## Where Do AFNI Datasets Come From?

- Method 1: Create datasets with program to3d [principal subject of this talk]
   \* Inputs are arrays of numbers image files
- Method 2: Realtime input from an external image source program (e.g., directly from the scanner's reconstructed images)
  - $\star$  AFNI program Imon reads image files from GE realtime EPI output, checks them for various errors, sends them into AFNI for display and formatting while acquisition continues
  - $\star$  Sample program <u>rtfeedme</u> can be used to write your own image source program
- Method 3: AFNI programs can read other formats for display and analysis
  - \* ANALYZE<sup>TM</sup> 7.5 format .hdr/.img file pairs
    - $\hookrightarrow$  Used by SPM and many other programs
    - $\hookrightarrow$  Major drawback: lack of spatial orientation and position information in header  $\Longrightarrow$  can be difficult to overlay ANALYZE datasets with other datasets
  - $\star$  MINC format .mnc files
  - $\hookrightarrow \mathsf{Used} \text{ by software from Montreal Neurological Institute} \longrightarrow \mathsf{Montreal Neurolo$
  - $\star$  CTF format <u>.svl</u> files
  - $\hookrightarrow$  Generated from CTF MEG data analysis software package

- $\star$  Dataset stored as columns of ASCII-formatted numbers .1D and .3D files
  - $\hookrightarrow$  Used to store datasets when knowing where the data points are in space isn't important for the analysis
  - $\hookrightarrow$  Example: node-wise analysis of group data on surfaces
  - $\hookrightarrow$  Each column corresponds to one sub-brick
  - $\hookrightarrow$  Each row corresponds to one voxel or node
  - $\hookrightarrow$  .1D files: just columns of numbers
  - $\hookrightarrow$  .3D files: contain an XML header with geometrical information
- \* NIFTI-1 format .hdr/.img file pairs or .nii files
  - $\hookrightarrow$  New format, modified from ANALYZE 7.5 to include more information
  - $\hookrightarrow$  Supposed to be mostly compatible with ANALYZE 7.5 compatible programs
  - ← Format just being finalized now [late 2003]; will be supported by SPM, AFNI, FSL, Brain Voyager
- Method 4: Output of most AFNI programs is AFNI-formatted datasets
  - \_HEAD/.BRIK file pairs
    - ★ AFNI utility programs exist to re-write AFNI-formatted datasets into ANALYZE, MINC, and .3D formats
    - $\star$  In the future, AFNI programs will be able to write out NIFTI-1 .nii formatted datasets directly

## Creating AFNI Datasets with Program to3d

- to3d reads image files each containing 1 or more 2D slices and assembles them into AFNI datasets
- The collection of all the 2D slice data forms the .BRIK file
   ★ An AFNI dataset can contain a single slice
- You must also provide to3d with some auxiliary data (for the .HEAD file):
  - $\star$  Orientation of the slices in space
  - $\star$  Size of the slices or of the voxels
  - ★ Slice offset where is the dataset volume located in space?
  - $\star$  For 3D+time datasets, also need slice timing information
  - $\star$  to3d 'knows' how to get some of this auxiliary information from image file headers for some image file formats:
    - $\hookrightarrow$  ANALYZE 7.5 .hdr/img pairs contain voxel size information
    - $\hookrightarrow$  Siemens <u>.ima</u> image arrays contain voxel size and orientation information
    - $\hookrightarrow$  GE [ ]. files contain voxel size and orientation information
    - → DICOM files contain lots of relevant information
       ▷ Manufacturers' variations on DICOM are frustrating

- to3d runs in two modes:
  - $\star$  Command line mode: you provide all auxiliary information on command line

— Useful to get things done fast, and for putting into scripts

- $\star$  Graphical user interface (GUI) mode: you provide auxiliary information by filling out an on-screen form
  - Useful for explaining concepts, and for AFNI neophytes
- $\bullet$  Sample #1: data from NIH GE 3 Tesla scanner
  - $\star$  Files stored in archive <code>AFNI\_sample\_01.tgz</code>
    - unpack with command gzip -dc AFNI\_sample\_01.tgz | tar xf -
    - unpacks into directory AFNI\_sample\_01/
  - $\star$  Anatomical (SPGR) data  $\Rightarrow$  3D dataset (no time; 1 sub-brick)
    - 124 axial slices in subdirectory SPGR\_anat
  - $\star$  Functional (EPI) time series data  $\Rightarrow$  3D+time dataset (160 sub-bricks)
    - 2880 images (18 coronal slices, 160 reps) in subdirectory EPI\_run1
    - Visual stimulation task: rotating hemifield flashing checkerboard



