Where do AFNI Datasets Come From?

- Method 1: Create datasets with program **to3d** [principal subject of this talk]
  - ★ Input files are arrays of numbers --- i.e., image files
- Method 2: Realtime input from an external image source program (e.g., directly from scanner's reconstructed images)
  - ★ AFNI programs like **Imon**(for I-files) and **Dimon** (for DICOM files) read image files from GE realtime EPI output, checks them for various errors, sends them into AFNI for display and formatting --- while acquisition continues
  - ★ Sample program **rtfeedme** can be used to write your own image source program
- Method 3: AFNI programs can read other formats for display and analysis
  - ★ ANALYZE™ 7.5 format ⇒ **.hdr/.img** file pairs
    - ➥ Used by SPM and many other programs
    - ➥ Major drawback: lack of spatial orientation and position information in header
      - ➪ Can be difficult to overlay ANALYZE datasets with other datasets
  - ★ MINC format ⇒ **.mnc** files
    - ➥ Used by software from Montreal Neurological Institute --- mnitools
  - ★ CTF format ⇒ **.svl** files
    - ➥ Generated from CTF MEG data analysis software package

- ⋆ Dataset stored as columns of ASCII-formatted numbers ⇒ **`.1D`** and **`.3D`** files
  - ➥ Used to store datasets when knowing where the data points are in space isn't important for the analysis
  - ➥ Example: node-wise analysis of group data on surfaces
  - ➥ Each column corresponds to one sub-brick
  - ➥ Each row corresponds to one voxel or node
  - ➥ .1D files: just columns of numbers
  - ➥ .3D files: contain an XML header with geometrical information
- ⋆ NIfTI-1 format ⇒ **`.hdr/.img`** file pairs or **`.nii`** files
  - ➥ New format, modified from ANALYZE 7.5 compatible programs
  - ➥ Supposed to be mostly compatible with ANALYZE 7.5 compatible programs
  - ➥ Format finalized 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
  - ⋆ 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):
  - ★ Orientation of slices in space
  - ★ Size of slices or of the voxels
  - ★ Slice offset -- where is the dataset volume located in space?
  - ★ For 3D+time datasets, you also need slice timing information
  - ★ **`to3d`** 'knows' how to get some of this auxiliary information from image file headers for some image file formats:
    - ➥ ANALYZE 7.5 **`.hdr/.img`** pairs contain voxel size information
    - ➥ Siemens **`.ima`** Files contain voxel size and orientation information
    - ➥ GE **`I`**. Files contain voxel size and orientation information
    - ➥ DICOM **`.dcm`** Files contain lots of relevant information
      - ➪ But manufacturers' variations on DICOM are frustrating

- **`to3d`** runs in two modes:
  - ⋆ *Command line mode:* you provide all auxiliary information on command line
  - ⋆ *Graphical interface (GUI) mode:* you provide auxiliary information by filling out an on-screen form
- **`Sample Study:`** data from NIH GE 3Tesla Scanner
  - ⋆ Files stored in directory **`AFNI_data3/`**
  - ⋆ Anatomical (SPGR) data ⇒ 3D dataset (no time; 1 sub-brick)
    - ➥124 axial slices in subdirectory **`MPRAGE_anat/`**
  - ⋆ Functional (EPI) time series data ⇒ 3D+time dataset (67 sub-bricks/time pts)
    - ➥2278 images (34 axial slices, 67 reps) in subdirectory **`EPI_run1/`**

- Cognitive Task: Subjects see photographs of two people interacting. The mode of communication falls in one of 3 categories: telephone, email, or face-to-face. The affect (emotion) portrayed is either negative, positive, or neutral in nature.
  - ★ Factor A: CATEGORY - (1) Telephone, (2) E-mail, (3) Face-to-Face
  - ★ Factor B: AFFECT - (1) Negative, (2) Positive, (3) Neutral

AFFECT

CATEGORY	Negative	Positive	Neutral
Telephone	"Your project is lame, just like you!"	"You are the best project leader!"	"You finished the project."
E-mail	Ugh, your hair is hideous!	Your new haircut looks awesome!	You got a haircut.
Face-to-Face	"I curse the day I met you!"	"I feel lucky to have you in my life."	"I know who you are."

- Experiment log, taken at scanner:

NIMH-LBC--Methods FMRI Research **RUN DATA**

Exp Code: sb23 Date/Time: March 20, 2007 9 am Investigator: J.J.

Scanner: 3T Coil: Wong/MAI/ GE

ANAT Scan1: Type: SPGR /FSE/MPIR TE(ms):____ TR(ms):____Flip:____ FOV(mm): 240

Matrix: 256x256 #slices: 124 Plane: Ax/Cor/ Sag Thickness(mm): 1.2 First: 62.7 I

Last: 84.9 S

EPI Scan: GE-EPI /SE-EPI/ GE RT EPI TE(ms):____ TR(ms): 3.0 sec Flip:___

Plane: Ax/ Cor/ Sag FOV(mm): 240 Matrix: 64 Thickness(mm): 3.5

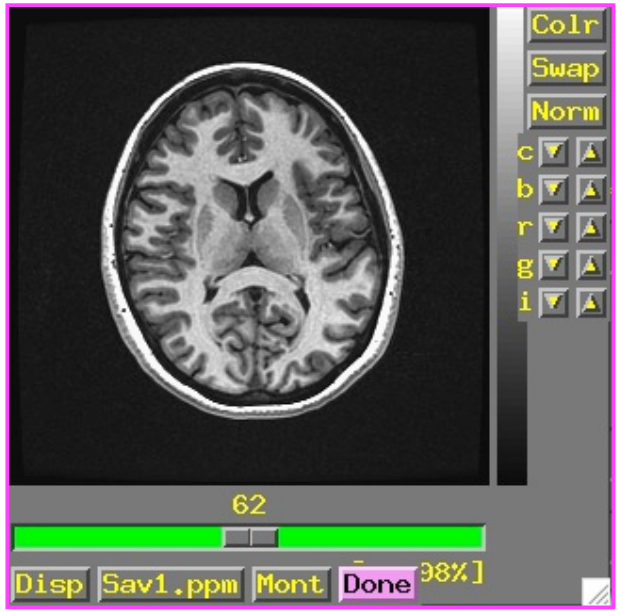
#slices: 34 (67 reps each) First 43.9 I Last: 71.6 S

Notes:

* Data Axes Orientation for anat: RAI, Data Axes Orientation for epi: RAI
* 9 EPI runs
* EPI scans first, followed by anatomical scan
* Subject sneezed during first EPI run

