

About Scanning at the Lucas Center

Our general operating procedure

(This will contain some information for new lab members about how we scan, and maybe links to informative web pages.)

Coils We Use

(A coils list here, w/ comments) Posthead Transmit/Receive (Tx/Rec): Posthead Receive-Only (Rec): fmriCoil: RessCoil2000:

Protocols We Use (last updated Feb-2004): (List of recent protocols here)

Getting Started

Preparations

Before you start, you should make sure:

- 1. The subject has completed a <u>consent form</u>.
- 2. You know which protocols you are going to use. 3. There is free <u>disk space</u> to store your data on lab computers.
- 4. You have stimulus code/machine present and ready.

Consent forms:

- Subject should sign 2 copies of the consent form. One goes to the subject and one stays in the lab. (These are kept in the filing cabinet in room 457 when you get back to Jordan.)
- Subject has to fill the yellow form in the scanner. All the answers to medical questions should be .no. to be able to scan Subject have normal or corrected-to-normal vision. If the subject would normally require correction, they have two options: 1) They
- can wear contacts or 2) They can use the set of magnet-compatible lenses stored in the black binder in the rear of the control room. These have a plastic frame (in the middle of the binder), and a set of L/R lenses -- all in integer # of diopters, so some subjects may need to round off. The glasses may be better if the subject worries about eyes drying out while using contacts (which will be exacerbated if the fan is kept on).
 - Put clean sheets on the scanner table and on coil .pillow. • Subjects should go to the restroom before the scan.
 - · Subjects should take off the shoes. There are small slippers if
 - the subject doesn't have socks. All subjects must wear ear plugs. There are new 37 dB
 - protection ear plugs on the top left shelf at the 3T. Check carefully that subjects do not have anything metallic
 - items on them such as jewelry, coins, piercing, knives, credit
 - cards, etc. before they enter the scanner room Keep the scanner door closed at all times.

Stimulus Setup

Button Box:

- 1. Connect the button box (large black box, usually near projector switches) to the usb port (It may sometimes be near Ochre3, the Heeger/Wandell lab G3 on the side; but this is rarely used as of 02/04)
- 2. Check that the button box is operating before you landmark the subject. Note that the keys stick sometimes, and sometimes matlab has problems getting the USB input. Test out the inputs while running
- matlab before continuing. Serial port 3. Connect keyspan device to USB port of the computer
- 4. Connect the serial connection (labeled "scan trig", located by the
- audio box) to the number 1 keyspan port Visual Display: 5. Connect the laptop to the video in of the vga splitter
- 6. The monitor connects to video out 2 of the vga splitter (this is
- ususally permanently connected) 7. Connect the lcd projector to video out 1 of the vga splitter
- 8. Switch the dial to select the projector source to the laptop position 9. After you landmark the subject and put him in the correct position in

the scanner run in matlab: mm demo

Check that the stimulus is centered & focused - Check that the subject can:

See all the display area Read the text

See the fixation

Close the lights in the scanner room!

Starting the Scan

- Enter scanner mode: click scanner icon in upper-left corner of display • If exam is in progress, select End Exam in Rx Manager and Confirm.
- Click New Patient.

of birth)

- In Patient Position area: Patient ID: K. GrillSpector xxx (xxx are your initials).
 - · Patient Name: subject's full name .
- Weight: subject's weight. Exam description: brain dob mm/dd/yyyy (date of subject's date

Protocol Selection (schematic representation of human body)

- Protocol set to Site (not GE).
- Click the head of the body schematic (protocols will appear).
- Select appropriate protocol (make sure it has the right coil selected) • Click the head of the body schematic (protocols will appear).

• Accept.

- Put subject in scanner (make sure subject has earplugs)
 - Landmark subject.
 - Clean out P-files from mrsic3t before funning functionals: Go to tools (icon, upper-left)
 - Open c-shell (button, lower-right of tools)
 - >> cd /usr/g/mrraw >> rm P*
 - >> rm E*

Do not remove Header Pool file. Check that Header Pool file exists. If it doesn't, stop now and page Anne/Gary for help.

Functional Session: Running Anatomicals

Localizers

There are a few different types of localizers that are used. Most KGS-lab scans start with a 3-plane scan.

3pln (3-plane)

This scan will give you 9 slices from one of each plane:sagittal; coronal; axial. It's useful for verifying that the subject's head is properly placed in the center of the scanner bore, and for proscribing other localizers (or, if needed, inplanes can sometimes be directly proscribed off of these).

