

Data Transfer Notes for GE 3T

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Transferring Data to the server if you are at the scanner:

IMPORTANT NOTE: Automatic data transfer to the AW workstation really slows things down. always disable this feature.

In general you will want to grab all images in either an exam or a series. To copy images use the perl script **gecopy** from the scanner. To facilitate the transfer process and make the scanner available for the next study, it's a good idea to copy each series when it is done. You can do this while the next series is running.

1. In the patient browser highlight the series that you need to transfer.
2. Open a unix shell, by right clicking on the desktop background and choosing the command window option from the menu
3. Type: `gecopy -s <server name> -r <raid number> -d <dir name> <username>`

An Example Session:

```
{sdc@fmri3tw}[3] gecopy -s fmrserver -r raid1 -d studies emang
```

```
You are about to copy the following Exam Directory=/export/home1/sdc_image_pool/images/p203414/e2112293
```

```
*****
```

```
*****
```

```
Type <exam> to copy the whole exam to fmrserver  
or Choose a number to copy the corresponding study
```

```
Choose <1> to copy s2112294
```

```
Choose <2> to copy s2112310
```

```
exam
```

```
mycommand=scp -rp /export/home1/sdc_image_pool/images/p203414/e2112293
```

```
emang@fmrserver.ucsd.edu:/mnt/raid1/emang/data/studies
```

```
emang@fmrserver.ucsd.edu's password:
```

Converting to AFNI

Images are in DICOM format, so that AFNI can grab the geometry information from the DICOM header. This makes conversion into BRIKS relatively painless.

Note: DICOM files generated by the upgraded 3T scanners (HDx, 14x) are not saved in sequential order. For the AFNI to3d program to create a AFNI BRIK with the correct slice order, these dicom files need to be reordered. We have developed a Perl script 'imseq' for this purpose. For more information and downloading the script use the following URL:

<http://fmri.ucsd.edu/Howto/reorder.shtml>

Anatomical images:

```
scp the images and run to3d
```

```
to3d -prefix [anatbrikname] i*
```

Warning: At present, there is a problem with processed images (such as surface coil intensity corrected (SCIC) images). An interim fix is as follows.

1. Read the FOV values and actual BRIK orientation from the header of a BRIK of non-processed images.

2. Rename files so that they are listed in the order indicated by the suffix. For example, rename processed fspgr image series i2136970.MRDC.1-i2138170.MRDC.120 to MRDC.001-MRDC.120. Renaming can be done from the matlab command window or by using the UNIX renfunc command.
3. Use a to3d command that ignores the headers: e.g.

```
to3d -prefix brikrname \  

    -zFOV eR-fL -xFOV aA-bP -ySALB cS-dI \  

    '3Ds:-1:0:256:256:1:M*'
```

The FOV/SLAB values (a,b,c,d,e,f) can be determined from the header of a brik created from raw images.

Functional images:

```
to3d -prefix XXX -time:zt #slices #timepts TR sliceorder i*
```

example for BIRN protocol interleaved slices:

```
to3d -prefix birn2 -time:zt 35 200 3000 alt+z i*
```

NOTE: The default fMRI scan uses interleaved slices and bottom to top slice ordering, so alt+z is *usually* the correct choice for sliceorder.

WARNING: If you are using an old version of AFNI, the slice order may not come out correctly. We've had problems with AFNI 2.51d that disappear when we use AFNI 2.55g. So if you run into problems, make sure you are using the latest version of AFNI.

Note: If you get argument list being too long error message, enclose the reference to the files by a back-quote ` , Example:

```
to3d -prefix birn2 -time:zt 35 200 3000 alt+z `i*`
```

Copying Images remotely (Not the preferred method):

If the scanner is busy and you need to transfer data from a previous study, you can log on to fmriserver, then ssh to the scanner and use the secure copy command to copy your data.

Instructions:

```
ssh sdc@fmri3tw.ucsd.edu
```

```
cd /export/home1/sdc_image_pool/images
```

```
ls -ltr (to determine the patient directory name by the time the data was acquired)
```

the tree structure looks like this:

```
./p127418/e127419/s127420/i127421.MRDC.1
```

where:

p127418 is the patient directory

e127419 is the exam directory

s127420 is the series directory

i127421.MRDC.1 is the first image in the study directory.

```
scp -r <dir path> username@fmriserver.ucsd.edu:/mnt/raid#/userdir/whatever
```

Enter your password

Example: copying an exam

```
cd export/home1/sdc_image_pool/images/p127418/
```

```
scp -r e127419 dummy@fmriserver.ucsd.edu:/mnt/raid1/dummy/data/testdata
```

```
Password: dummypassword
```

Example: copying a series

```
cd /export/home1/sdc_image_pool/images/p127418/e127419
```

```
scp -r s127420 dummy@fmriserver.ucsd.edu:/mnt/raid1/dummy/data/testdata
```

```
Password: dummypassword
```