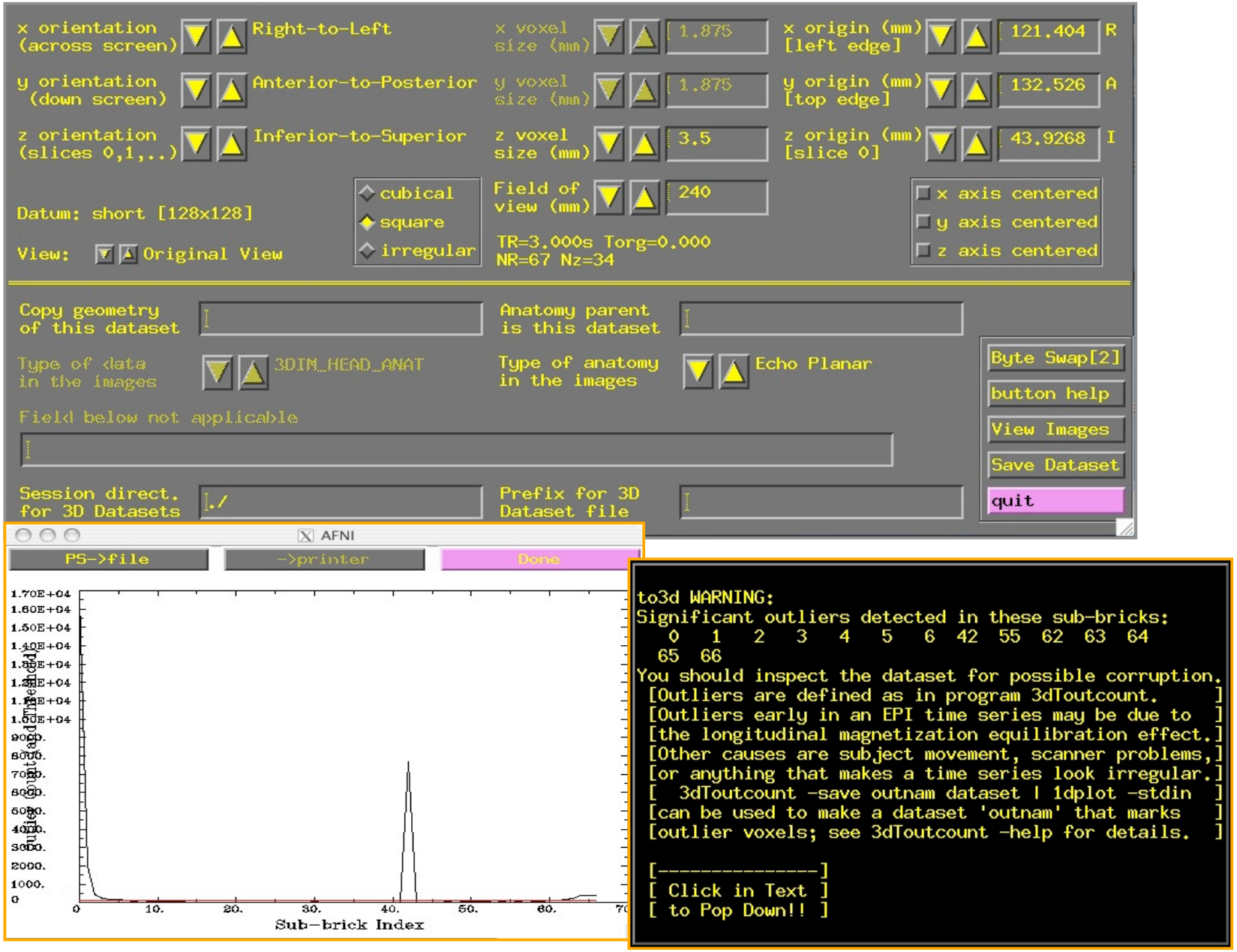
- Using **to3d** to assemble the anatomical (MPRAGE) dataset:
  - ★ **cd AFNI_data3/MPRAGE_anat** ⇒ change directory, to get at images
  - ★ **ls** ⇒ to see what files are there:
    - ➥ `MPRage_12mm-00001.dcm ... MPRage_12mm-00124.dcm`
  - ★ **to3d *.dcm** ⇒ run **to3d**, reading in all the images files --- GUI pops us:

  - ➥ **to3d** understands **Dicom** files, and so has filled in some of the GUI
  - ➥ Note: z-origin field **62.7 I** corresponds to experiment log

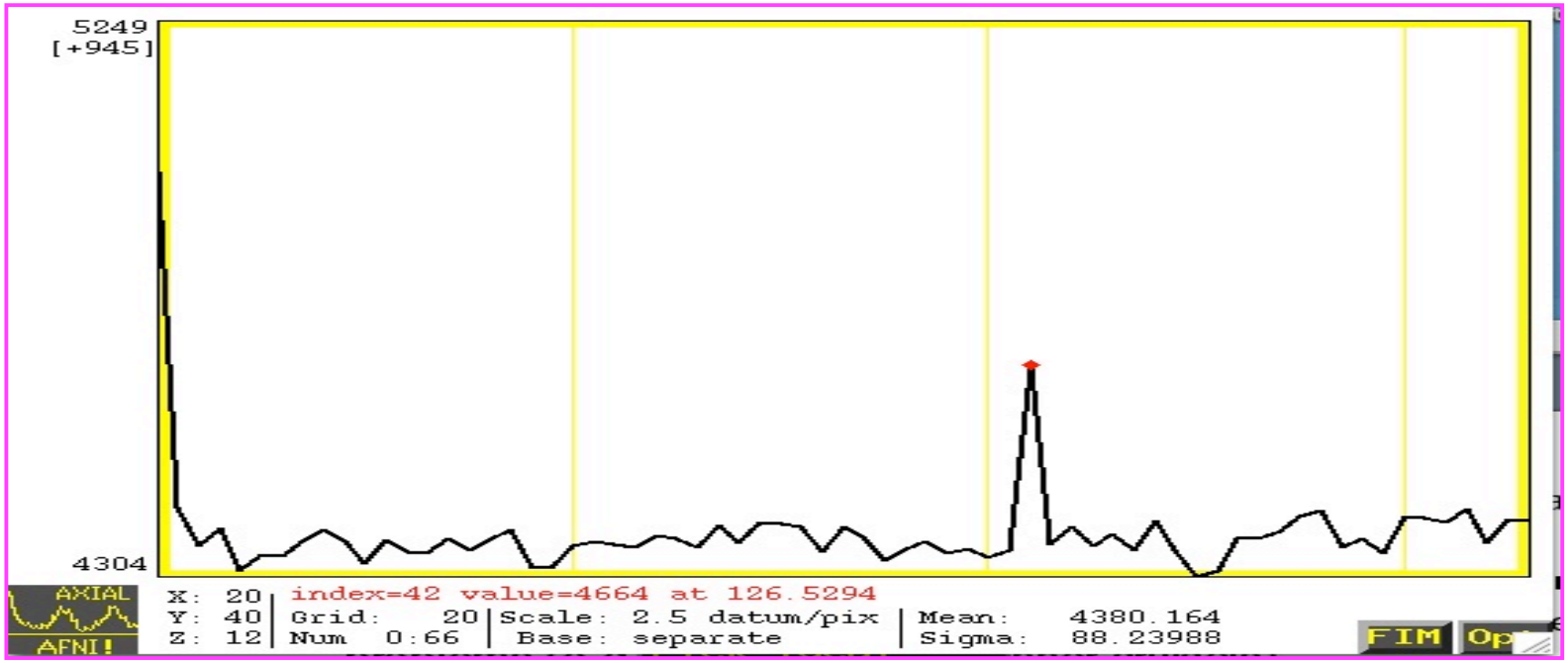


- ★ To check images that were just input, click the **[View Images]** button in the **to3d** GUI
  - ➥ Window is the same as the AFNI image viewer
  - ➥ Slider below image lets you move between slices
- ★ In this example, **to3d** has all the information needed from the ***.dcm** headers
  - ➥ All you need to do is supply the data Prefix , then press **[Save Dataset]**
    - ➪ Look at the bottom right of the **to3d** GUI for these controls
    - ➪ I suggest the prefix **anat**
  - ➥ Dataset files **anat+orig.HEAD** and **anat+orig.BRIK** will be created
  - ➥ Then press **[quit]** button *twice* to exit **to3d** GUI
- ★ Script version (no GUI): **to3d -prefix anat *.dcm** would create a dataset with no user intervention
- ★ To save the dataset as a NIfTI (.nii) file, include the .nii suffix in the prefix name, e.g., **to3d -prefix anat *.dcm** . You can also do this in the GUI.