• Experiment log, taken at scanner:

NIMH-CBC-METHODS FMRI RESEARCH		RUN DATA
ExpCode: ARZS	Subject: •	\$ 8AM.
	7 Am Investigator: Shruti Tech: _ZSS	
Scanner: Coil: Wong/MAI/		
Anat Scan 1       Type:       SPGR/FSE/MPIR/       IR       PSP         Matrix:       256       x       256       #Slices:       124       Plane:       Ag/Cor/Sag         Anat Scan 2       Type:       SPGR/FSE/MPIR/	TE(ms): TR(ms): Flip: NEX:	- Taken last FOV(mm):
	TE(ms):     Z5     TR(ms):     2     Flip:     90     NEX:       54     Thickness(mm)     4     #Slices:     18     First:     696.8	VTE:
Timing: #Reps: Skip#: #C)	/cles:#Conditions/Cycle:#Reps/Condition/Cycl	
	Stimulus File (38, on command Lin, 8xc. Sugard) Response File	T. 2. P
Run# Time Conditions	003/I.019 -> 043/I900	
- ccw	43/901 -> 103/783	- <u>1</u>
Cw	103/784 -> 163/666	
C.w	163/667->223/549 + may have been ~ loce of	Biting scan
	223/550->283/432	
Ccw	283/433-343/315	
ςω;	343/3/6 -> 403/198	
ςω	403 /199 -> 463/081	

• Using to3d to assemble the SPGR dataset:

\*

- \* cd AFNI\_sample\_01/SGPR\_anat change directory, to get at images
- $\star$  1s to see what files are there (should see files I.001 ... I.124)
  - to3d I.\* run to3d, reading in all the image files GUI pops up:

- to3d		• 🗆 🗙
x orientation (across screen) 🔽 🛆 Right-to-Left	x voxel size (mm)	375 × origin (mm) 🔽 🛕 [119.5312]R [left_edge]
y orientation (down screen)	y voxel size (mm)	375 y origin (mm) 🔽 🛕 119.5312 A [top edge]
z orientation (slices $0,1,$ ) $\square$ $\square$ Inferior-to-Superior	z voxel size (mm)	z origin (mm) $\checkmark$ $\checkmark$ 50.6 I [slice 0]
Datum: short [256x256]	Field of view (mm)	■ x axis centered ■ y axis centered
View: 🔽 🖾 Original View 🔷 irregular		🗖 z axis centered
Copy geometry of this dataset	Anatomy parent is this dataset	
Type of data in the images 🔽 🛆 3DIM_HEAD_ANAT	Type of anatomy in the images	Spoiled GRASS Byte Swap[2] button help
Field below not applicable		View Images
Session direct. for 3D Datasets	Prefix for 3D Dataset file	Save Dataset

- $\hookrightarrow$  to3d understands GE I.\* files, and so has filled in some of the GUI
- $\hookrightarrow$  Note: z origin field 50.6 l corresponds to experiment log

- ★ To check images that were just input, click the View Images button in the to3d form
  - → Window is the same as the AFNI image viewer
  - $\hookrightarrow$  Slider below image lets you move between slices



- $\star$  In this example, to 3d has all the information needed from the I.\* headers
  - → All you need to do is supply the dataset Prefix, then press Save Dataset
    ▷ look at the bottom right of the to3d GUI for these controls
    - $\triangleright$  I suggest the prefix anat
  - $\hookrightarrow$  Dataset files anat+orig.HEAD and anat+orig.BRIK will be created
  - $\hookrightarrow$  Then press quit button twice to exit to3d GUI
- \* Script version (no GUI): to3d -prefix spgr I.\* would create a dataset with no user intervention
- \* Later: will give more complicated example of assembling data from 'naked' image files, where no header information is available

