fMRI Data

WHERE'S IT COMING FROM
AND WHATCHA' DOIN' WITH IT?

AFNI FOR IRTAS
02/07/14
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Things I wish someone had told me…

- Learn a computer language (or two). Yesterday.
  - A must: UNIX
  - Common: Matlab, Python, T-Shell
  - Less Common: TCL, Perl
- Blindly trust NO ONE!
  - Don’t push buttons without asking questions
- When you get stuck, use your resources wisely:
  - Ask Google before you ask your friend
  - Ask your friend before you ask your supervisor
- Think deeply about organization BEFORE you start.
  - File structure
  - Naming conventions
  - Documentation for your progress and posterity

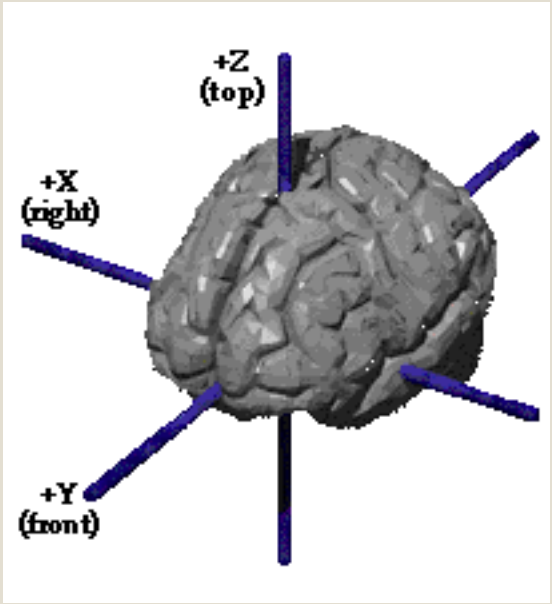
Variety of Analysis Programs

(basic preprocessing steps are more or less the same)

- **AFNI**
- SPM
- FSL
- BrainVoyager

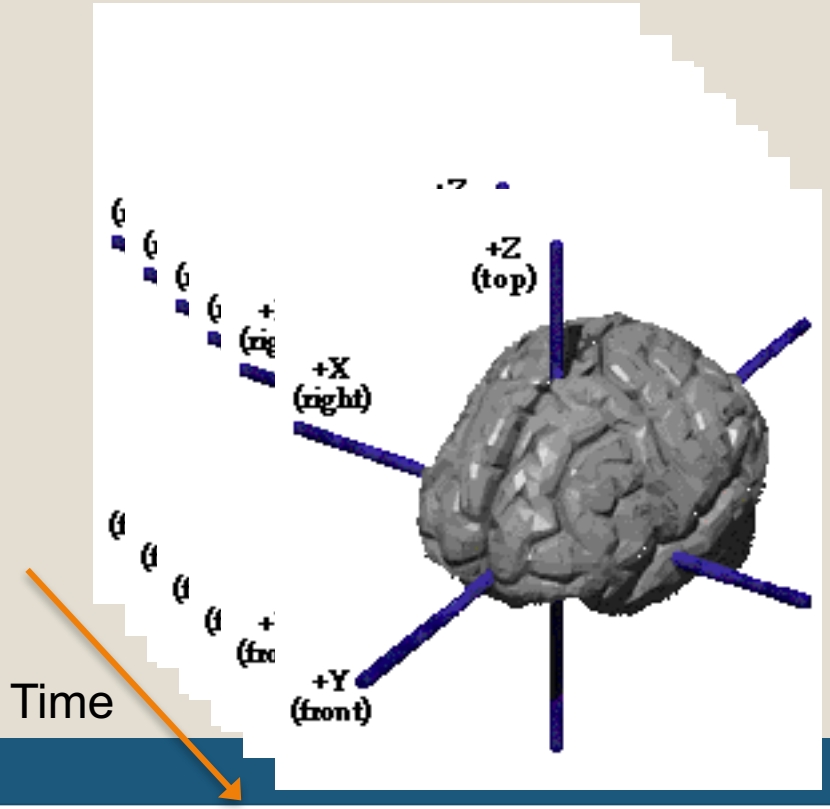
Data Collection

- Anatomical Scan
  - AKA: Structural
  - Data collected without task
  - 3-D



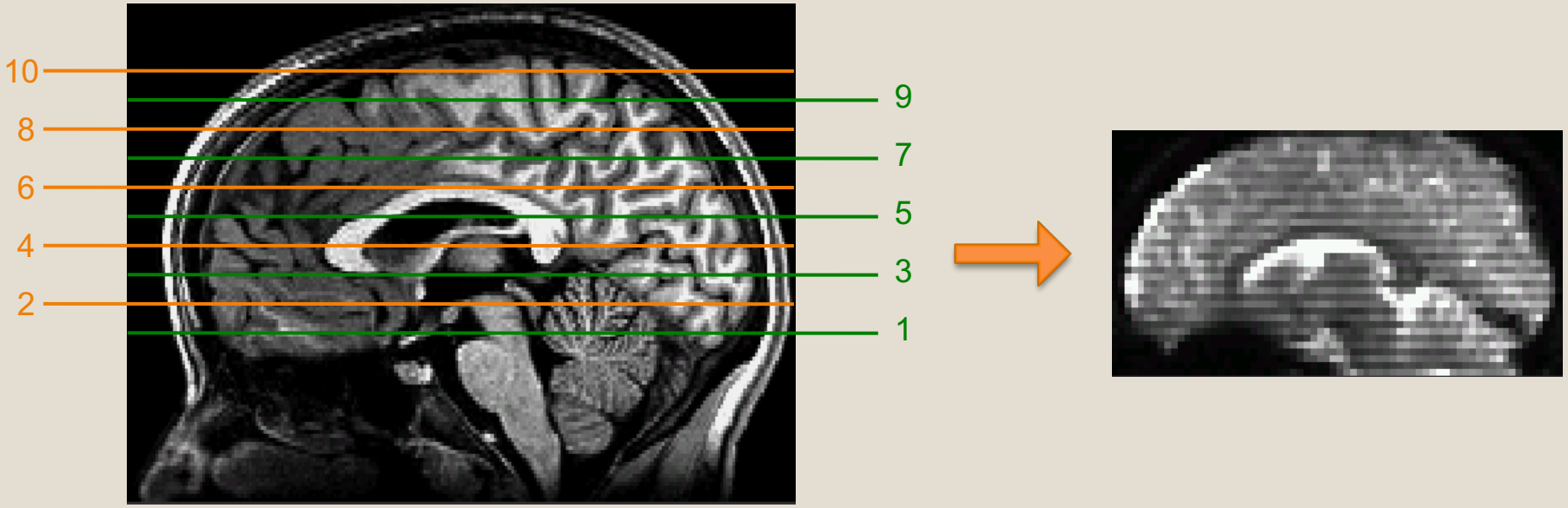
Data Collection

- Functional Scan
  - AKA: EPI (echo planar imaging)
  - Data collected during task (or resting state)
  - 4D (3D + time)



