# Where do AFNI Datasets Come From?

- Method 1: Create datasets with program **to3d** or **Dimon**
  - ★ **to3d** can work with "raw" image files – if you are clever enough – we will not talk about that in this presentation
  - ★ **Dimon** will work with DICOM formatted image files, and will run **to3d** for you, after it organizes the images

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- Method 2: Realtime input from an external image source program (e.g., directly from scanner's reconstructed images)
  - ★ **Dimon** can read image files output by realtime EPI reconstruction, check them for various errors, then send them into AFNI for display and formatting – while image acquisition continues
  - ★ Sample program **rtfeedme.c** can be used to write your own image source program if **Dimon** isn't right for you

# Creating AFNI Datasets with Program Dimon

- **Dimon** reads DICOM image files and assembles them into AFNI datasets (using program **to3d**)
  - ★ Can also read GEMS 5.x I-files; plus NiFTI and AFNI datasets if needed
- The collection of all 2D slice data forms the `.BRIK` file
  - ★ An AFNI dataset *can* contain a single slice
- **Dimon** has many different ways of being run, to deal with different situations that come up in the input files
- But we will only have 2 simple examples (next slides)

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- Program **dicom_hdr** is used to write out a formatted table of the header information from a DICOM file
  - ★ This information can help when there are problems
    - ➥ Sample output near end of presentation

# Example 1 – EPI Time Series

- Switch to the directory with the sample data:
  - ★ `cd ~/AFNI_data6/EPI_run1`
- Run this command
  - ★ `Dimon -infile_prefix 8HR -gert_create_dataset`
- The **Dimon** program does these things:
  - Scan the input files (all files with names starting with **8HR**), determines where each 3D volume ends (one TR)
  - Runs **to3d** to assemble all the input files into one AFNI dataset, with 68 3D volumes, each one with 34 slices
  - Saves the dataset with a default prefix name **OutBrick_run_003+orig**
    - You can choose the output prefix yourself – see next example

# Example 2 – T1-Weighted Anatomical Volume

- Switch to the directory with the sample data:
  - ★ `cd ~/AFNI_data6/DICOM_T1`
- Run this command (almost the same as Example 1)
  - ★ `Dimon -infile_prefix I -gert_create_dataset`
- The **Dimon** program fails!
  - The reason: the filenames (**I1000000**, **I1000001**, …) are not in the correct order to make up a 3D volume
  - To see this disorder (chaos 混沌), run command `aiv I*` and scroll through the slices (**aiv** = **A**FNI **I**mage **V**iewer)
- To fix this problem, the **run_Dimon.csh** script was written
  - To run this script, type **tcsh run_Dimon.csh**
    - See next slide for script

# Example 2 – run_Dimon.csh

```
uniq_images I*[0123456789] > uniq_image_list.txt

Dimon -infile_list uniq_image_list.txt \
      -gert_create_dataset             \
      -gert_write_as_nifti             \
      -gert_to3d_prefix T1.3D          \
      -gert_outdir ..                  \
      -dicom_org                       \
      -use_last_elem                   \
      -save_details Dimon.details      \
      -gert_quit_on_err
```

# Example 2 – **run_Dimon.csh** – Unique Images

```
uniq_images I*[0123456789] > uniq_image_list.txt
```

```
Dimon -infile_list uniq_image_list.txt \
```

- From the list of input image files, creates a list of files with ***unique*** images
- To avoid a problem where systems can output more than one copy of the same image file, but with different names
- The use of **uniq_images** is not needed in this example, but it was needed in some other data from the same scanner

```
      -gert_quit_on_err
```

# Example 2 – **run_Dimon.csh** – Sorting Input Files

```
uniq_images I*[0123456789] > uniq_image_list.txt

Dimon -infile_list uniq_image_list.txt \
      -gert_create_dataset             \
      -gert_write_as_nifti             \
      -gert_to3d_prefix T1.3D          \
      -gert_outdir ..                  \
      -dicom_org                       \
```