- Using to3d to assemble the EPI 3D+time dataset:
  - $\star$  cd ../EPI\_run1 change directory, to get at images
  - $\star$  1s to see what files are there (should see files I.00001 ... I.02880)
  - $\star$  We do not just do to3d I.\* to create a 3D+time dataset
  - ★ For historical reasons, the time-axis information must be given on the to3d command line
  - $\hookrightarrow$  Cannot be modified from GUI
  - **\star** Command line: to3d <u>-time:zt 18 160 0 alt+z</u> I.\*
  - $\star$  <u>-time:zt</u> means slices will be presented in order of space (z) then time (t)
  - $\hookrightarrow$  This is the usual way slices are ordered, but <u>-time:tz</u> is needed at some sites
  - → If in doubt, do to3d I.\* or aiv I.\*, use viewer to look at slices and see their order [aiv=AFNI Image Viewer program]
  - $\star$  <u>18</u> <u>160</u> means that there will be 18 slices in z, 160 in t (2880 total)
  - $\star$  <u>O</u> means that the TR for volume acquisition will be read from the image headers
  - $\hookrightarrow$  If not available, could put <u>2s</u> instead of this <u>0</u>
  - $\star$  <u>alt+z</u> means that the slices are gathered in alternating order in the +z direction
  - $\hookrightarrow$  Most EPI acquisitions are really 2D multislice, spread out through time
  - $\hookrightarrow$  AFNI header can contain information about slice timing offsets
  - $\hookrightarrow$  Other possible modes: <u>zero</u> (for 3D), <u>@filename</u> (to specify each slice)

🗝 to3d			• 🗆 🕺
x orientation (across screen)	x voxel size (nnn)	x origin (mm)	[118,125]R
y orientation (down screen)	r y voxel size (mm) 🛛 🛕 3.75	y origin (mm) 🔽 🛕	118.125 5
z orientation (slices 0,1,)	or z voxel size (mm) 🔽 🛆 4	z origin (mm) [slice 0]	96.8 P
Datum: short [64x64]	Field of view (mm)	a second a s	s centered s centered
View: 🔽 🖾 Original View 🔷 irregul	ar TR = 2.000 (s) NR = 160 Nz = 18		s centered
Copy geometry of this dataset	Anatomy parent is this dataset		
Type of data 3DIM_HEAD_ANAT in the images	Type of anatomy 🔽 🔼 E in the images		Byte Swap[2] button help
Field below not applicable			View Images
Session direct.	Prefix for 3D		Save Dataset
	Dataset file		<pre>- help ************************************</pre>
- AFNI - Dime PS->file ->printer Dome			<pre>* time series * * outliers *</pre>
700. 600. 600. 100. 0 0 10. 20. 30. 40. 50. 60. 70. 60. 90. 100. 110. 120. 130. 140. 150. 160. Sub-brick Index		7 8 9 10 11 19 20 21 22 23 37 141 142 146 148 156 157 158 159 t for possible corruptio program 3dToutcount. me series may be due to ion equilibration effect vement, scanner problems me series look irregular dataset   1dplot -stdin et 'outnam' that marks	

- $\star$  Outliers are data values that are very different from other values in the same time series
  - $\hookrightarrow$  to3d reports sub-bricks (time points) that have a lot of outliers
  - → You should use AFNI to look at these time points to see if there are major problems (e.g., head motion, scanner artifacts)
  - $\hookrightarrow to 3d \ \texttt{-skip\_outliers} \ option \ \texttt{lets} \ you \ \texttt{skip} \ \texttt{outlier} \ \texttt{detection} \ \texttt{step}$
  - → Utility program <u>3dToutcount</u> can also report outliers and can even make a dataset with the 'outlier-ness' of each voxel value



 $\star$  Again, fields in GUI were filled in from data in the I.\* headers



★ Coronal slices; will work with SPGR axials in AFNI
← Programs <u>3dresample</u> and <u>3daxialize</u> can rewrite datasets in new orientations
★ Note slice thickness and slice offset ("z origin")
← Values match experiment log (that's good)
★ Time information is displayed in GUI, but not editable
★ Have set "Type of anatomy" to "Echo Planar"
← Just acts as a reminder to user (not used elsewhere)

\* Script version: to3d -time:zt 18 160 0 alt+z -prefix epi I.\*

- \* Program <u>3drefit</u> can be used to change some header items in an AFNI dataset after it is created
- $\hookrightarrow$  Example: 3drefit -TR 1s epi+orig will change the TR of the dataset to 1 second

## Assembling 'Naked' Images into AFNI Datasets

- 'Naked' image  $\equiv$  image file without header data that AFNI understands
- User must supply geometrical information to to3d

 $\star$  This is when the written experiment log is critical!