Data Collection

- Time repetition (TR) / Single whole-brain volume
  - Amount of time required to collect an image of the whole brain
  - Comprised of interleaved slices

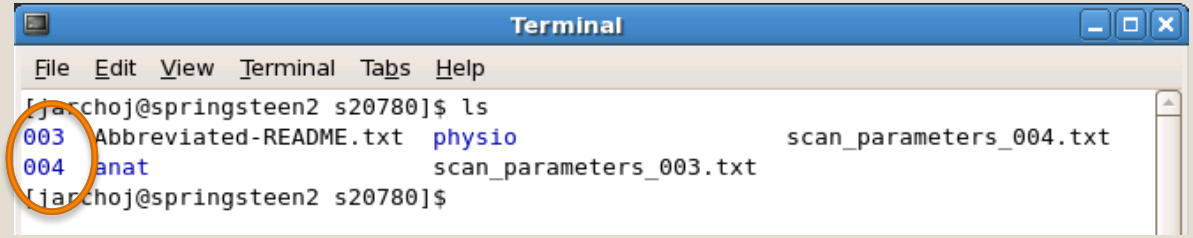


Data Transfer

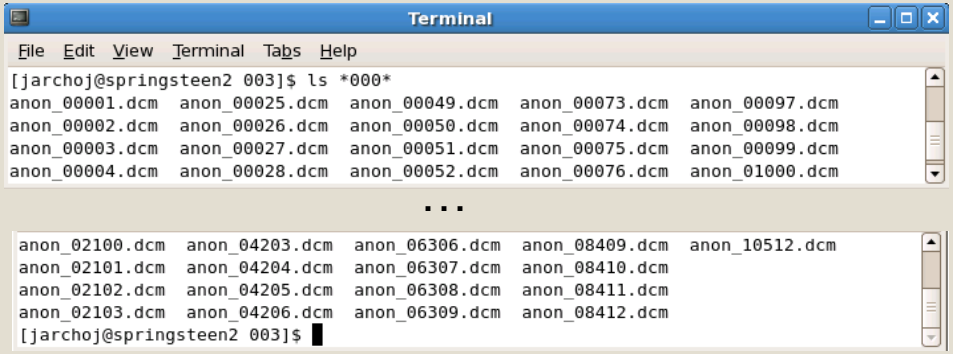
- Raw data is temporarily stored on the scanner
- Transferred to the group's raw data repository
  - Typically via secure copy (scp) or something similar
- Compressed to save space
  - .tar
  - .gz
  - .tar.gz

Raw Data

- Must be de-compressed
  - untar, unzip
  - “open_sesame”

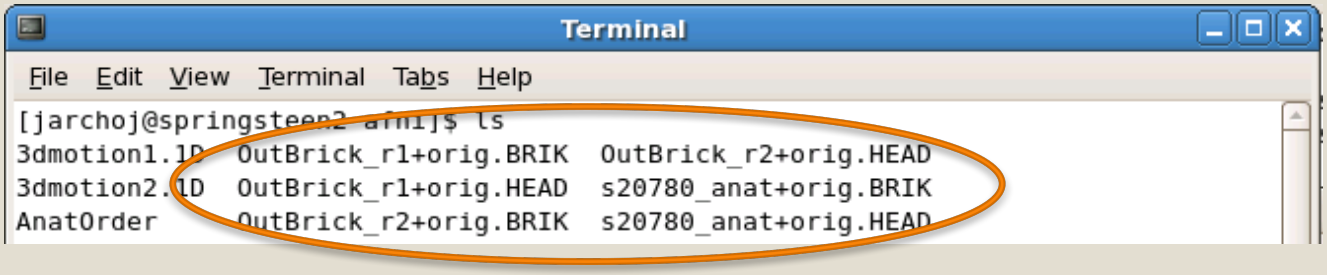


- DICOM format
  - One folder per run
  - One file per slice (.dcm)
  - Big ass folders!