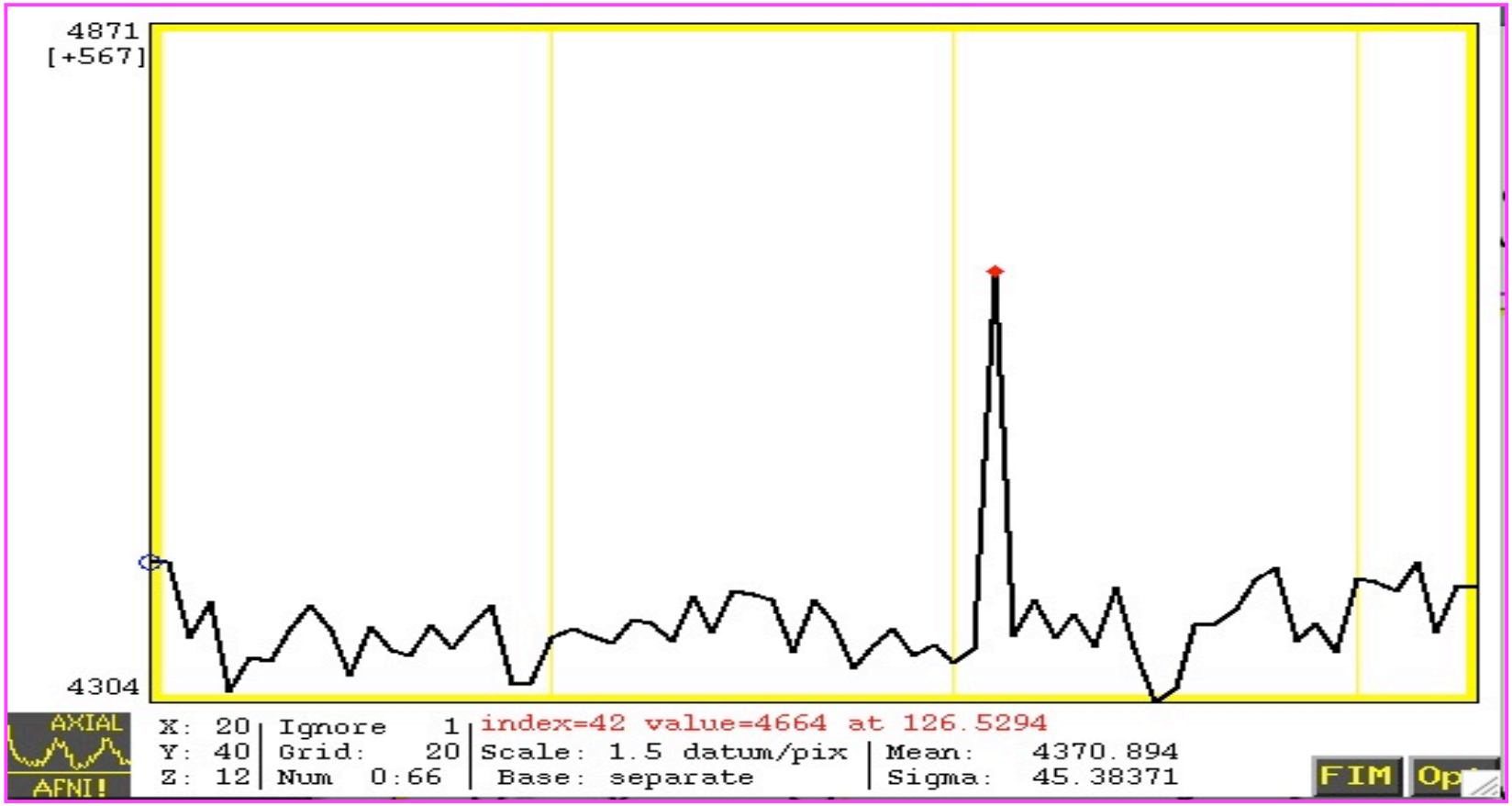
- Using **to3d** to assemble the EPI 3D+time dataset:
  - ★ **cd ../EPI_run1** ---> change directory to get at images
  - ★ **ls** ---> to see what files are there (should see files `8HRBRAINAx2DGRE-00001.dcm ... 8HRBRAINAx2DGRE-02278.dcm`)
  - ★ We do not just do **to3d *.dcm** to create a 3D+time dataset
  - ★ For historical reasons, the time-axis information must be given on the **to3d** command line.
    - ➥ Cannot be modified from the GUI
  - ★ Command line: **to3d -time:zt 34 67 0 alt+z *.dcm**
    - ➥ `-time:zt` ⇒ slices usually presented in order of space (z), then time (t)
      - ➪ `-time:tz` 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]
    - ➥ `34 67` ⇒ there are 34 slices in space (z) and 67 over time (t) = 2278 total
    - ➥ `0` ⇒ tells **to3d** to read the TR for volume acquisition from the image headers
      - ➪ If not available, the user puts `3.0s` or `3000` instead of this `0`
    - ➥ `alt+z` ⇒ slices are gathered in alternating order in the +z direction
      - ➪ Most EPI acquisitions are really 2D multislice, spread out through time
      - ➪ AFNI header can contain information about slice timing offsets
      - ➪ Other possible modes: `zero` (for 3D), `@filename` (to specify each slice)


x orientation (across screen)
Right-to-Left
y orientation (down screen)
Anterior-to-Posterior
z orientation (slices 0,1,..)
Inferior-to-Superior
x voxel size (mm)
1.875
y voxel size (mm)
1.875
z voxel size (mm)
3.5
x origin (mm) [left edge]
121.404
R
y origin (mm) [top edge]
132.526
A
z origin (mm) [slice 0]
43.9268
I
Datum: short [128x128]
View: Original View
cubical
square
irregular
Field of view (mm)
240
TR=3.000s Torg=0.000
NR=67 Nz=34
x axis centered
y axis centered
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
Echo Planar
Field below not applicable
Byte Swap[2]
button help
View Images
Save Dataset
quit
Session direct. for 3D Datasets
./
Prefix for 3D Dataset file
AFNI
PS->file
->printer
Done
Sub-brick Index
to3d WARNING:
Significant outliers detected in these sub-bricks:
0 1 2 3 4 5 6 42 55 62 63 64
65 66
You should inspect the dataset for possible corruption.
[Outliers are defined as in program 3dToutcount.]
[Outliers early in an EPI time series may be due to]
[the longitudinal magnetization equilibration effect.]
[Other causes are subject movement, scanner problems,]
[or anything that makes a time series look irregular.]
[3dToutcount -save outnam dataset | 1dplot -stdin]
[can be used to make a dataset 'outnam' that marks]
[outlier voxels; see 3dToutcount -help for details.]
[----------]
[Click in Text]
[to Pop Down!!]