- The <u>SPGR\_naked</u> directory contains the same SPGR images as before, but stripped of all header information
  - $\star$  Each file has 131072 bytes = 256 imes 256 16-bit integers ('shorts')

$\star$ cd SPGR_naked, then to3d N.*					
		to3d 🗉			
	x orientation (across screen) 🔽 🛕 Right-to-Left	x voxel size (num) 🔽 🛕 (0.9375) x origin (num) 🔽 🛕 119.5312 R			
	y orientation 🔽 📐 Right-to-Left (down screen)	y voxel size (mm) 🔽 🛕 (0.9375 y origin (mm) 💟 🛕 119.5312 R			
	z orientation (slices 0,1,)	2 voxel size (mm) 🔽 🛕 (0.9375) 2 origin (mm) 💟 🛕 57.65625 R [slice 0]			
	Datum: short [256x256] <ul> <li>◆ cubical</li> <li>◆ square</li> <li>◆ irregular</li> </ul>	Field of 240 view (mm) 240 y axis centered z axis centered view common 240			
	Copy geometry of this dataset	Anatomy parent is this dataset			
	Type of data in the images DIM_HEAD_ANAT Field below not applicable	T i to3d WARNING: 602237 negative voxels (7.41081%) were read in images of shorts. It is possible the input images need byte-swapping.			
	Session direct. for 3D Datasets	** I recommend that you View Images. **			







SGI/Sun/etc. computers

- On Linux/Intel computers: the peculiar appearance of the image shows that something is wrong:
  - **\*** MR images from scanners are stored as <u>shorts</u>: 2 bytes per number
  - $\star$  Like a 2 digit decimal number: "93" means "9 imes10+3"
    - $\hookrightarrow$  By universal custom, we write the "9" first
    - $\hookrightarrow$  Could also write the same number as "39" (if we had a different custom)
  - $\star$  Customs for computers are not so universal
    - $\hookrightarrow$  Sun and SGI systems store 2 byte numbers in reverse order from Intel
    - $\hookrightarrow$  Result is that numbers are mangled (and some show up as negative)
    - $\hookrightarrow$  Solution: press to3d's Byte Swap[2] button, and images are fixed!

• Same to3d control panel (without the negative voxel warning):

		to3d			1
x orientation (across screen)	ft	x voxel size (mm)	0.9375 ×	origin (mm) left edge]	V 🛕 119,5312 R
y orientation (down screen) 🔽 🛆 Right-to-Lef	ft	y voxel size (mm)	0.9375 y	origin (mm) top edge]	V 🛕 119,5312 R
z orientation (slices 0,1,)	ft	z voxel size (nm)	0.9375 <sup>2</sup>	origin (mm) slice ≬]	V 🛕 57,65625 R
Datume chart	cubical square	Field of view (mm)	240		x axis centered  y axis centered
View: 🔽 🛆 Original View 🔷	irregular				z axis centered
Copy geometry of this dataset		Anatomy parent is this dataset	Ĭ		
Type of data in the images	_anat	Type of anatomy in the images	Spoi	led GRASS	Byte Swap[2] button help
Field below not applicable					View Images
		NO.CONTRACTOR ADDRESS			Save Dataset
Session direct. for 3D Datasets		Prefix for 3D Dataset file	Ĭ		quit

- Above the double line: must fill out 3 types of geometry information:
  - $\star$  Left column: orientation of the dataset axes
  - $\star$  Middle column: size of the dataset images or voxels
  - $\star$  Right column: offset of the first slice



- Screen shot above shows correct orientation for this dataset
  - $\star$  Use the image viewing window to judge how images are laid out
  - $\star$  Click the arrows to scroll through the 6 possible options for each orientation to set the correct values
  - $\star$  "x orientation" of dataset is across the screen (left to right)
  - $\hookrightarrow \mathsf{Must}\ \underline{\mathsf{know}}\ \mathsf{subject's}\ \mathsf{right}\ \mathsf{from}\ \mathsf{left}$
  - $\star$  "y orientation" of dataset is down the screen
  - $\star$  "z orientation" of dataset is in increasing slice index order
  - $\hookrightarrow$  determine this by using the slider at the bottom of image window



- To set dataset geometrical size/location, experiment log sheet is essential
- $\bullet$  Screen shot above shows setting slice thickness to 1.1 mm
  - \* Default Field of view (FOV) of 240 mm is correct for these images
  - $\star$  Default voxel geometry of "cubical" is incorrect
  - ★ Must set geometry to "square" (x size = y size, z size different)
  - $\star$  Then set "z voxel size" to correct value (by typing in box)
- Screen shot shows setting center of first slice to 50.6 mm in Inferior (I) direction
  - $\star$  Default is that slices are centered in the magnet
  - $\star$  Probably not the case in the z direction
  - $\star$  Click "z axis centered" off
  - $\star$  Enter offset (here, 50.6 mm) into the "z origin" box