Convert Data from DICOM to AFNI format

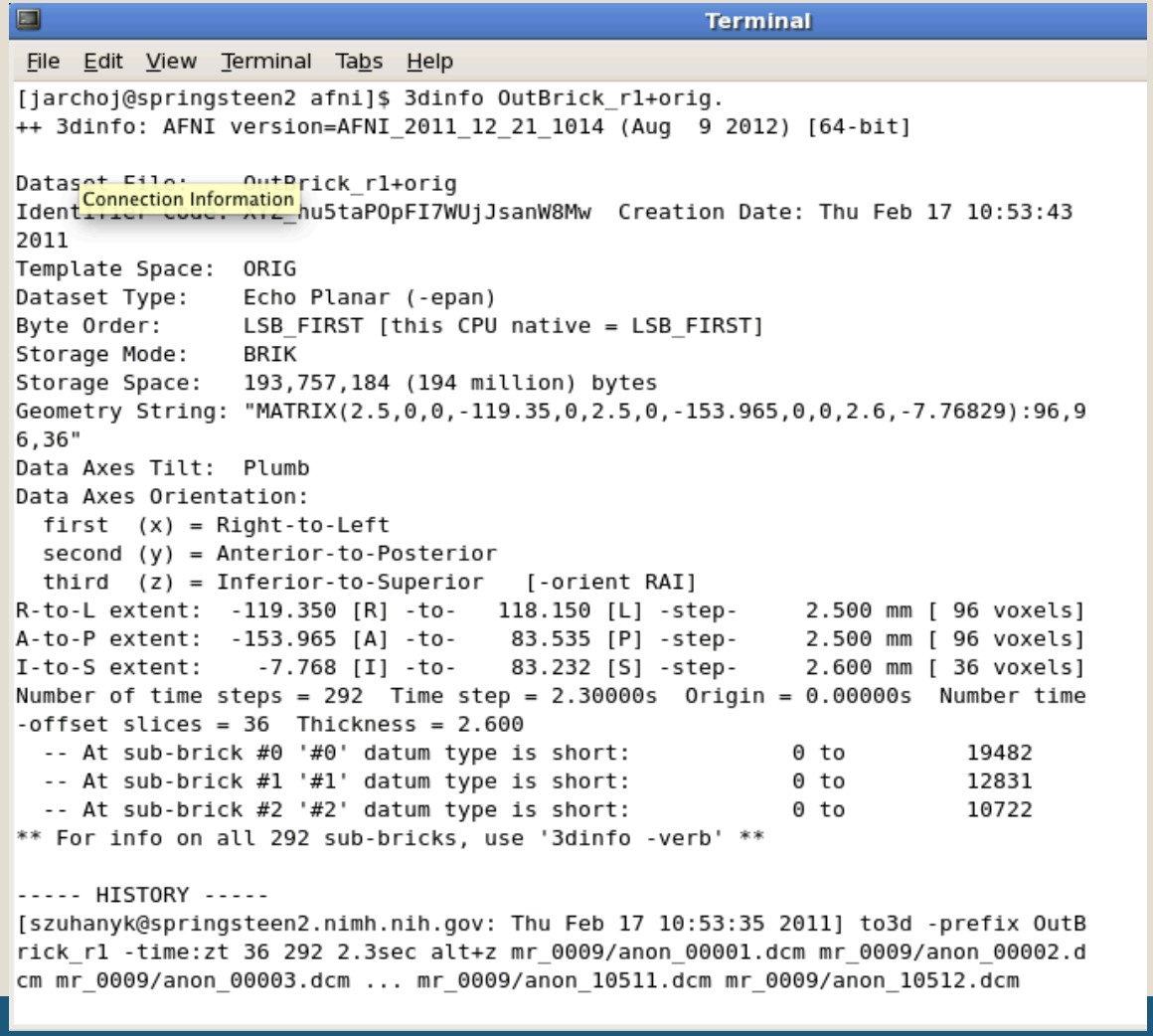
- AFNI format: .BRIK and .HEAD
- DICOM files from each run: 1 set / run
- DICOM files anatomical scan: 1 set
  - Use AFNI commands to do this
  - dicom_datacheck



  - OutBrick_r1+orig

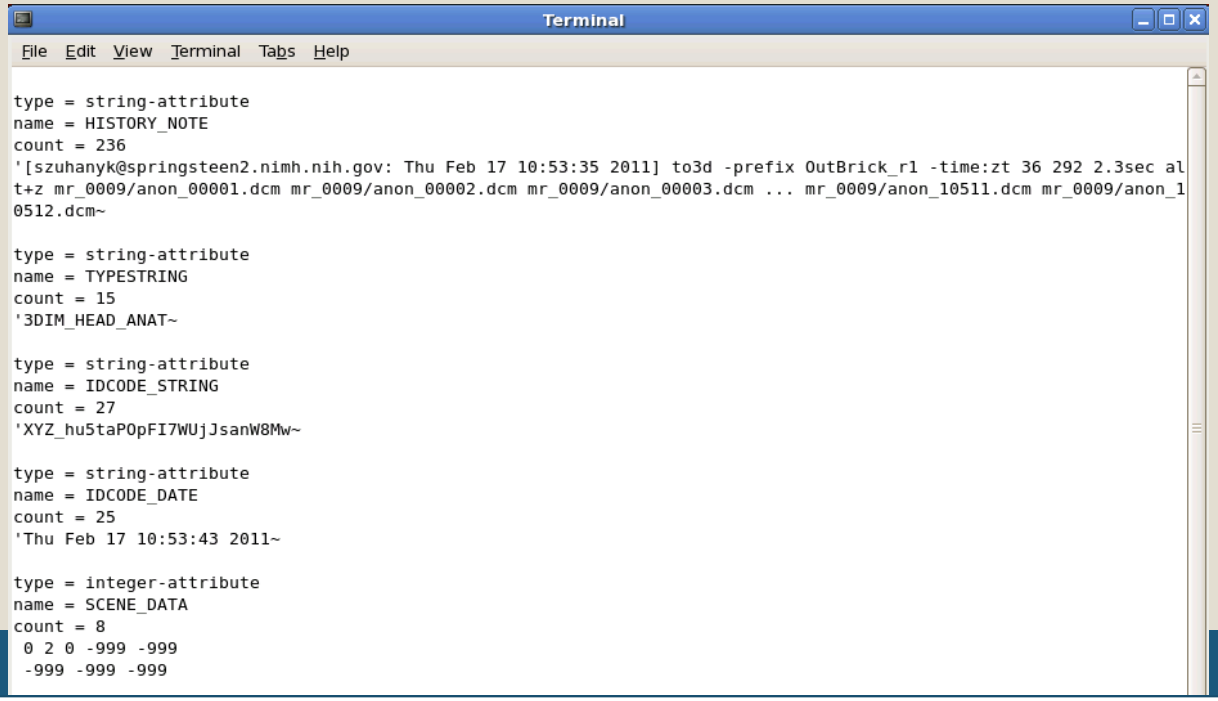
Information about your data…

- 3dinfo….



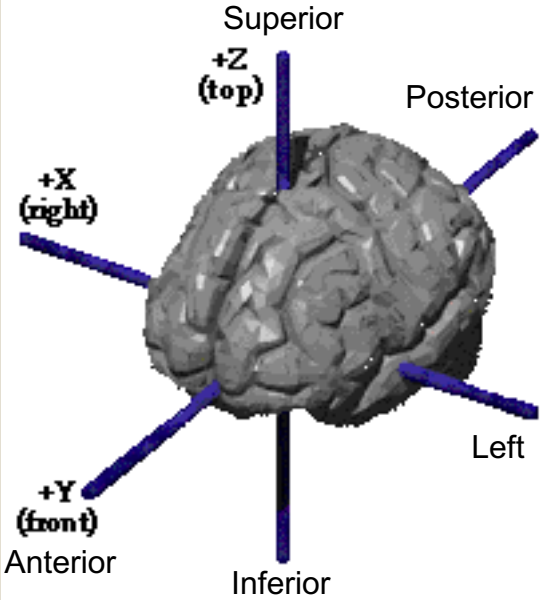
Information about your data…

- BRIK
  - File that contains data
- HEAD
  - Text file that contains attributes *about* the data

