AFNI & SUMA

Concepts, Principles, Demos

Analysis of Functional NeuroImages

by

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AFNI User

AFNI is a research tool.

Clinical uses are not supported or advised.

http://afni.nimh.nih.gov/afni

Some Goals of FMRI Analyses

- **Task-based experiments**
  - **Per subject:** estimate amplitude of BOLD response to each different type of stimulus
  - Find+model inter-regional correlations between fluctuations in BOLD responses
- **Resting-state experiments**
  - Measure spatial patterns in coherent fluctuations in spontaneous BOLD
- **Group level**
  - Combine and contrast per subject results

pre-processing

Conceptual Basis - 1

- **Time shifting** = pretend get 3D snapshot
- **Despiking** = remove large blips
- **Image Registration** (AKA alignment)
  - intra-EPI time series, and EPI-Structural
- **Blurring in space** = lower resolution :-(*&* less noise :-) *&* more group overlap :-)
- **Masking** = ignore non-brain voxels
- **Scaling** = normalizing data amplitude
  - Makes inter-subject comparisons more valid

Conceptual Basis - 2

- **Time series regression**
  - model of the BOLD response in the data = **H**emodynamic **R**esponse **F**unction ⊗ stimulus timing
  - plus baseline (null hypothesis) model
  - plus physiological noise
  - plus allowing for serial correlation

- **Talairach-ing =** Spatial Normalization
  - Talairach, MNI-152, …
  - affine and nonlinear spatial transformations

Conceptual Basis - 3

- **Group Analyses** = Putting it all together
  - **ANOVA**, **LME**, Meta-Analyses, …
- **Blobs** = Spatial models of activation
  - Assigning statistical significance to blobs
- **Connectivity** = Inter-regional analyses
  - **SEM**, **PPI**, **SVAR**, **DCM**, Granger, …
  - Resting state FMRI (Connectome*!*)
- **Dimensional factorization**
  - Components, such as **PCA**, **ICA**, …

Conceptual Basis - 4

- **Data Formats** = NIfTI-1.x is your friend
- **Software** for FMRI analyses: **open-source*
  - **AFNI***, **BrainVoyager**, **FSL***, **SPM***, **…**
  - Whichever you use, **don't blindly assume** the software works perfectly all the time
- Most important thing I will say today

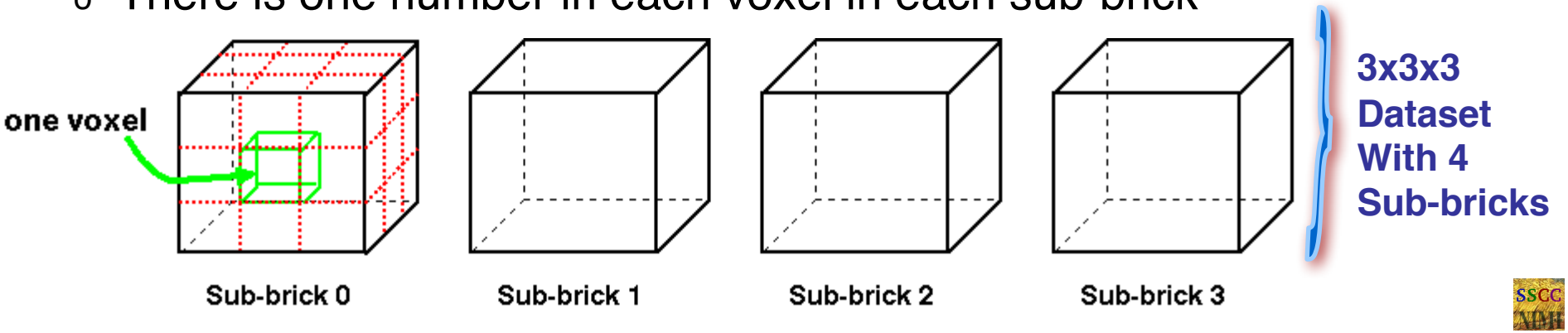
  Understand and check the steps applied to your data!
- 2nd most important: **Is no "best" way to analyze data, just "reasonable" *ways***

AFNI = Analysis of Functional NeuroImages

- Developed to provide an environment for FMRI data analyses
  - And a platform for development of new software tools
- AFNI refers to both the program of that name and the entire package of external programs and plugins (more than 200)
- The Prime Directive in the development of **AFNI**:
  - Allow users to stay close to their data and view/analyze it in many different ways
- SSCC = Scientific Computing and Statistical Core
  - Our mission is help NIH (and beyond) investigators carry out the analyses of their (F)MRI data
  - Development of data analysis methods and putting them into usable and (reasonably) reliable software
  - Consulting and question answering and hand-holding

Fundamental **AFNI** Concept

- Basic unit of data in **AFNI** is the **dataset**
  - A collection of 1 or more 3D arrays of numbers
    - Each entry in the array is in a particular spatial location in a 3D grid (a voxel = 3D pixel)
    - Image datasets: each array holds a collection of slices from the scanner
      - Each number is the signal intensity for that particular voxel
    - Derived datasets: each number is computed from other dataset(s)
      - e.g., each voxel value is a *t*-statistic reporting "activation" significance from an FMRI time series dataset, for that voxel
  - Each 3D array in a dataset is called a sub-brick
    - There is one number in each voxel in each sub-brick



