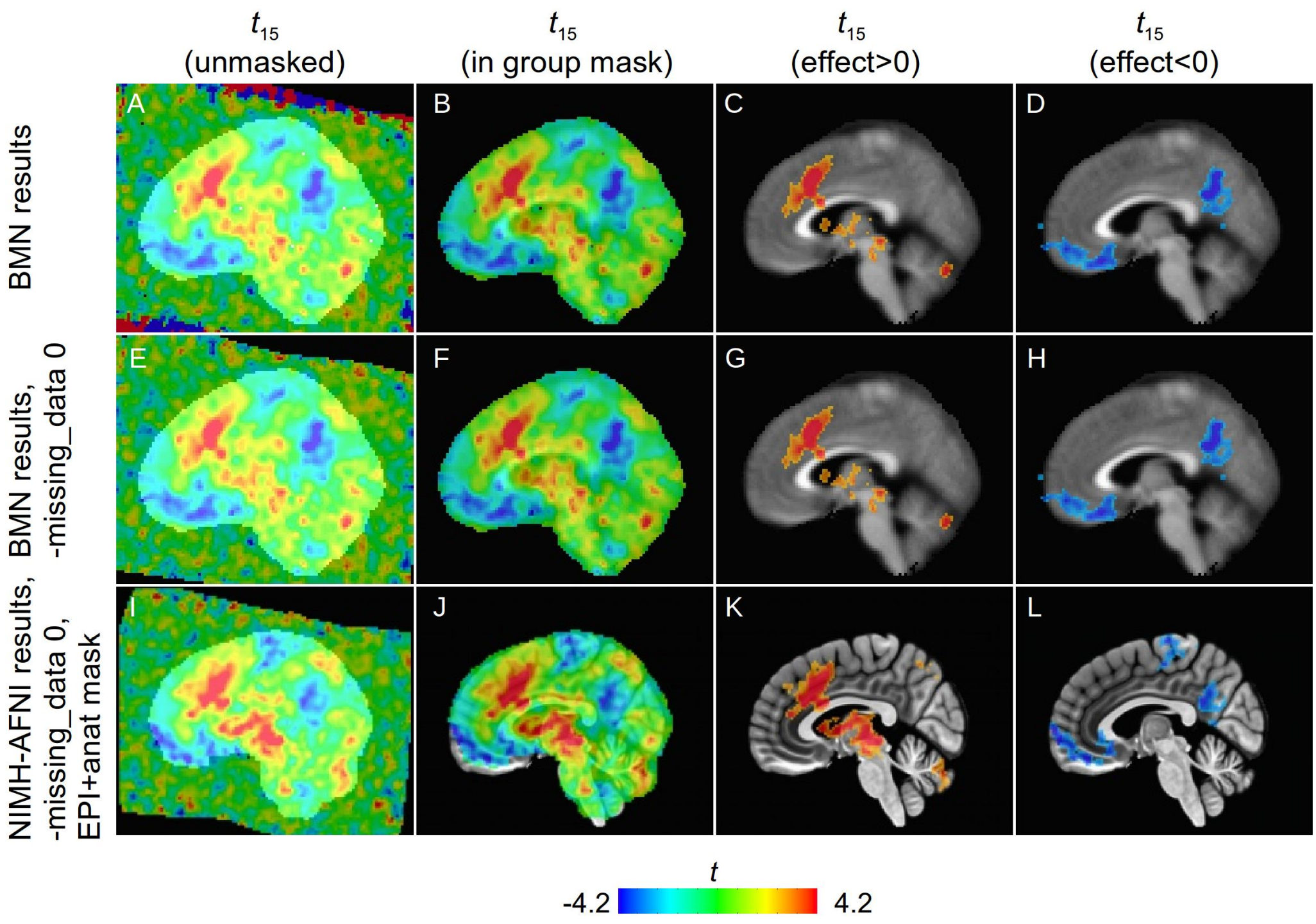
- https://www.biorxiv.org/content/biorxiv/early/2018/04/28/308643.full.pdf
- https://afni.nimh.nih.gov/pub/dist/doc/htmldoc/codex/main_det_2018_TaylorEtal.html