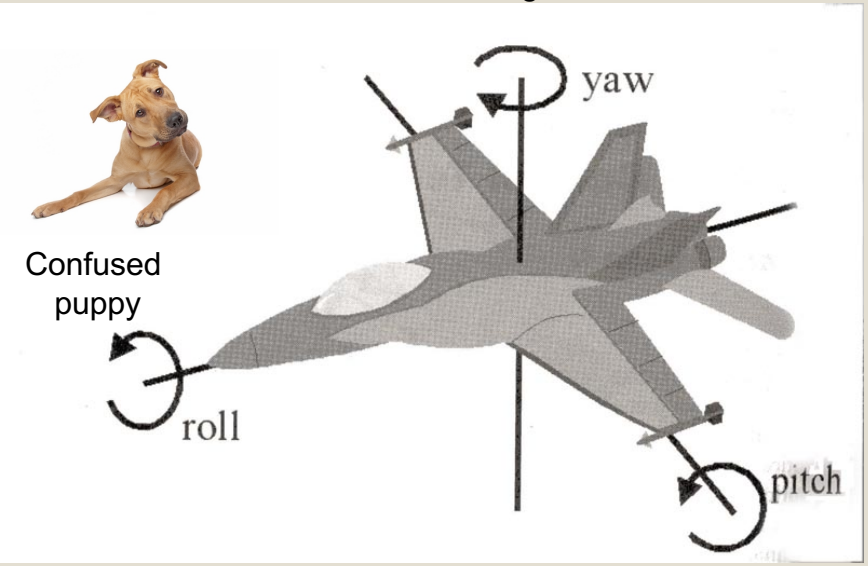


Initial Check of Raw AFNI Data

- Basic idea about motion



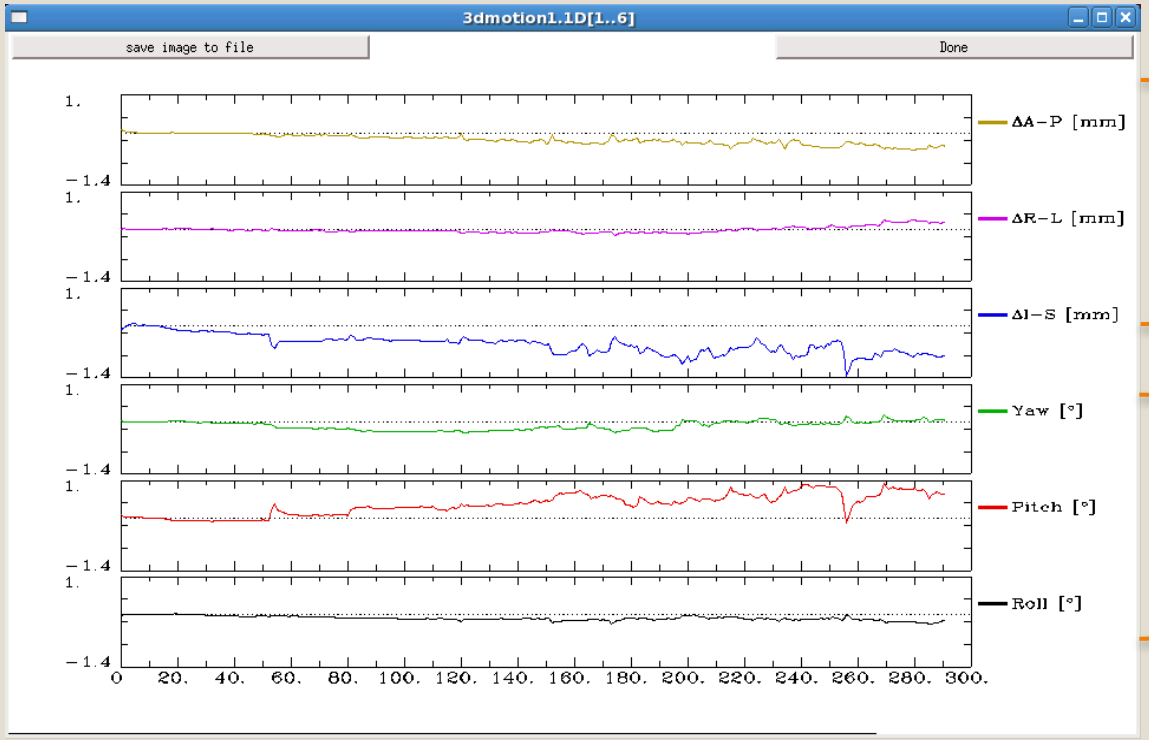
Turning L/R

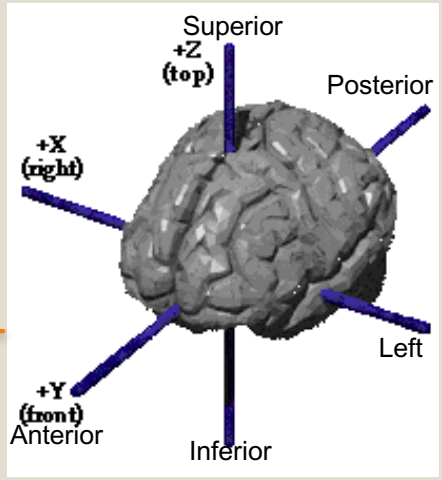


Nodding

Initial Check of Raw AFNI Data

- Basic idea about motion
  - Motion plots (.1D files)