Parts of **AFNI**

- Interactive visualization and analysis — **AFNI** and **SUMA**
  - For looking at data and results
  - **AFNI** is based on 3D volumes = data as gathered by MRI
  - **SUMA** is based on 2D surfaces = models of cortical surfaces
  - A few kinds of analysis can be done by pointing+clicking
- Batch mode programs and scripts
  - Are run by typing commands directly to computer, or by putting commands into a text file (script) and later executing them
  - Most **AFNI** complex analyses are done in batch programs
- Plugins and Plugouts
  - Separate programs that attach themselves to **AFNI** and/or **SUMA** to provide extra capabilities

AFNI & SUMA

Interlude

AFNI Batch Programs

- Many many important capabilities in **AFNI** are **only** available in batch programs
  - A few examples (of more than 100)
- Über-scripts: **afni_proc.py** and **align_epi_anat.py**
  - FMRI time series pre-processing and analysis
  - Driver for 3D image registration tools
- **3dDeconvolve** + **3dREMLfit** = multiple *linear* regression on 3D+time datasets; fits each voxel's time series to activation model, tests these fits for significance (**3dNLfim** = nonlinear fitting)
- **3dvolreg** = 3D+time dataset registration, to correct for small subject head movements, and for inter-day head positioning
- **3dANOVA** + **3dLME** + **3dMEMA** = ANOVA/*t*-test group analyses: combining & contrasting datasets in Talairach space
- **3dsvm** = SVM multi-voxel pattern analysis program
- **3dDWItoDT** = compute diffusion tensor from DWI (nonlinearly)

Analysis by Super-Script – by hand

- Script to analyze one imaging run (5 min) of data from one subject [`cd AFNI_data6/afni ; tcsh quick.s1.afni_proc`]

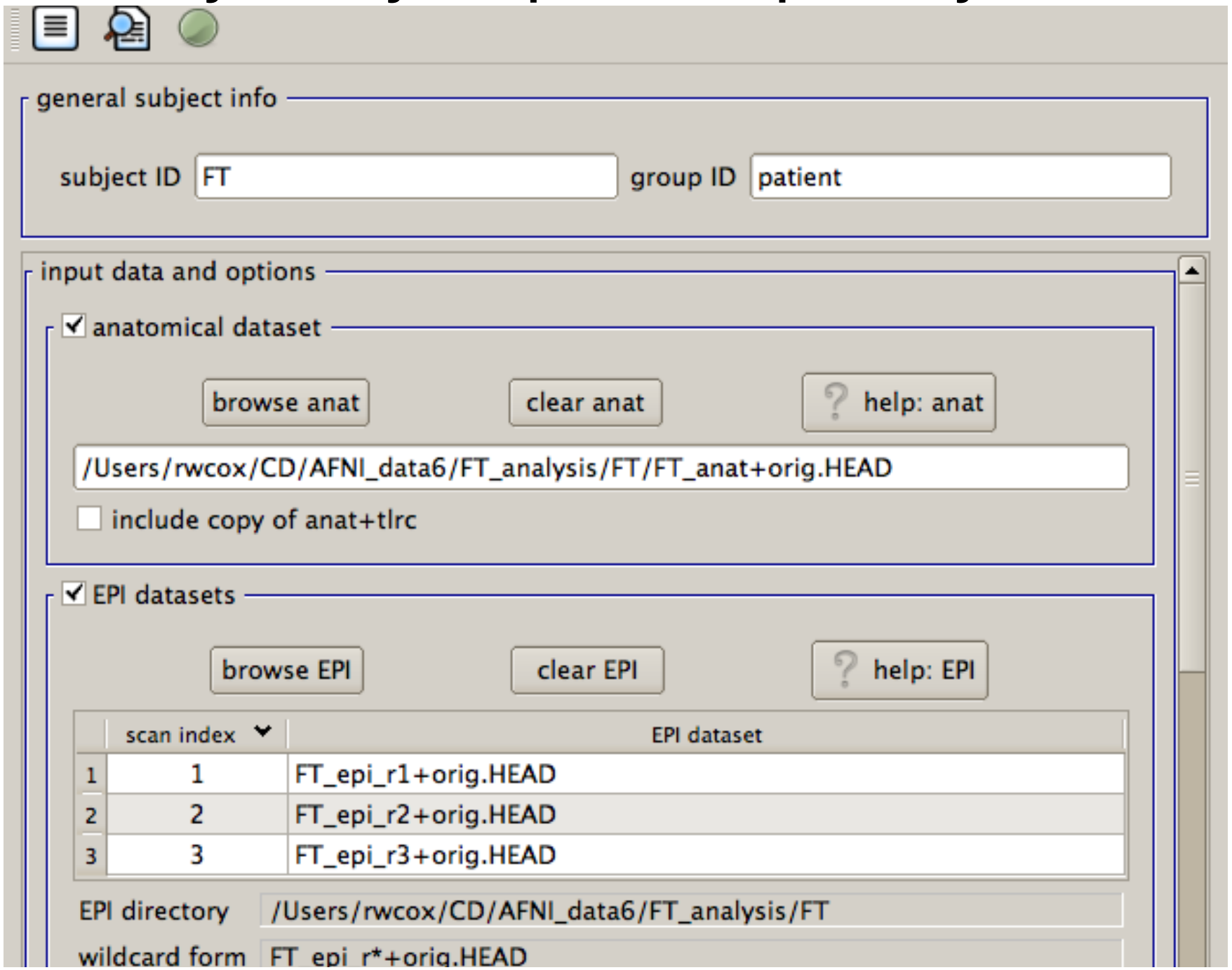
```
afni_proc.py -dsets epi_r1+orig -copy_anat anat+orig \
             -tcat_remove_first_trs 2                \
             -do_block align                         \
             -regress_stim_times quick.r1_times.txt  \
             -regress_basis 'BLOCK(20,1)'            \
             -execute
```