Recommendations

- **Making a group mask**
- create a group mask from the intersection of each subject's EPI masks, with the mask_epi_anat dataset
- Include a mask in the group analysis level
- Make a group level mask for reporting results. This also determines the volume over which multiple comparisons corrections for voxelwise stats are done.
- 3dmask_tool -prefix mask -input `ls ${TOPDIR}/sub*.results/mask_epi_anat.*.HEAD` -frac 1.0

Recommendations

- Marking missing data to avoid erroneous modeling
  - there will be zero values outside the warped volume's field of view (FOV), and the warped FOV edges may not exactly overlap across the group. Simply leaving those (one or more) zero values of missing data in the model would lead to erroneous and meaningless results at those voxels (due to divisions by zero); such cases could be recognized as producing t-statistics with extreme values at or near ±100
  - the option “-missing_data 0” should be used when running 3dMEMA; for 3dttest++, the analogous option is “-zskip”


t_{15} (unmasked)
t_{15} (in group mask)
t_{15} (effect>0)
t_{15} (effect<0)
BMN results
BMN results, -missing_data 0
NIMH-AFNI results, -missing_data 0, EPI+anat mask
A
B
C
D
E
F
G
H
I
J
K
L
t
-4.2
4.2

- **Alignment to standard space**
  - nonlinear registration ("warping") for the alignment of subject anatomical volumes to standard space ("intersubject registration")
  - nonlinear warping of each single subject's anatomical through the @SSwarper
    - 1) aligning each subject's anatomical to a standard space target and 2) skull-stripping that anatomical volume
    - the MNI152_2009_template volume (1x1x1 mm3 voxels)

- Alignment of EPI to anatomical: cost function selection
  - lpc+ZZ

- **EPI volume registration for motion correction (and alignment)**
  - select the volume with the fewest number of outliers in the initial EPI time series (denoted by the following option and keyword "-volreg_align_to MIN_OUTLIER“)
  - avoid having a very poor quality or motion-corrupted volume play the dual reference role

- do not recommend upsampling the data by large amounts during processing (e.g. -volreg_warp_dxyz 2)

- often beneficial *not* to remove pre-steady state TRs
  - can be very useful as a reference volume for alignment to the subject's anatomical

- To better account for motion, recommend applying -regress_motion_per_run in afni_proc.py

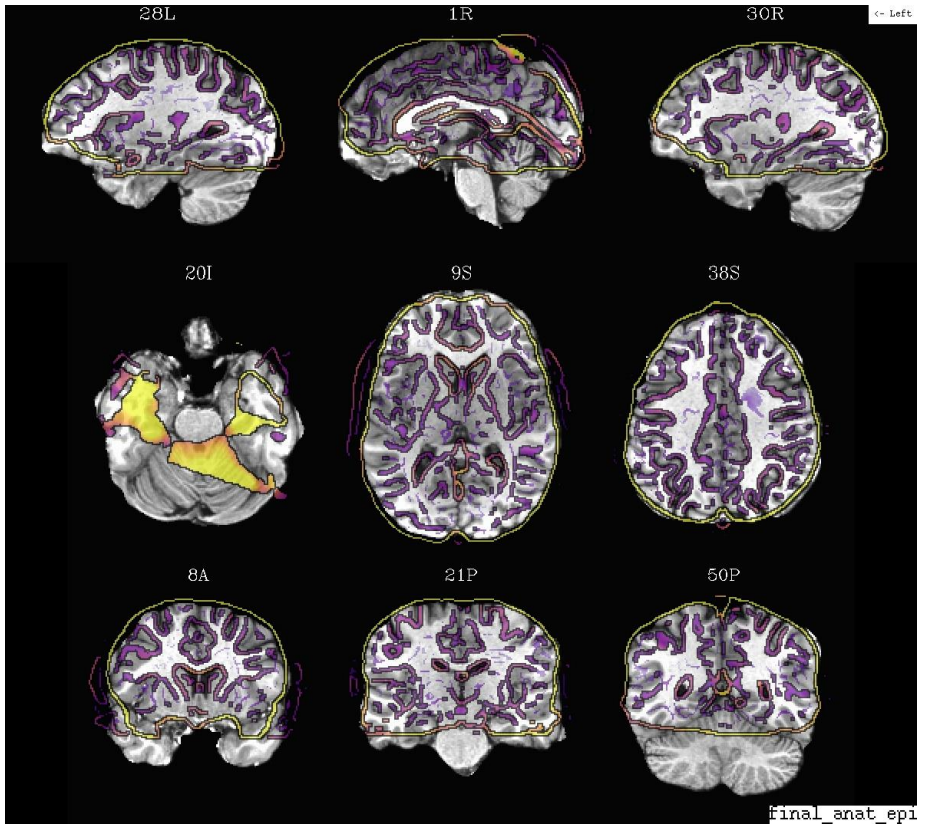
gen_ss_review_table.py

```
gen_ss_review_table.py  \
-infiles Subject*/Subject*.results/out.ss_review* \
-tablefile ss_review_stats.txt
```