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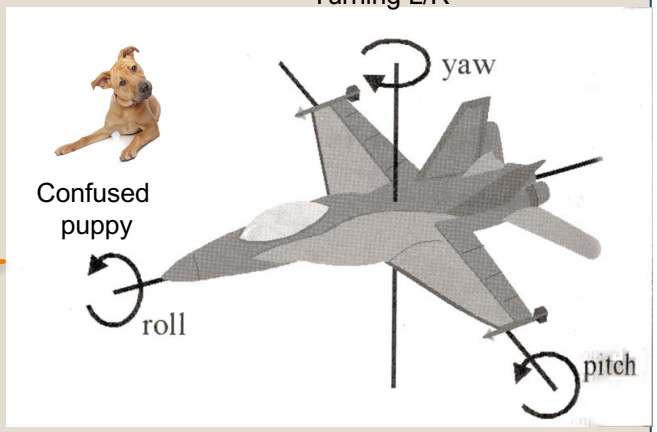
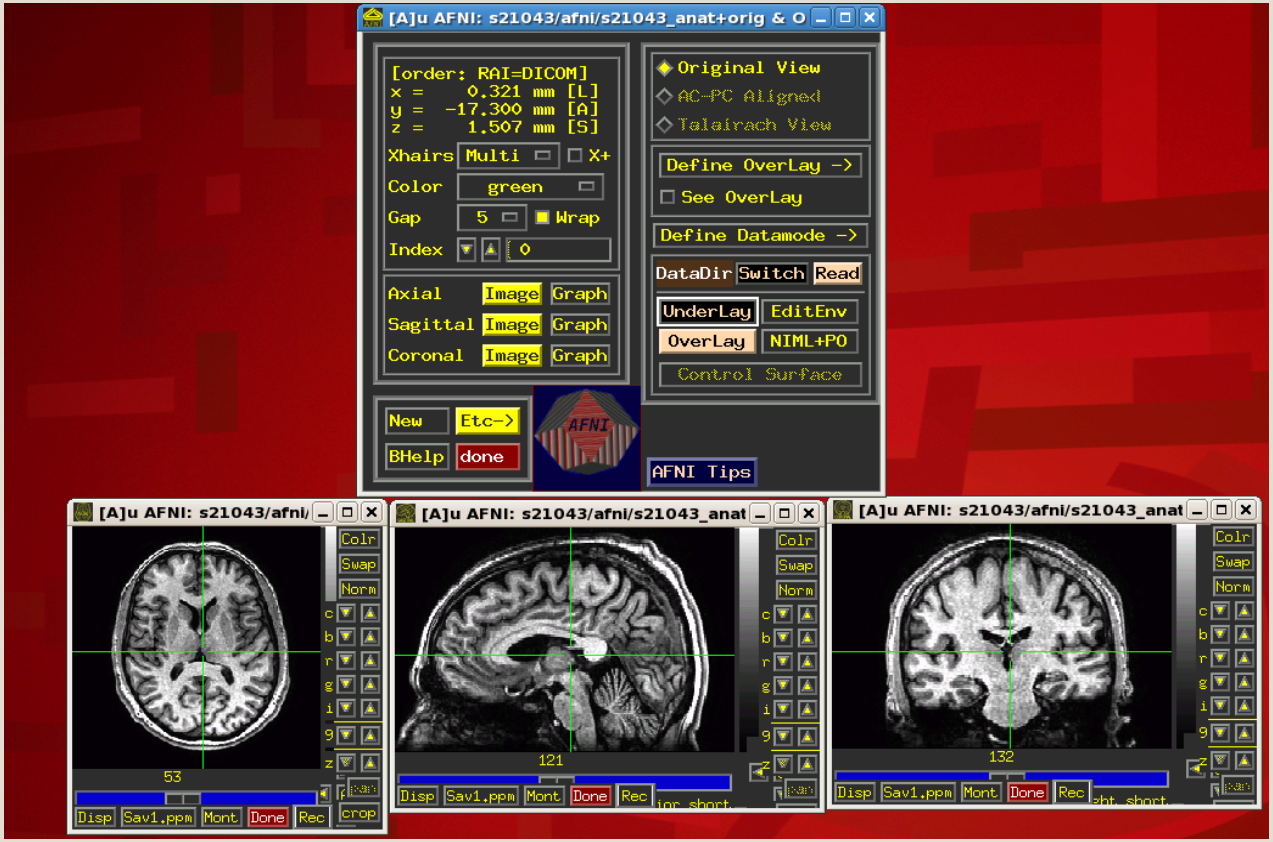