- Tells **Dimon** to organize the image files by the information stored in their DICOM headers, rather than by filenames
- This step usually fixes problems with slices being out of order when the scanner (or PACS) creates the filenames

# Example 2 – **run_Dimon.csh** – Other Details

```
uniq_images I*[0123456789] > uniq_image_list.txt

Dimon -infile_list uniq_image_list.txt \
      -gert_create_dataset             \
      -gert_write_as_nifti             \
      -gert_to3d_prefix T1.3D          \
      -gert_outdir ..                  \
      -dicom_org                       \
      -use_last_elem                   \
      -save_details Dimon.details      \
      -gert_quit_on_err
```

- Write NiFTI output
- Prefix for output dataset
- Write in parent directory

# Other **Dimon** Options

- **-dicom_org** tells **Dimon** to “organize” the files
  - Which can be used when all the files in one directory might be from different imaging runs and need to be put into different datasets
- **-sort_method XXX** tells **Dimon** how to sort the files for arrangement in space and time (if **-dicom_org** does not work)
  - Most useful possibilities for **XXX** are **default** and **acq_time**
- **-save_details PREFIX** tells **Dimon** to save the information about how the DICOM files are organized (into a few files whose names start with **PREFIX**)
  - So you can look at this information when there is a problem
  - If you need help from us, we will need these details

# How to Use **Dimon** at Your Site

- Experiment with the program until it works for your DICOM files
  - Read the help and ask for help on the AFNI message board
- Write a script that makes **AFNI** or NiFTI datasets from the files you get from your scanner
- Keep using that script forever, or until it stops working for you
- Advanced Usage:
  - You can use the "realtime" options (**`-rt -host`** …) to read DICOM files written out during scanning
  - And **Dimon** will send them into the **AFNI** graphical interface, so you can look at the data and at subject head movement while the subject is still being scanned
  - **`AFNI_data6/realtime.demos`** has 2 examples, with scripts showing how to run **Dimon** sending realtime data to **AFNI**

# Example 3 – Using **dicom_hdr**

- This program is for finding information in the DICOM header of an image file
  - **dicom_hdr I9900000 | more** (in directory **DICOM_T1/**)
  - Small part of the output (describes 2D image format)

```
Group: 0028, Length:      200
0028 0002   2 [2864    ] //          IMG Samples Per Pixel// 1
0028 0004  12 [2874    ] // IMG Photometric Interpretation//MONOCHROME2
0028 0010   2 [2894    ] //                      IMG Rows// 256
0028 0011   2 [2904    ] //                   IMG Columns// 256
0028 0030  14 [2914    ] //             IMG Pixel Spacing//0.9375\0.9375
0028 0100   2 [2936    ] //            IMG Bits Allocated// 16
0028 0101   2 [2946    ] //               IMG Bits Stored// 12
0028 0102   2 [2956    ] //                  IMG High Bit// 11
0028 0103   2 [2966    ] //     IMG Pixel Representation// 0
0028 1050   2 [2976    ] //             IMG Window Center//94
0028 1051   4 [2986    ] //              IMG Window Width//164
0028 1052   2 [2998    ] //         IMG Rescale Intercept//0
0028 1053   2 [3008    ] //             IMG Rescale Slope//1
-------------------------------------------------------------
Group: 7fe0, Length:   131080
7fe0 0010 131072 [17920] //                PXL Pixel Data//Data on disk
```

# Another Program to Try – **dcm2niix**

- **dcm2niix** = DICOM to NiFTI converter
  - **https://www.nitrc.org/projects/dcm2nii/**
  - **https://github.com/neurolabusc/dcm2niix**
- It works with more DICOM formats than Dimon does
  - For example, color images (from perfusion studies)
  - Philips PAR/REC format files
- **dcm2niix** is *not* from the **AFNI** group
  - It is from Chris Rorden at University of South Carolina (USA)
  - Someday *soon*, we will include it with **AFNI** ☺
- One advantage of using **Dimon**
  - Creates datasets (**AFNI** or NiFTI formats) with extra information in the header