	A	B	CP	CQ	CR	CS	CT	CU	CV
1	group	subject ID	TSNR average	global correlation (GCOR)	anat/EPI mask Dice coef	maximum F-stat (masked)	blur estimates (ACF)		
2	value	value_1	value_1	value_1	value_1	value_1	value_1	value_2	value_3
3	1	sub01	145.961	0.061	0.704	20.964	0.820	3.689	13.639
4	2	sub02	134.894	0.046	0.751	32.915	0.807	3.630	13.425
5	3	sub03	147.863	0.065	0.672	28.720	0.848	3.714	15.372
6	4	sub04	161.558	0.033	0.682	46.975	0.864	3.646	14.648
7	5	sub05	143.556	0.097	0.694	68.014	0.859	3.617	14.016
8	6	sub06	162.671	0.100	0.698	17.466	0.863	3.624	14.330
9	7	sub07	116.644	0.190	0.705	27.741	0.824	3.635	13.372
10	8	sub08	143.888	0.054	0.695	33.795	0.812	3.706	14.533
11	9	sub09	127.048	0.070	0.694	30.761	0.829	3.660	12.870
12	10	sub10	159.629	0.060	0.686	34.677	0.781	3.692	13.634
13	11	sub11	160.800	0.070	0.682	20.358	0.804	3.659	13.324
14	12	sub12	136.494	0.152	0.711	22.832	0.750	3.707	13.713
15	13	sub13	150.658	0.085	0.708	23.472	0.810	3.776	13.248

@snapshot_volreg

- quickly evaluating alignment between two datasets (e.g. a subject's anatomical and an EPI volume)



gen_group_command.py

- gen_group_command.py - generate group commands: 3dttest++, 3dMEMA, 3dANOVA2, 3dANOVA3
  - generate generic commands
  - todo (maybe): 3dttest, GroupAna

- This program is to assist in writing group commands. The hardest part (or most tedious) is generally listing datasets and such, particularly including sub-brick selection, and that is the main benefit of using this program.

- 3dANOVA3 -type 4

  This is a simple example of a 2-way factorial ANOVA (color by image type), across many subjects. The colors are pink and blue, while the images are of houses, faces and donuts. So there are 6 stimulus types in this 2 x 3 design:

  pink house pink face pink donut
  blue house blue face blue donut

  Since those were the labels given to 3dDeconvolve, the beta weights will have #0_Coef appended, as in pink_house#0_Coef. Note that in a script, the '#' character will need to be quoted.

  There is only one set of -dsets given, as there are no groups.

```
gen_group_command.py -command 3dANOVA3                    \
  -dsets OLSQ*.HEAD                                        \
  -subs_betas                                              \
    "pink_house#0_Coef" "pink_face#0_Coef" "pink_donut#0_Coef" \
    "blue_house#0_Coef" "blue_face#0_Coef" "blue_donut#0_Coef" \
  -factors 2 3
```

- New executable script **@grayplot** reads a results directory created by afni_proc.py and creates a grayplot of each errts*+tlrc.HEAD dataset it finds. The output Grayplot.*.png images have a motion magnitude trace on top (with the censored intervals marked), and the time series grayscale plot
- below. The voxels (downwards) are ordered with Gray Matter on top, White Matter below, and CSF at the bottom, with tissue types separated by black-and-white dashed lines. These images are quick way to see if there are any strange artifacts left in the data
- after processing, and also to see how much the censoring has affected the dataset time series.