Nodding

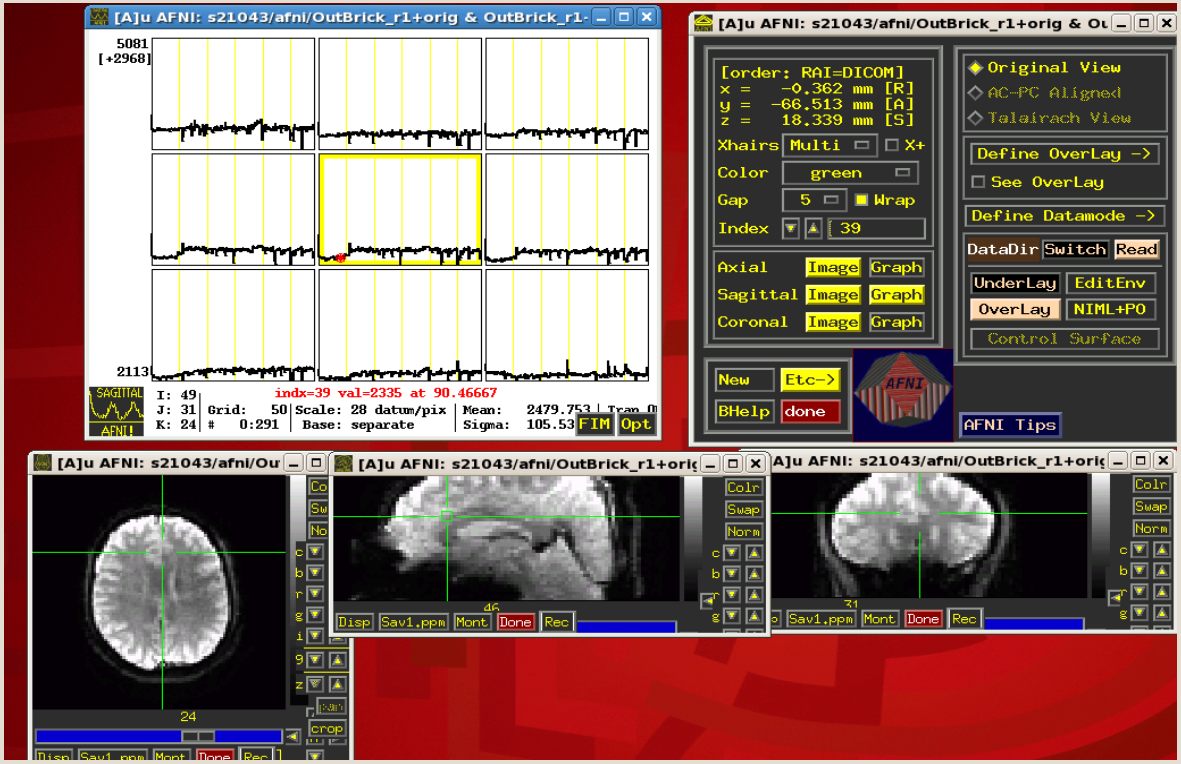
Initial Check of Raw AFNI Data

- Basic idea about quality of anatomical scan



Initial Check of Raw AFNI Data

- Basic idea about quality of functional data
  - EPI (echo-planar imaging) data

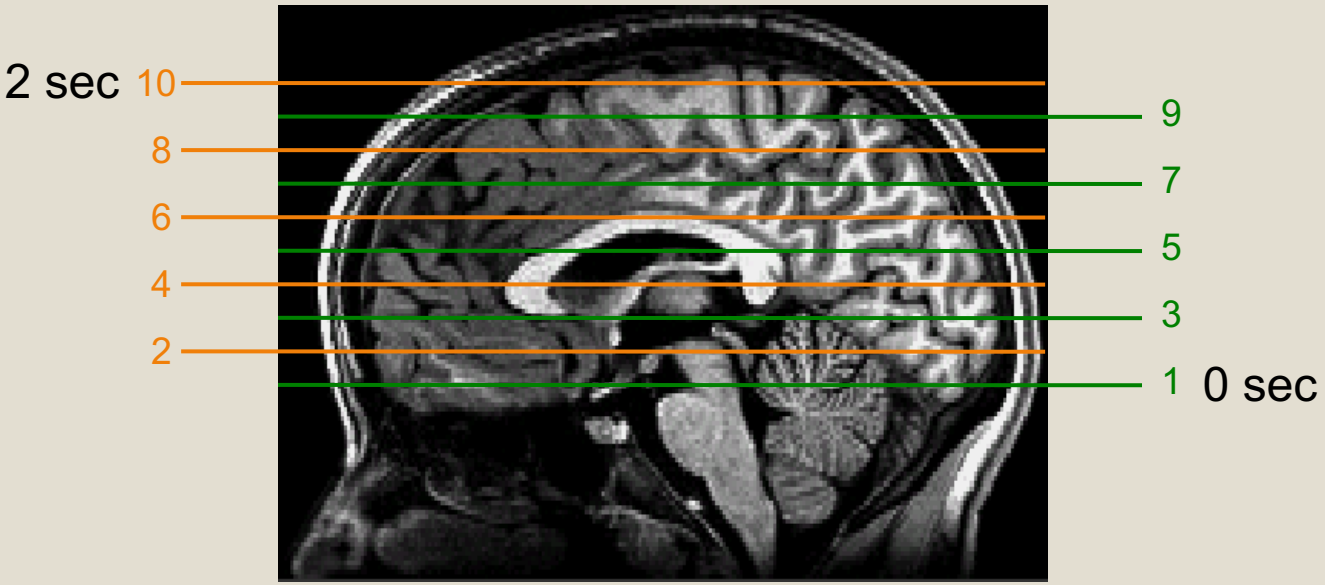


Preprocessing

- Choice of parameters is often subjective
- There is no “right” answer, but some are righter than others…
- For AFNI, specified with afni_proc.py
- Basic preprocessing steps (“blocks” in AFNI)
  - Slice timing correction (3dTshift)
  - Align EPI to anatomical scan (align_epi_anat.py)
  - Warp data into standard space (done manually or @auto_tlrc)
  - Volume registration (volreg)
  - Spatial smoothing by blurring (blur)
  - Scaling

Slice Timing Correction

- Shifts start time of each slice to have the same temporal origin (e.g., 0 sec)
- Allows more straightforward analysis of event-related studies



Align EPI to Anatomical Scan

- Aligns the two datasets in space
- Works best when data are in similar space
  - This is why you determine if the anatomical was collected before or after the EPI
- Computes the alignment between EPI and anatomical scans
  - Transformation matrix
- Applies the transformation matrix to anatomical scan
  - Anatomical is now in the same space as EPI data

Warp Data Into Standard Space

- Everyone has a different brain
- For group analyses, everyone's brain needs to standardized
- Spatially warp brains into standard space
  - Talairach-Tournoux Atlas Space
  - Space of a specific, single subject (TT_N27+tlrc)
- Warping is applied to EPI and anatomical data
  - Generates files with +tlrc suffix

Volume Registration

- Register (align) all EPI volumes
  - Align them so they are the same across all runs, different scan days, etc.
- Think of each EPI volume as a piece of paper
  - These pieces of paper are in a messy stack
  - They are messy because of movement
    - The subject was in one position for one volume, then another position for next volume
  - They are messy because of repositioning across scans
    - The subject was placed in a slightly different spot for each scan

Volume Registration (cont'd)

- Volume registration does a good job of correcting for motion correction by straightening up this stack
- If some volumes are too far away from the rest of the stack, registration may fail
  - Eliminate subject because they moved too great of a distance
- There is no way to correct for motion that occurs within a TR – that volume will be noisy
  - Censor TRs with too much *within* TR motion
- How define too much motion? A difficult decision to make…

Spatial Smoothing by Blurring

- Helps eliminate noise
- Helps further normalize brains so they are more similar to one another

Scaling

- Converts activation map to % signal change
  - Everyone on the same “scale”
- Allows for pooling of subjects for group analyses