- Final required steps:
  - ★ Enter prefix for new dataset into "Prefix" text box at lower right of to3d control window
    - $\hookrightarrow$  Choosing a good prefix is important for keeping datasets organized
  - $\star$  Press "Save Dataset" button
  - $\star$  Press "quit" (twice) to exit to3d
  - $\star$  The new dataset files should show up when you use command 1s
  - $\star$  You might want to move them to some other directory
  - $\stackrel{\mbox{\sc mv }*+\mbox{\sc orig. }* \ ../\mbox{\afni}}{\mbox{\low level above}} \ to \ move \ datasets \ to \ directory \ named \ afni, \ one \ level \ above$
  - $\hookrightarrow$  this directory was created when you unpacked AFNI\_sample\_01.tgz; it contains pre-made AFNI datasets from EPI and SPGR images

- Geometry parent lets you copy the geometry data from a pre-existing dataset and apply it to the dataset now under construction
  - \* Enter name of pre-existing dataset into the Copy geometry of this dataset field
  - $\hookrightarrow$  If in another directory, must include that in filename
  - ★ When you press 'Enter' or move the cursor from the text-entry field, to3d tries to read geometry parent dataset header
  - $\star$  If geometry parent has same spatial dimensions as current dataset, all geometry fields will be filled out
    - $\hookrightarrow$  Does not affect the time fields, which must still be set using <u>-time:zt</u> or -time:tz on the command line
  - $\star$  Geometry parent very useful when constructing multiple EPI datasets from a single scanning session
- Using to3d in command line mode
  - $\star$  You can specify all needed inputs to to3d using command line options
    - $\hookrightarrow$  For a full list of options, type to3d -help
  - $\star$  If enough information is present on command line to define a dataset, then the GUI will not be opened, and the dataset will be written to disk
  - $\hookrightarrow$  If the command line is incomplete, then the GUI will be opened

★ For the SPGR dataset example:

to3d -xFOV 120R-L -yFOV 120A-P -zSLAB 50.6I-84.7S

-prefix anat -2swap -spgr N.\*

(this is all on one command line)

- $\hookrightarrow$  –xFOV 120R–L says that the x axis of the images runs from 120 mm Right to 120 mm Left
- $\hookrightarrow$  <u>-yFOV</u> 120A-P says that the y axis of the images runs from 120 mm Anterior to 120 mm Posterior
- $\hookrightarrow$  <u>-zSLAB 50.6I-84.7S</u> says that the z axis of the slices runs from 50.6 mm Inferior to 84.7 mm Superior
  - ▷ <u>FOV</u> means the distances apply from edge-to-edge of the images in that direction (x and y, in most cases)
  - ▷ <u>SLAB</u> means that the distances apply to the centers of the outermost voxels (z=slice direction, in most cases)
- $\hookrightarrow$  <u>-prefix anat</u> gives the prefix for output dataset filenames (in this case, anat+orig.HEAD and anat+orig.BRIK)
- $\hookrightarrow$  -2swap means to byte-swap the images while reading them
- $\hookrightarrow \texttt{spgr}$  means to label this data as being of SPGR type
- $\hookrightarrow$  N.\*, as before, means to read the images from the files whose names start with the string "N." and end with anything ("\*" is a wildcard)

\* For the EPI dataset example (if image files were 'naked'):

to3d -xFOV 120R-L -yFOV 120S-I -zSLAB 96.8P-28.8P

-time:zt 18 160 2000 alt+z -prefix epirun1 -2swap -epan I.\*

(this is all on one command line)

 $\hookrightarrow$  Options (with their arguments) can appear in any order

 $\hookrightarrow$  Input image filenames always appear last

• Once you get used to it, command line usage for to3d is more useful than the GUI

 $\star$  Usually need to create many datasets at once

- $\star$  Can put commands in a script file and execute them
- $\star$  Then edit that file to change a few things, and run it again
- ★ Just create the file with your favorite Unix text editor (emacs, nedit, vi), typing each command on a separate line
- $\hookrightarrow$  Long commands can be split across multiple lines by ending all but the last line with the "\" character
- $\hookrightarrow$  There <u>must not</u> be a blank after the "\" !!!
- \* You can execute a script file by typing a command like <u>source filename</u>, which just means to read commands from "filename"
- $\star$  As time goes on, you build up a set of scripts that automate various tasks for you, and ensure you do things the same way each time