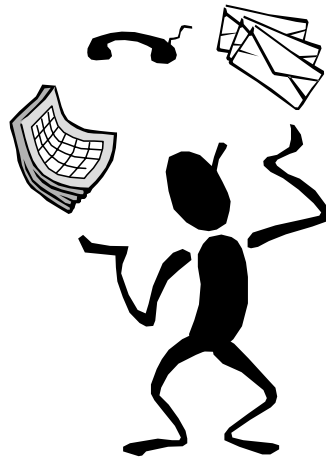


# fMRI data shuffling @ MRC



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### Before scanning

1. Login on *cicada* or *ladybird*. (user name and password is obtained from Stefan Skare). *Cicada* is the SUN Ultra 1 workstation in the room between the two MR Scanners at the MR Center. *Ladybird* is the SUN Enterprise 250 server, whose keyboard and monitor is placed next to MR-scanner 2 (MRC2).
2. All fMRI data is automatically transferred from the MRC1 scanner to ladybird:/raw\_images. Type df -k to check that there is enough free space on the disk /raw\_images. 'Enough' depends on your experiment, but think twice if there is less than 1-2 GB free. If there is not enough space, then you may erase other peoples data, as this disk is intended to temporary storage of data. Please start by erasing the oldest files first and only as much as is needed for the experiment. Hopefully, this should never be necessary since 18GB during 4 days should be sufficient. Do not make a habit of erasing the entire contents of /raw\_images before scanning – you will end up with very few friends!
3. Most users use the 64x64-image resolution. Beware of that the maximum number of images (=slices x # volumes) possible to acquire (using the epibold or epiboldseq sequence) per scan is about 5000 images. This is due to internal memory limitations. For higher resolution, the number of images is less.

### During scanning

1. You are encouraged to use the fMRI standard protocol #59. It consists of  
Series #1: Sagittal scout  
Series #2: 3D SPGR (optimized for gray/white matter contrast)  
Series #3: epiboldseq (The fMRI pulse sequence. 'seq' means that the slices are excited 1,2,3,...,n rather than 1,3,5,7,...,n-1,2,4,6,...,n in order to be able to do time adjustments in SPM for event related fMRI.)  
Series #4: 2D T1-w SPGR. To get T1-weighted images with bright signal from the vessels. Not everybody wants to use this series; that's why it is after the epiboldseq.
2. The most common changes you have to do to fit your needs will be to change some parameters for the epiboldseq sequence:
  - \* On User CV page: Change the number of BOLD reps to the number of image volumes (time points) you have in your paradigm. NOTE: The number of BOLD reps MUST be an even number; otherwise the scanner won't start.
  - \* On Scan timing page: Change the TR to the time resolution you want to have in your experiment. The lower TR, the fewer slices that can be used = less brain coverage. Approx. 10 slices can be acquired per second.
  - \* On Scanning range page: Change the number of slices.
3. When you are on the Scan Ops page of series 3, you should not press Cancel until you have scanned all fMRI series on your volunteer. Do the following:
  - \* Press Scan (AutoPrescan will start, and one image volume will be scanned and stored in the image database)
  - \* Press Modify CV, type boldscan [ENTER], type in the value '1' [ENTER], press Backup (NOT Cancel). Now you have instructed the pulse sequence to scan all image volumes you have requested and dump all data to disk instead of putting them in the image database. Raw data dumping is necessary because the image database cannot store more than 512 images at a time.
  - \* Press Prep for Scan to prepare the scanner to start immediately when the Scan button is pressed. If the Scan button is not pressed within 30 sec you have to press Prep for Scan again.
  - \* Inform the volunteer that the scan will start
  - \* Press Scan (and the button on your computer keyboard)
  - \* After each completed scan, data is transferred to ladybird:/raw\_images/<patID>/<exam number>/fmriX, where X=1 for the first scan, 2 for the next, etc.
  - \* If you want to do another fMRI scan with the same scan parameters, you can press Prep for scan followed by Scan again. If you want to change the number of image volumes (time points) you can do it by pressing Modify CV. Type opuser4 [ENTER] and type in the number of image volumes (remember, an even number). Press backup. Note that other parameters, e.g. TR (Modify CV: optr) cannot be altered without a new prescan. If you need to change the TR, set boldscan=0 and do an AutoPrescan, set boldscan=1, followed by Prep for scan and Scan.
  - \* After each successful transfer of raw data to ladybird:/raw\_images you will get a notification window on the plasma screen.

## After scanning

### STEP 1: Your fMRI data:

When the raw data files (*P:xxxxx*) have been transferred to */raw\_images* they are erased on the MR scanner. Data is stored under */raw\_images/<patID>/<exam number>/fmriX*. To reconstruct MR images from the raw data, type:

```
cd /raw_images/<patID>/<exam number>/fmriX
epirecon -F -f Pxxxxx &
```

The *-F* flag stand for Fermi filter. Unless you know better, use it.

After the images have been reconstructed they are named: *I.001.s01, I.002.s02...I.0nn.smm*, where

*I.\*.s01* = all images (in time) for the first anatomical slice

*I.001.s\** = all slices for the first image volume

Note: The images have no image header, unlike the anatomical images transferred from the image database which have a header size of 7904 bytes.

The pixels are 16-bits signed short.

### STEP 2: Your anatomical images:

To get your anatomical images in the same directory as your fMRI series, type:

```
cd /raw_images/<patID>
getmr
```

After this the directory */raw\_images/<patID>* will now contain:

```
001 002 003 fmri1 fmri2 fmri3 ...
```

### STEP 3: Convert fMRI data to Analyse format

Data is stored according to the radiological convention.

For the anatomical series, type:

```
cd /raw_images/<patID>/<exam number>/002 (where series 002 is the 3D SPGR)
ge2spm
```

For each fMRI series, type:

```
cd /raw_images/<patID>/<exam number>/fmriX
ge2spm -hdr ../003/I.001 (where series 003 is the single EPI volume that was stored in the image database when boldscan=0)
```

*ge2spm* uses the header information (slice thickness, orientation, resolution ...) from that image in the conversion process.

After conversion, you can erase all *I.0XX.sXX* files, by typing

```
rm I.???.s?? in each fmriX directory.
```

It is recommended not to delete the *P*-file or the *.dat*-files since other reconstruction methods may be available later.

### STEP 4: Move or burn your data

*Alternative 1:* Copy the directory tree */raw\_images/<patID>* to your disk using *cp -r* (if you can access your disk via NFS) or *gftp* (Graphical ftp program that can transfer an entire directory tree).

*Alternative 2:* Login on *cicada* (SUN Ultra 1 in the room between the two scanners).

Insert a blank CD (not one of ours!) into the CD-R drive next to *cicada*.

Open a terminal shell and type:

```
burncd /raw_images/<patID>
```

*Alternative 3:* Use the Linux PC (*bee*, Linux account required) next to *cicada*. From this PC you are able to burn CD-R, CD-RW, DVD-R (recommended) and DVD-RW (again, bring your own media even though there are empty CD's within the length of an arm). Use the command *burncd* to burn CD's and *burndvd* to burn DVD-R's. NOTE: For DVD's there is no support for multi-session. With current settings all swedish characters (åäö) are converted to '\_' and all filenames will be in lower case. The advantage is that it is faster to read on your PC. If you need 'åäö' and case sensitivity, use *burndvd2* instead.

**NOTE! All images older than 4 days are erased every night automatically from */raw\_images* in order to maintain free space on the disk (18 GB). As a courtesy to the next researcher doing fMRI, please erase your data after you have moved/burned it.**