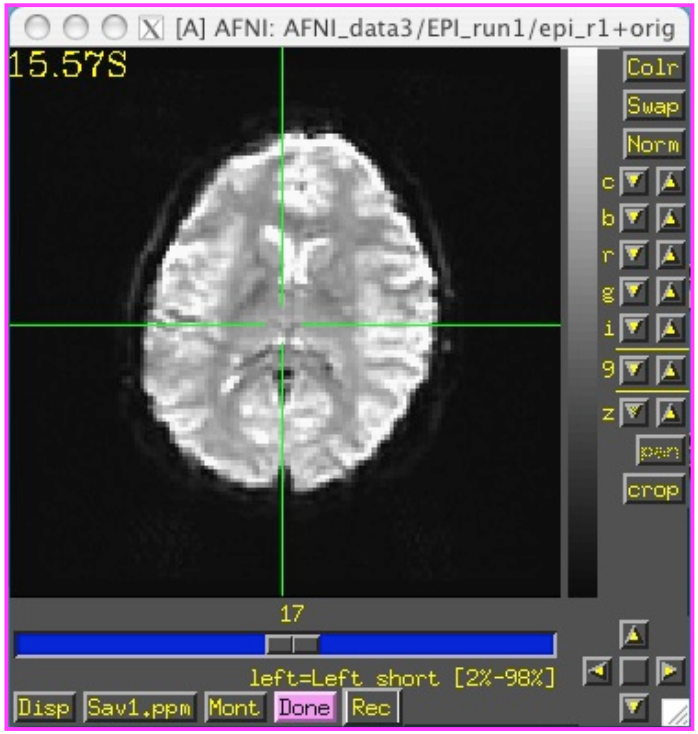
- **Outliers** are data values that are very different from other values in the same time series
  - **`to3d`** reports sub-bricks (time points) that have a lot of outliers
  - You should use AFNI to look at these time points to see if there are major problems (e.g., head motion, scanner artifacts)
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



- The outlier becomes much more obvious in this example when the first time point of the time series (which shows possible scanner artifacts) is removed.
  - ★ Remove time point by selecting (from the graph viewer): **FIM-->Ignore-->1**



- ★ Again, fields in the GUI were filled from the **`*.dcm`** headers



- ★ In this example, the EPI and anatomical datasets are both axial slices. However, AFNI can work with anat/EPI datasets that have different planes (e.g., if anat is coronal and EPI is axial)
  - ➥ Programs **`3dresample`** and **`3daxialize`** 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

- ★ Script version: **`to3d -time:zt 34 67 0 alt+z -prefix epi_r1 *.dcm`**
- ★ Program **`3drefit`** can be used to change some header items in an AFNI dataset after it is created
  - ➥ Example: **`3drefit -TR 1s epi_r1+orig`** will change the TR of the dataset to 1 second

Processing DICOM Image Files with **Dimon**

- **NIH - new file format (since 2005)**:
  - ★ The file format for images coming out of the GE scanners at the NIH has changed from **I-files** to **DICOM** (note: some of the scanners still output I-files. For more information regarding the processing of I-files, see pg. 32 of the appendix).
  - ★ Hence, most images are no longer saved as **`I.0001, I.0002`**,…etc. Instead, they appear with a **`.dcm`** suffix. For example:

Anatomical Data:	Time Series (EPI) Data:
`MPRage_12mm-00001.dcm`	`8HRBRAINAx2DGRE-00001.dcm`
`MPRage_12mm-00002.dcm`	`8HRBRAINAx2DGRE-00002.dcm`
`MPRage_12mm-00003.dcm`	`8HRBRAINAx2DGRE-00003.dcm`
. . .	. . .
`MPRage_12mm-00124.dcm`	`8HRBRAINAx2DGRE-02278.dcm`

➥ The .dcm suffix appears for both anatomical and time series data.

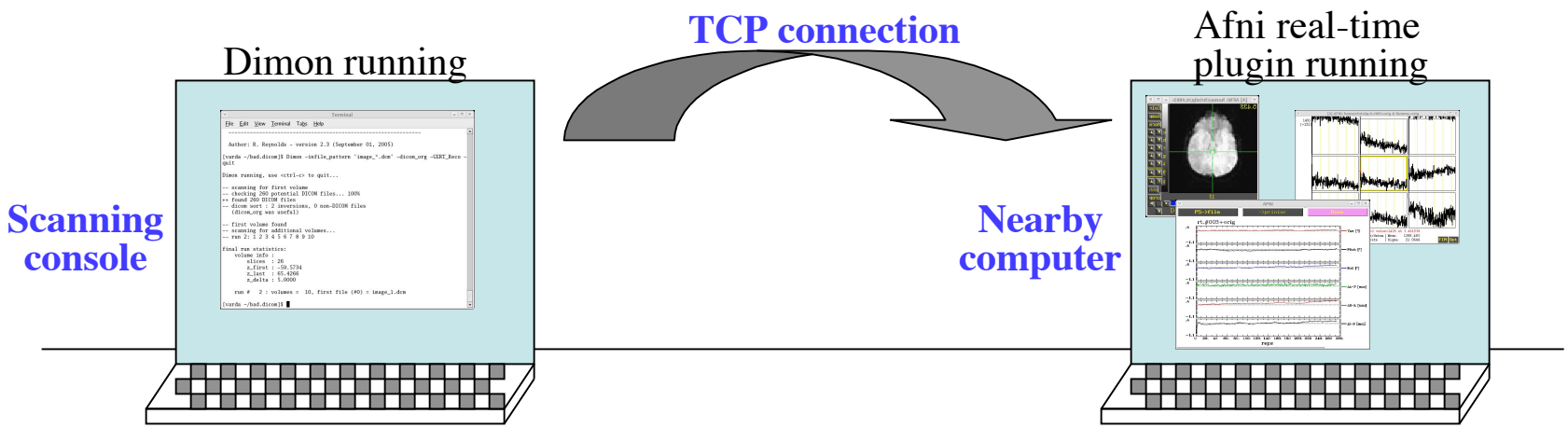
➥ Irrespective of whether you're dealing with I.* files or *.dcm files, programs like **`to3d`** still work in the same way:

```
to3d -prefix fred_anat  I.*
to3d -prefix fred_anat  *.dcm
```

Processing DICOM Image Files with **Dimon**

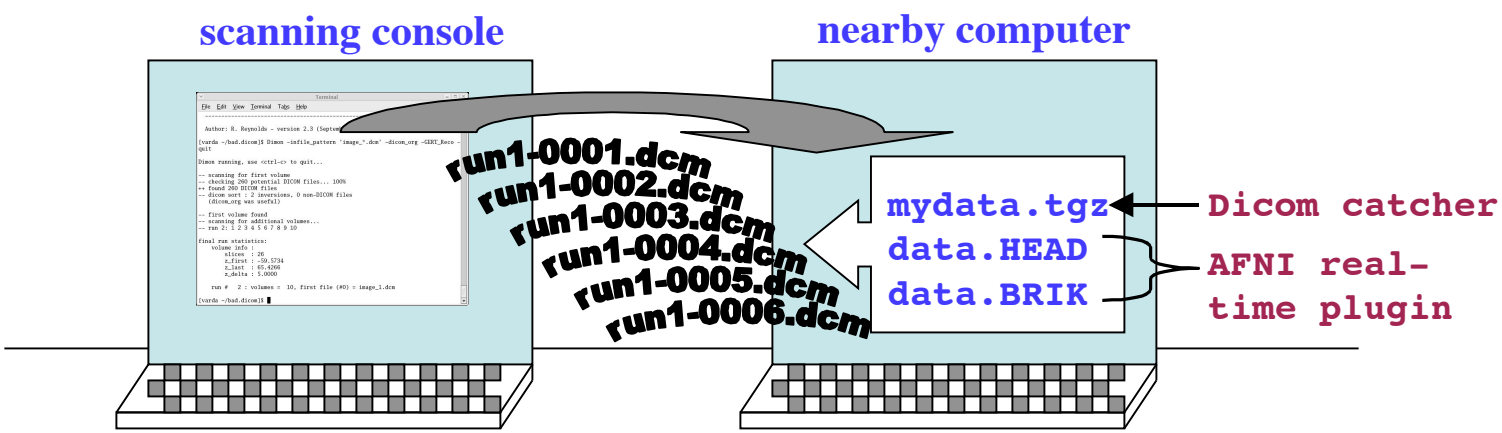
- **What is Dimon?**
  - ★ **Dimon** is an AFNI program (by Rick Reynolds) intended to be run in ***real time*** (i.e., during a scanning run), to monitor the collection of DICOM image files. The user will be notified of any missing slices or any slices that are acquired out of order.
    - ➥ Dimon also communicates with the realtime plugin in afni, allowing users to:
      - monitor subject head motion
      - create AFNI datasets
  - ★ **Dimon** can also be used ***off-line*** (i.e., away from the scanner), either to verify the integrity of `DICOM` files, or to create AFNI 3D and 3D+time datasets by using the **-GERT_Reco** option (or you can use `to3d`).
  - ★ Type **Dimon -help** for more information