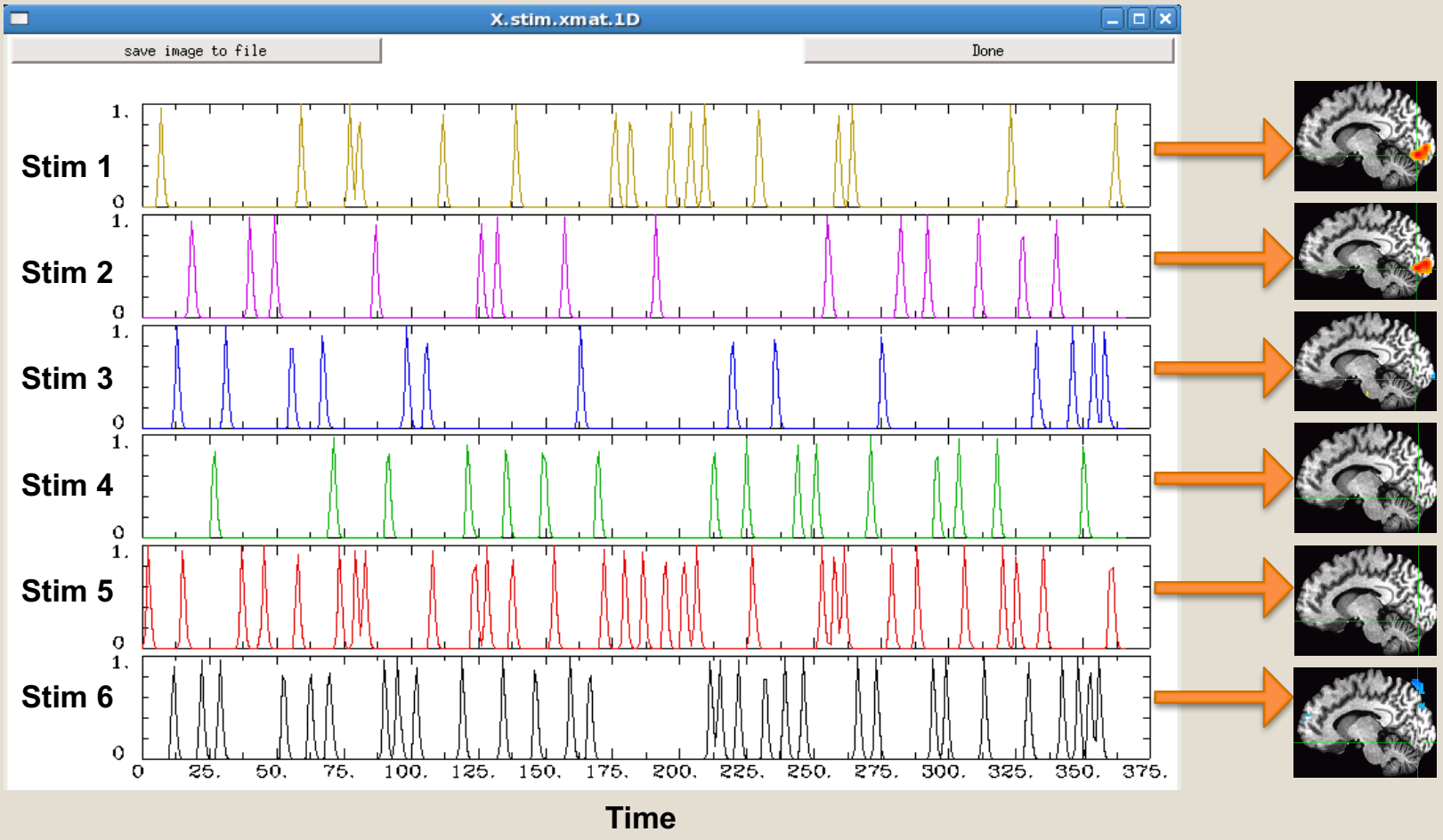
Model Subject's Data

- After pre-processing all EPI data are in a single set of BRIK and HEAD files, typically within a directory called: **sdan.results**
  - pb04.sdan.r01.scale+tlrc.BRIK
  - pb04.sdan.r01.scale+tlrc.HEAD
- Obtain onset times for each type (class) of stimulus from the subject's Edat file
  - Typically with Excel, SPSS, Matlab, TCL
  - Each type of stimulus is parsed into its own .txt file
  - Each .txt file has a row of timing information for each run the subject completed

Model Subject's Data (cont'd)

- Model (deconvolve, regress) the EPI data by binning the subject's brain activity by stimulus type (AKA: class type, event type)
  - We know what brain activity is associated with each stimulus type from the onset time files

Model Subject's Data (cont'd)

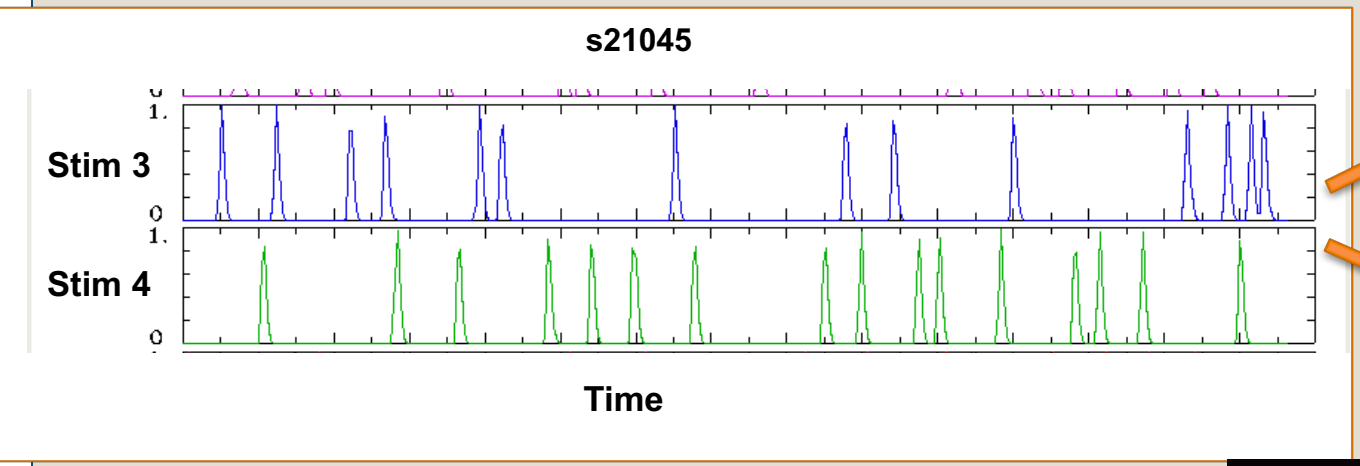


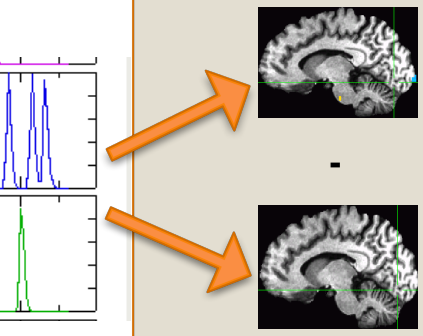
Individual Level Analysis

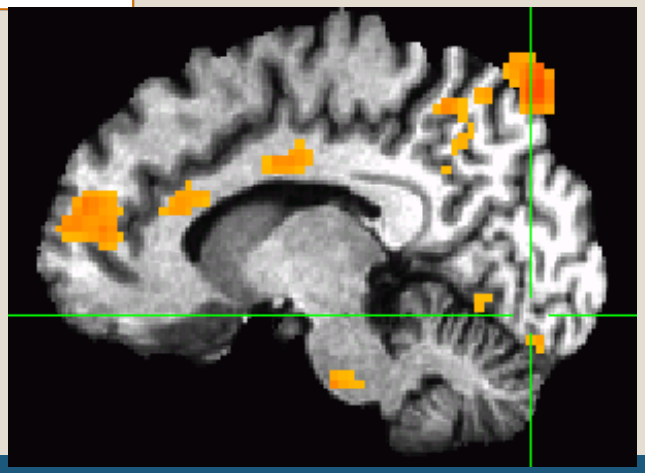
- AKA first level analysis
- Now that we've binned data by stimulus type we can generate contrasts for that subject:

Individual Level Analysis (cont'd)

- Is there greater activity for Stim 3 vs Stim 4?