- Stimulus timing in file **`quick.r1_times.txt`**

```
0 30 60 90 120 150 180 210 240 270
```

  - 20 s of stimulus per block, starting at the given times
- FMRI data in file **`epi_r1+orig`**
  - Anatomical volume in file **`anat+orig`**
- **Actions**: Align slices in time; align Anat to EPI; motion correct EPI; blur in space; activation analysis (thru time) in each voxel

Analysis by Super-Script – by GUI



FMRI Experiment Design and Analysis

All on one unreadable slide!

- **FMRI experiment design**
  - Event-related, block, hybrid event-block?
  - How many types of stimuli? How many of each type? Timing (intra- & inter-stim)?
  - Will experiment show what you are looking for? (Hint: bench tests)
  - How many subjects do you need? (Hint: the answer does *not* have 1 digit)
- **Time series data analysis** (individual subjects)

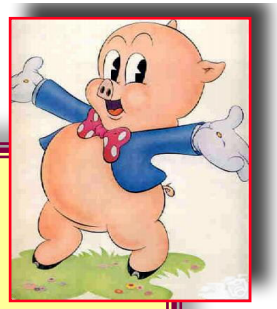
  afni_proc.py & uber_subject.py
  - Assembly of images into AFNI datasets; Visual & automated checks for bad data
  - Registration of time series images (AKA motion correction and EPI-anat alignment)
  - Smoothing & masking of images; Baseline normalization; Censoring bad data
  - Catenation of multiple imaging runs into one big dataset
  - Fit statistical model of stimulus timing+hemodynamic response to time series data
    - Fixed-shape or variable-shape response models [pattern matching in time]
  - Segregation into differentially activated blobs (i.e., what got turned on – or off?)
    - Threshold on statistic + clustering and/or Anatomically-defined ROI analysis
  - Visual examination of maps and fitted time series for validity and meaning
- **Group analysis** (inter-subject)
  - Spatial normalization to Talairach-Tournoux atlas (or something like it; e.g., MNI)
  - Smoothing of fitted parameters
    - Automatic global smoothing + voxel-wise analysis or ROI averaging
  - ANOVA+ to combine and contrast activation magnitudes from the various subjects
  - Visual examination of results (usually followed by confusion)
  - Write paper, argue w/ mentor, submit paper, argue w/ referees, publish paper, …

Getting and Installing **AFNI**

- **AFNI** runs on **Unix** systems: Linux, Sun, Mac OS X
  - Can run under Windows with Cygwin Unix emulator
    - This option is really just for trying it out — not for regular use***!***
- **If you are at the NIH**: SSCC can install **AFNI** and update it on your system(s)
  - You must give us an account with ***ssh*** access
- You can download precompiled binaries from our Website
  - **http://afni.nimh.nih.gov/afni**
  - Also: documentation, message board, humor, data, …
- You can download source code and compile it
- **AFNI** is updated fairly frequently, so it is important to update occasionally
  - We can't help you with old versions***!***

AFNI at the NIH Scanners

- **AFNI** can take 2D (or 3D) images in "realtime" from an external program and assemble them into 3D+time datasets slice-by-slice at each TR – then update the images+graphs
- Jerzy Bodurka (ex-FMRIF) and Vinai Roopchansingh have set up the GE FMRI scanners (3 Ts, 1.5 T, and 7 T) to start **AFNI** automagically when scanning, and send reconstructed images over to the AFNI box as soon as they are available:
  - For immediate display (images and graphs of time series)
  - **Plus**: graphs of estimated subject head movement
  - **Also possible**: feedback to subject in realtime
- Goal is to let you see image data as they are acquired, so that if there are any big problems, you can fix them right away
  - Sample problem: someone typed in the imaging field-of-view (FOV) size wrong (240 cm instead of 24 cm), and so got garbage data, ***but only realized this too late*** (after scanning 8 subjects this way) — ***D'oh!***



That's All, Folks