- **Using Dimon in Real Time**
  - ★ During a scanning session, **Dimon** looks for potential problems with the output image files. Optionally, `Dimon` can be used to send the images (collected into volumes) to afni's `realtime plugin`.
    - ➥ At the NIH, `Dimon` is invoked for both of these purposes automatically.
  - ★ If `Dimon` has established a TCP connection with the real-time plugin to `afni`, then it will send each volume to the plugin, and will notify `afni` when a single run has ended. Note that `afni` will generally be running on a *separate* computer, not the scanning console where `Dimon` runs.



  - ★ The `realtime plugin` will show the volumes in `afni` as they arrive, along with a 3-D registration graph, allowing users to monitor subject motion.

- **Overview of Real Time Processing at the NIH**
  - ★ **Dimon** and `afni` are invoked automatically (via scripts written by Jerzy Borduka). No user intervention is required.
  - ★ All DICOM files are passed to the **DICOM catcher** (part of the **packrat** utilities, organized by John Ostuni). The catcher organizes the files into a directory tree, with useful filenames, and then creates a .tgz package of it.
  - ★ The incoming DICOM files are also assembled into AFNI datasets (created by afni's real-time plugin) and are available for the users to download.
    - ➥ Each EPI run (or anatomical scan) will be stored as a separate AFNI dataset (i.e., **.HEAD** and **.BRIK** files), created by the **realtime plugin**.



  - ★ Class demo of realtime plugin: **cd AFNI_data3/EPI_manyruns**
    tcsh demo.realtime

- **Using Dimon OFF-LINE**
  - ★ Sometimes, it may be necessary to run **Dimon** manually from the command line.
    - ➥ Suppose you receive some DICOM files that are obviously not sorted in the proper sequential order. For example:

```
cd AFNI_data3/bad.dicom
ls
```

```
image_1.dcm
image_10.dcm
image_100.dcm
image_101.dcm
    . . .
image_109.dcm
image_11.dcm
image_110.dcm
image_111.dcm
    . . .
image_119.dcm
image_12.dcm
image_120.dcm
image_121.dcm, etc…
```

- The problem here is that the image number for each slice is not "zero-padded" (e.g., **image_100.dcm** instead of **image_00100.dcm**).
- When non-zero-padded files are alphabetically sorted, you get this result.
- Use the **-dicom_org** option in Dimon to re-sort them by the sequential slice and time order.
- To then assemble the images into an AFNI dataset, include the **-GERT_Reco** option on the Dimon command line.

★ Example of **Dimon** :

```
Dimon -infile_pattern 'image_*.dcm'   \
      -dicom_org -GERT_Reco -quit
```

★ Output from **Dimon** command:

```
xterm
[varda:jj/AFNI_data3/bad.dicom] christip% Dimon -infile_pattern 'image_*.dcm' -dicom_org -GERT_Reco

Dimon running, use <ctrl-c> to quit...

-- scanning for first volume
-- checking 170 potential DICOM files... 100%
++ found 170 DICOM files
-- dicom sort : 2 inversions, 0 non-DICOM files
   (dicom_org was useful)

-- first volume found
-- scanning for additional volumes...
-- run 3: 1 2 3 4 5

final run statistics:
    volume info :
        slices  : 34
        z_first : -43.9268
        z_last  : 71.5732
        z_delta : 3.5000

    run #   3 : volumes =   5, first file (#0) = image_1.dcm

[varda:jj/AFNI_data3/bad.dicom] christip% []
```

- DICOM files are sorted (non-DICOM files are ignored).
- Dimon looks for missing or out-of-sequence DICOM files.
- Volume information is presented when `Dimon` terminates (-quit or ctrl-c).

- Explanation of **Dimon** arguments and options :

```
Dimon  -infile_pattern 'image_*.dcm'   \
       -dicom_org -GERT_Reco -quit
```

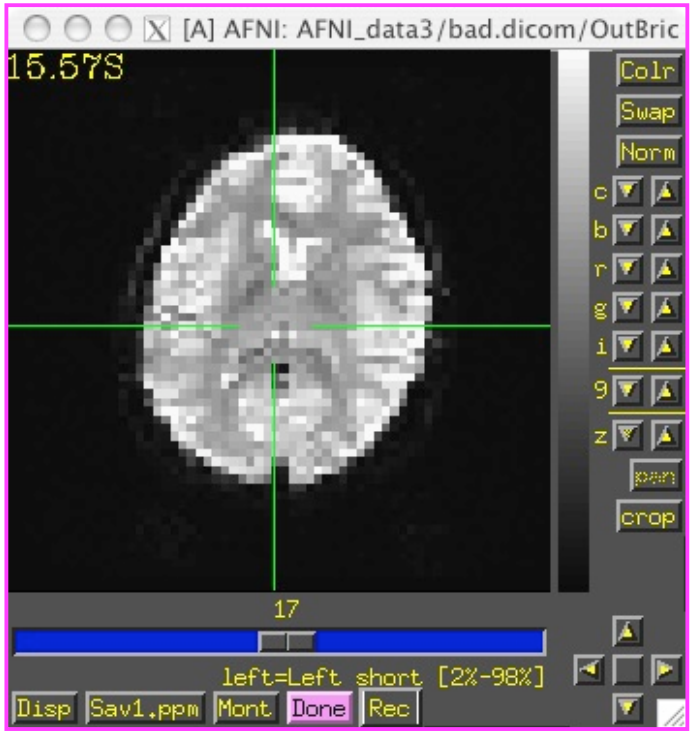
  - **-infile_pattern**: This argument tells Dimon where the DICOM files of interest are located, and how they are labeled. In this case, the DICOM files are found in directory **AFNI_data3/bad.dicom** and they all begin with the name "**image_**" and end with the "**.dcm**" suffix.
  - **-dicom_org**: This option tells Dimon to read the files specified by the -infile_pattern argument, and to determine if they are indeed DICOM files, and if so, to organize them in an ordered list of files per run.
  - **-quit**: will terminate **Dimon**, after all image files have been examined,
    - If -quit is not used, the program will forever wait for more images, until <ctrl-c> is used to terminate the program
  - **-GERT_Reco**: This option creates the **GERT_Reco_dicom** script in the same directory that Dimon was run.
    - To create AFNI datasets, just execute this script:

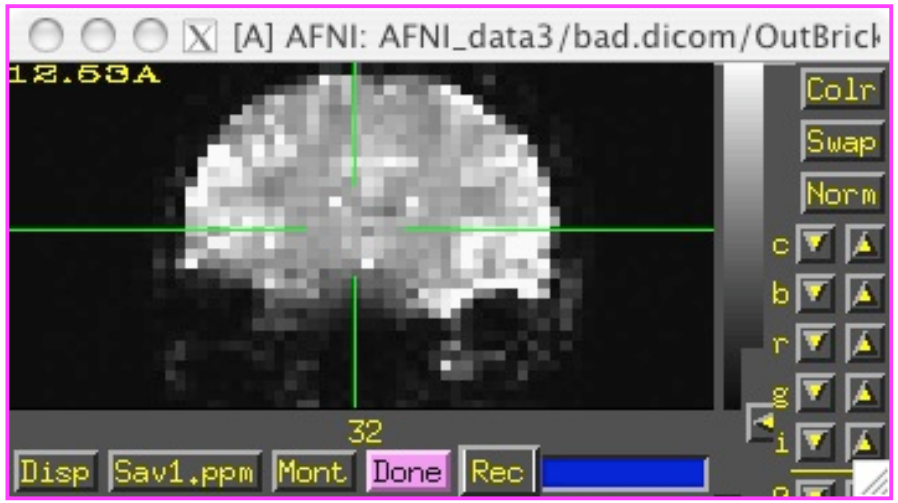
      ./GERT_Reco_dicom or **tcsh GERT_Reco_dicom**

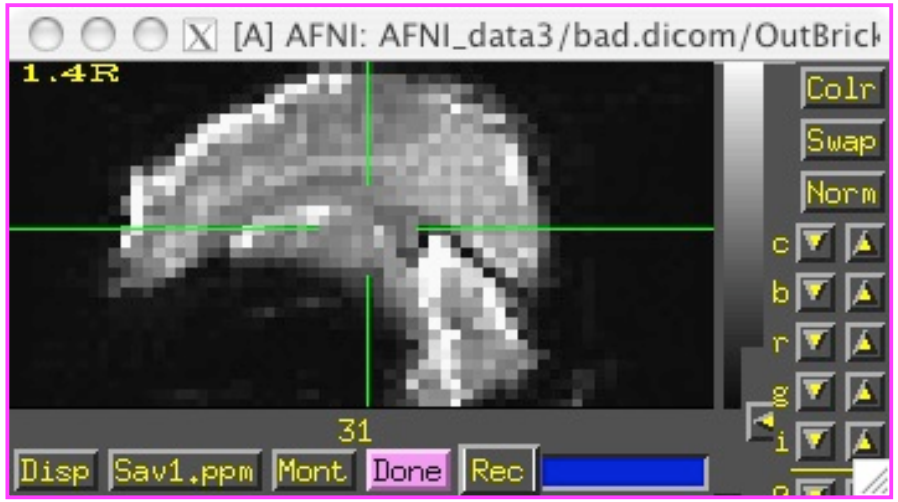
★ The result is an AFNI dataset created from the images in directory **bad.dicom/**

OutBrick_run_003+orig.HEAD

OutBrick_run_003+orig.BRIK







APPENDIX

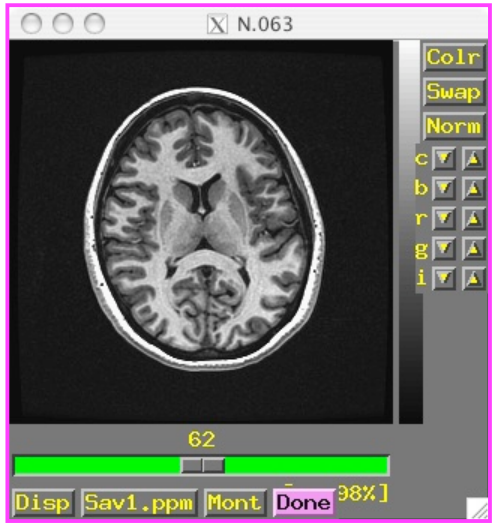
1. Assembling ‘Naked’ Images into AFNI Datasets
2. Creating New AFNI 3D+time Datasets with Program **Imon**

The appendix contains important topics pertaining to image input into AFNI and **`to3d`**, but may not necessarily be covered in the workshop due to time constraints

Assembling 'Naked' Images into AFNI Datasets

- 'Naked' image ⇒ image file without header data that AFNI understands
- User must supply geometrical information to **`to3d`**
  - ★ This is when the written experiment log is critical!
- The **`MPRAGE_naked/`** directory contains the same anatomical images as before, but stripped of all header information
  - ★ Each file has 131072 bytes = 256 x 256 16-bit integers ('shorts')
  - ★ **`cd ../MPRAGE_naked`** (to get at images `N.001...N.124`), then **`to3d N.*`**