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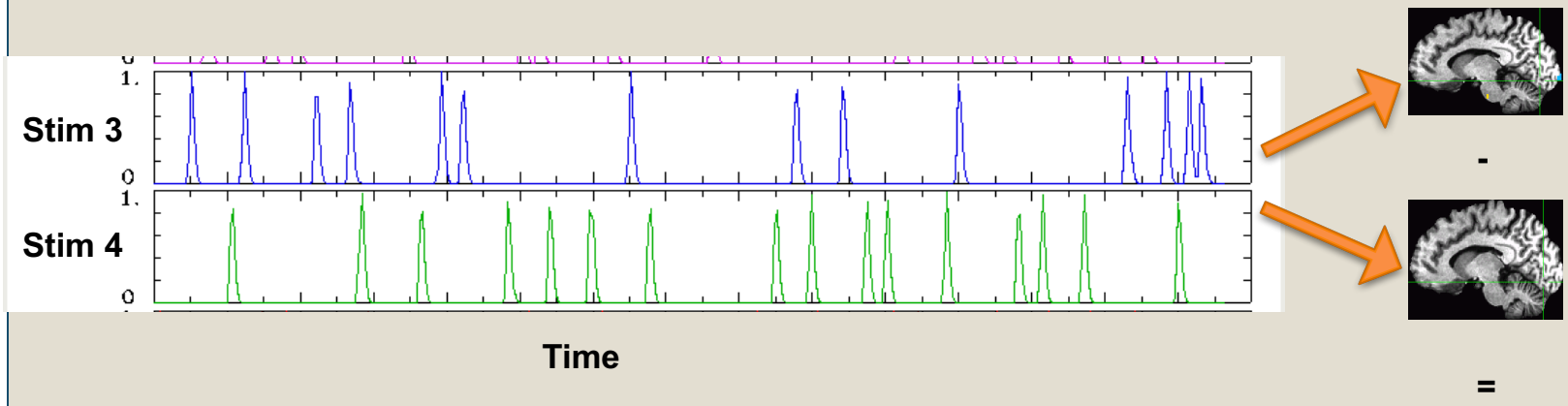

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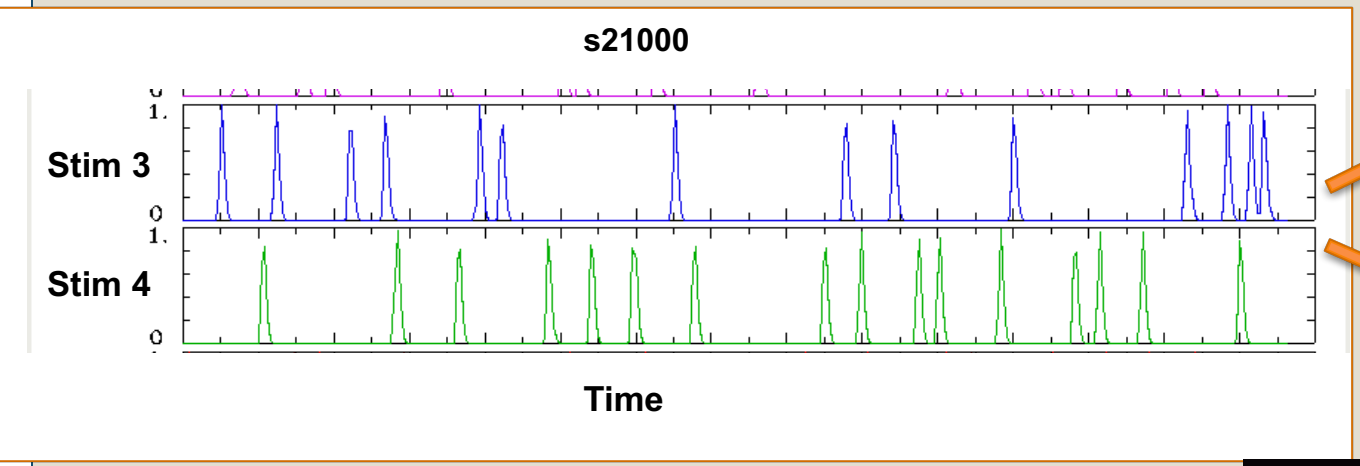

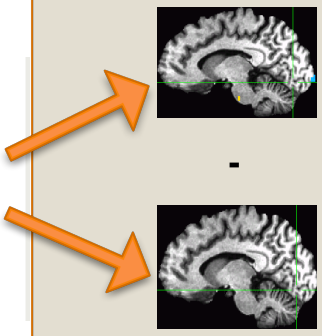

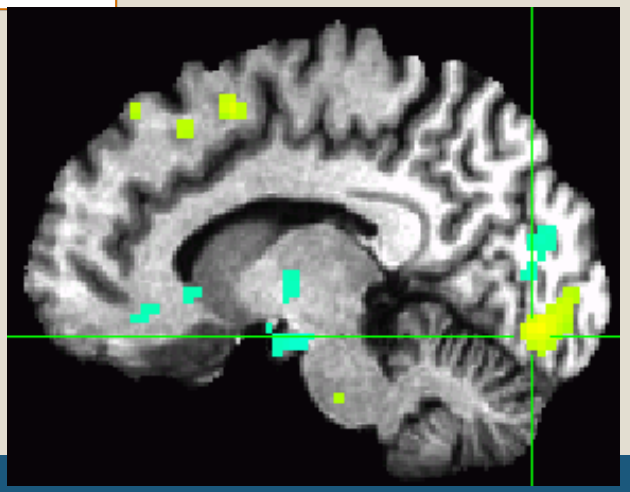

Group Level Analyses

- Do anxious subjects, compared with healthy subjects, have more activity for Stim 3 than Stim 4?