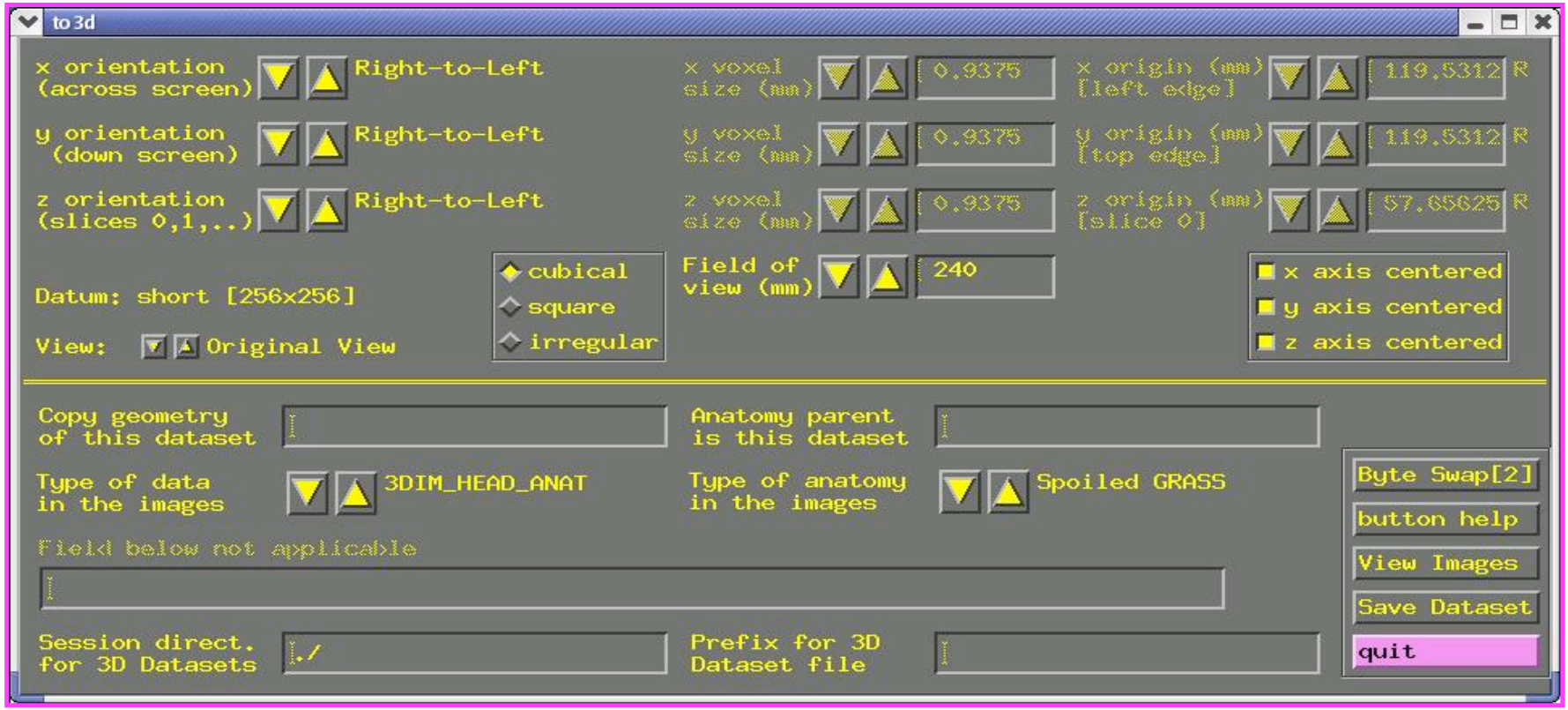
Linux/Intel computers



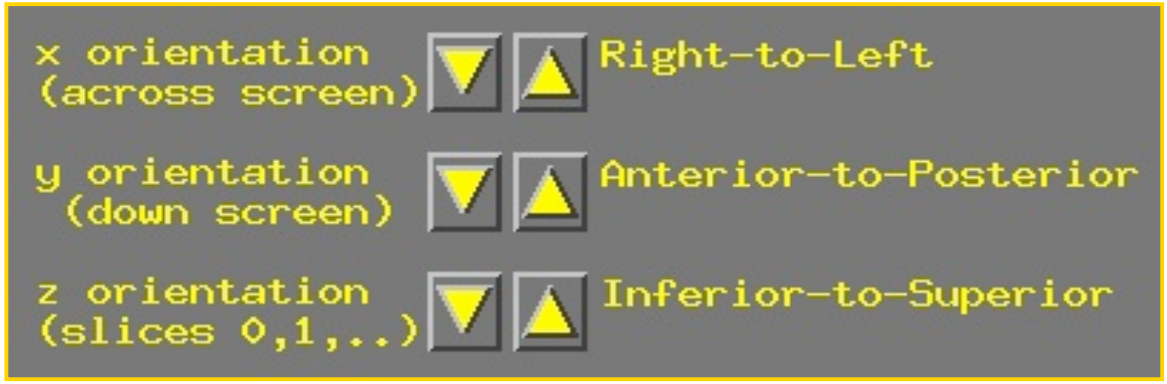
SGI/Sun/etc. computers

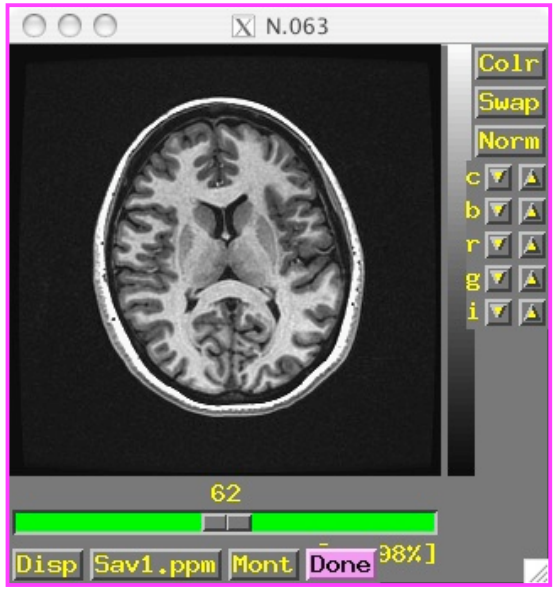
- On Linux/Intel computers: the peculiar appearance of images shows that something is wrong:
  - ★ MR images from scanners that are stored as shorts: 2 bytes per number
  - ★ Like a 2-digit decimal number: “93” means “9 x 10 + 3”
    - ➥ By universal custom, we write the “9” first
    - ➥ Could also write the same number as “39” (if we had a different custom)
  - ★ Customs for computers are not so universal
    - ➥ Sun and SGI systems store 2 byte numbers in reverse order from Intel
    - ➥ Result is that numbers are mangled (and some show up as negative)
    - ➥ Solution: press **to3d**’s **[Byte Swap[2]]** button and images are fixed!

- Same **`to3d`** control panel (without negative voxel warning):



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





- Screen shot above shows correct orientation for this dataset
  - ★ Use the image viewing window to judge how images are laid out
  - ★ Click the arrows to scroll through the 6 possible options for each orientation to set correct values
  - ★ “x orientation” of dataset is across the screen (Right-to-Left for this dataset)
  - ★ “y” orientation of dataset is down the screen (Anterior-to-Posterior)
  - ★ “z” orientation” of dataset is in increasing slice order (Inferior-to-Superior)
    - ➥ Note: You *must* know subject’s right from left, from experiment log sheet or vitamin E tablet placed on one side of the head. You cannot tell left from right by simply viewing the volume.

- To set dataset geometrical size/location, experiment log sheet is essential
  - ★ Field of view (FOV): Default is **240 mm** and also correct for these images
  - ★ Voxel geometry*:* Default is “cubical”, which is incorrect for this example
    - ➥ Must set geometry to “**square**” (x size = y size, z size different)
  - ★ z voxel size*:* Default is set to 0.9375, which is incorrect for this example
    - ➥ Must set z voxel size (a.k.a. “slice thickness”) to “**1.2 mm**”
  - ★ x,y,z centered: Default is that slices are centered in the magnet, which is incorrect in this example
    - ➥ Typically, the x and y axes are centered, and the z direction is not. In this example, *none* of the axes are centered.
    - ➥ Click “z axis centered”, “y axis centered”, and “z axis centered” off
    - ➥ Enter “**123.6**”, “**135.4**”, and “**62.7**” for x, y, z origins respectively

- Final required steps:
  - ★ Enter prefix for new dataset into **[Prefix]** text box at lower right of **to3d** control window
    - ➥ Choosing a good prefix is important for keeping datasets organized
  - ★ Press **[Save Dataset]** button
  - ★ Press **[quit]** (twice) to exit **to3d**
  - ★ The new dataset files should show up when you use command **ls**
  - ★ For organizational purposes, you may want to move your datasets to some other directory

- 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 **[Copy geometry of this dataset]** field
    - ➥ If in another directory, you must include that in the filename
  - ★ When you press 'Enter' or move the cursor from the text-entry field, **to3d** tries to read geometry parent dataset header
  - ★ If geometry parent has same spatial dimensions as current dataset, all geometry fields will be filled out
    - ➥ Does not affect the time fields, which must still be set using **-time:zt** or **-time:tz** on the command line
  - ★ Geometry parent very useful when constructing multiple EPI datasets from a single scanning session
- Using **to3d** in command line mode
  - ★ You can specify all needed inputs to to3d by using command line options
    - ➥ For a full list of options, type **to3d -help**
  - ★ 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
    - ➥ If the command line is incomplete, then the GUI will be opened

- For the SPGR dataset example ('naked' image files):

```
to3d -xSLAB 123.6R-115.4L -ySLAB 135.4A-103.6P   \
     -zSLAB 62.7I-84.9S -prefix anatNaked -2swap \
     -spgr N.*
```

  - `-xSLAB 123.6R-115.4L` says that the x axis of the images runs from 123.6 mm Right to 115.4 mm Left
  - `-ySLAB 135.4A-103.6P` says that the y axis of the images runs from 135.4 mm Anterior to 103.6 mm Posterior
  - `-zSLAB 62.7I-84.9S` says that the z axis of the slices runs from 62.7 mm Inferior to 84.9 mm Superior
  - What is the difference between the *FOV* option and the *SLAB* option? (see to3d -help)
    - `FOV` refers to the coordinates of the outer edge of the first voxel to the outer edge of the last voxel along the relevant axis (x and y, in most cases)
    - `SLAB` refers to coordinates of the center of the outermost voxels (z=slice direction, in most cases)
  - `-prefix anatNaked` gives the prefix for output dataset filenames (in this case, **`anatNaked+orig.HEAD`** and **`anatNaked+orig.BRIK`**)
  - `-2swap` means to byte-swap the images while reading them
  - `-spgr` means to label this data as being of SPGR (or MPRAGE) type
  - `N.*` means to read the images from the files whose names start with string "N." and end with anything ("`*`" is a wildcard)

- ★ For the EPI dataset example (if image files were 'naked'):

```
to3d -xSLAB 121.4R-114.8L -ySLAB 132.5A-103.7P          \
     -zSLAB 43.9I-71.6S -2swap -time:zt 34 67 3000 alt+z \
     -prefix epiRun1 -epan *.dcm
```

  - ➥ Options (with their arguments) can appear in any order
  - ➥ Input image filenames always appear last (i.e., `I.*` or `*.dcm`)

- Conclusion
  - ★ With practice, command line usage for **`to3d`** becomes more useful than the GUI
    - ➥ Usually need to create many datasets at once
    - ➥ Can put commands in a script file and execute them
    - ➥ Then edit the 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
    - ➥ Long commands can be split across multiple lines by ending all but the last line with the "\" character
    - ➥ There must not be a blank after the "\"!!!
  - ★ You can execute a script file by typing a command like `tcsh <filename>`, which just means to read commands from "filename"
  - ★ 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

Creating New AFNI 3D+time Datasets with Program **Imon**

- **`Imon`** can be run during a scanning session on a ***GE scanner,*** to monitor the collection of time series **`I.*` files**. The user is notified of any missing or out-of-sequence slices
- **`Imon`** can also be run separate from scanning, either to verify the integrity of `I.*` files, or to create AFNI 3D+time datasets by using the **`-GERT_Reco2`** option
  - ★ **`Imon`** is run in command line mode
    - ➥ The **`-GERT_Reco2`** option is added to the command line so that `I.*` files examined by **`Imon`** can then be assembled into an AFNI 3D+time dataset
    - ➥ When not being used in real-time mode, the **`-quit`** option is added so that Imon will terminate after processing all of the `I.*` files

- Why not use **to3d** directly to create AFNI datasets?
  - ★ EPI images collected using GE's real time EPI sequence are saved in a peculiar fashion
    - ➥ Only 999 image files can be stored in a single directory
    - ➥ If a run consists of 110 volumes of 27 slices each, we have 2970 image files
    - ➥ With a limit of 999 `I.*` files per directory, a run made up of 2970 images would have to be saved in 3 separate directories (numbered **001/**, **021/**, and **041/**):
      - ➪ E.g., **001/**`I.028…I.999` + **021/**`I.001…I.999` + **041/**`I.001…I.999` = 2970 `I.*` files total
    - ➥ The second run would be stored in directories **061/**`I.001` ⇒ **101/**`I.973`, the third run in **101/**`I.974` ⇒ **161/**`I.946`, and the nightmare continues…
    - ➥ This setup already makes it difficult to delineate between runs. Now image what happens if the scanner hiccups, if you stop a scan in the middle and start a new one, or start collecting scans with a different number of slices!
- **Imon** attempts to identify complete scans from the images in those directories. It also monitors missing or out-of-order images, and generates the commands necessary to turn them into AFNI bricks using the script **GERT_Reco2**

- Using **Imon** to assemble the EPI 3D+time datasets
  - ★ **cd AFNI_data3/EPI_manyruns** ⇒ change directory to get at GE subdirectories containing images
  - ★ **ls** ⇒ to view the GE subdirectories containing 4 runs worth of `I.*` files
    - ➥ Directories are numbered in multiples of 20 (default naming system used by the GE scanner): `001/ 021/ 041/ 061/. . . 201/ 221/`
  - ★ Command line: **Imon -start_dir 001 -GERT_Reco2 -quit**
    - ➥ `-start_dir` specifies the starting directory where **Imon** will begin monitoring the images. In this example, our start directory is `001/`
    - ➥ `-GERT_Reco2` will create a script called '`GERT_Reco2`', similar to the one that program **Ifile** creates (for more info on **Ifile**, type **Ifile -help**).
      - ➪ The `GERT_Reco2` script may be run to create the AFNI datasets corresponding to the `I.*` files
    - ➥ `-quit` will terminate **Imon**, after all image files have been examined,
      - ➪ If `-quit` is not used, the program will forever wait for more images, until `<ctrl-c>` is used to terminate the program
  - ★ For a full list of **Imon** options, type **Imon -help**

- Output from **Imon** command:

```
File  Edit  View  Terminal  Go  Help
[morwen EPI_manyruns]$ Imon -start_dir 001 -GERT_Reco2 -quit

Imon running, use <ctrl-c> to quit...

-- scanning for first volume

-- first volume found
-- scanning for additional volumes...
-- run 1: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 2
7 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53
54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80
 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 10
5 106 107 108 109 110
-- run 2: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 2
7 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53
54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80
 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 10
5 106 107 108 109 110
-- run 3: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 2
7 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53
54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80
 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 10
5 106 107 108 109 110
-- run 4: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 2
7 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53
54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80
 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 10
5 106 107 108 109 110

final run statistics:
    volume info :
        slices  : 27
        z_first : 69.0000
        z_last  : -61.0000
        z_delta : -5.0000

    run #   1 : volumes = 110, first file = 001/I.028
    run #   2 : volumes = 110, first file = 061/I.001
    run #   3 : volumes = 110, first file = 101/I.973
    run #   4 : volumes = 110, first file = 161/I.946

[morwen EPI_manyruns]$
```

```
run# 1: volumes 110, first file = 001/I.028
run# 2: volumes 110, first file = 061/I.001
run# 3: volumes 110, first file = 101/I.973
run# 4: volumes 110, first file = 161/I.946
```

- **Imon** will search for missing or out-of-order images.
- Any errors will be noted on the screen
- The starting point for each run is reported at the end of **Imon**'s examination

- **`ls EPI_manyruns`** ⇒ to view the newly created **`GERT_Reco2`** script
  - ⋆ This script contains the commands that will automatically create bricks from the complete scans and store them in a newly created subdirectory called **`afni/`**
  - ⋆ To run the script, type **`./GERT_Reco2`**

- **`cd afni`** ⇒ to get at datasets
- **`ls`** ⇒ to view the AFNI 3D+time datasets:

`Outbrick_r1+orig.HEAD`	**`Outbrick_r1+orig.BRIK`**
`Outbrick_r2+orig.HEAD`	**`Outbrick_r2+orig.BRIK`**
`Outbrick_r3+orig.HEAD`	**`Outbrick_r3+orig.BRIK`**
`Outbrick_r4+orig.HEAD`	**`Outbrick_r4+orig.BRIK`**