- 1. Select 3pln/localizer scan. 2. Save Series.
- 3. Prepare to Scan. 4. Alert subject that localizers are coming.
- 5. Select Scan in Scanner Control area.
- 6. Scanner will automatically run a prep for about 30seconds followed by the localizer scan. When scanner stops, images should be displayed in miniviewer in upper-right of display¹
- 7. Maximize to enlarge display 8. Scroll through localizer images. Use scroll bar on the right-hand side of the viewer. Select the coronal slice which is the center of the brain. Write down the image number. You will use this slice to prescribe the sagital localizer scan

Sagittal localizer

1.

In different protocols they have slightly different names. These are 60 sagittal T1 weighted images. We collect them for 2 purposes:

• To use them to prescribe the inplanes & functional slice orientation and location. • Align the volume collected in this scan to the 3D hires volume anatomical from which the subject's brain was reconstructed.

- 1. Select localizer series: sag localizer / 3D anatomy scan in Rx Manager. 2. If desired, enter/change slice-thickness (in millimeters) in bottom of Scan Parameters. 3. Select Graphic Rx in Scan Parameters
- 4. Select desired localizer image using the slider on the left-handside of display: should be the widest coronal slice; usually around the center of the brain. 5. Prescribe slab for the sagittal scan. Should cover the head left to right & up/down. If it doesn.t cover left to right change slice thickness. 6. Set Fallback to R0.²Accept.
- 7. Save Series
- 8. Protocol selection should automatically select and download the localizer scan. If this is the case, the Scanner Status area on the left-hand side of the display should indicate that series 2 had been downloaded. 9. Prepare to Scan.
- 10.Alert subject that localizers are coming.
- 11.Select Scan in Scanner Control area. Scanner will automatically run a prep for about 30seconds followed by the localizer scan. 12. When scanner stops, images should be displayed in miniviewer in upper-right of display. Maximize to enlarge display; scroll through localizer images. Use scroll bar on the right-hand side of the viewer. Adjust brightness and contrast. Press middle mouse button Drag target up/down to increase/decrease brightness. Drag target left/right to increase/decrease contrast. Select slice that extends most posterior (towards the back of the skull) and that has a good view of calcarine sulcus.
- 13.Note slice number (slice number appears on upper left corner of image display) for inplane prescription and screen save

Inplanes

Select Inplanes2D or Inplanes3D series in Rx Manager.

Select slice-orientation indicated by Plane under Imaging Parameters. If desired, enter/change slice-thickness (in millimeters) in bottom of Scan Parameters.

Select Graphic Rx in Scan Parameters. Select desired localizer image using the slider on the left-handside of display. Adjust brightness and contrast, if necessary.

1. Prescribe slices:

For 2-D inplanes: (inplane anatomicals)

· Click mouse left-button to make slice-prescription visible.

• Orient prescription into appropriate position³

For 3-D inplanes: (inplane 3d)

• Drop slab by clicking mouse left-button. • Orient slab into appropriate position. Note that here there will be 4 more slices than the functional inplanes! • In the CV panel make sure that gain is set to 10.

For both 2-D inplanes and 3-D inplanes:

• Set Fallback to R0

• Accept.

• Make sure Freq DIR in Acquisition Timing section below Autoview window is not set to R/L^4 • Save Series. For 3-D inplanes, you should print screen or write down obtain start-end locations (L/R; A/P; S/I).

2. PRINT SCREEN- save picture of Graphic Rx localizer: Print screen by hitting

3. Print 4. on the printer.

5. Prepare to Scan (wait while inplanes download). Scanner control display (small monitor to the right of scanner interface) should show timing for the new series. 6. Alert subject that he/she will move.

7. Move to Scan.

8. Alert subject scan is coming. 9. Scan. Prep will run for 30 seconds, followed by Inplane scan.

10. Functionals can be setup while Inplanes are being collected. See Functionals steps 1-5.

11. When scanner is done running, examine Inplanes in viewer or browser to make sure all is well⁵. 12.If manual prescan (2D inplanes only):

• Alert subject.

· Auto Prescan. • Manual Prescan.: Manual prescan window opens.

• In window, click on Scan TR (R1/R2) at top right. • Adjust Digital Gain slider so that R2 values fall within 30-70% range (typically30-40%).

Screen Save

* Save Screen

• Done.

Must be done prior to Data Management. Can be done as soon as Inplanes are done.

* Click browser icon in upper-left * Within image-view window, click browser left-hand side

* Select current patient in left-hand window * Select appropriate series in right-hand window

* Select chosen slice in bottom-window * Viewer

* With image slider, choose localizer image number that was used to do the inplane graphic Rx. * In blank area at lower-left of screen, type xr s# * (# = inplane series number, usually 2)

* Click browser and choose the screen save series when it appears Viewer Adjust brightness and contrast using middle mouse so that brain and slice prescription are easily visible Print screen by hitting Print on the printer. Write and protocol name on the back of the screen save and take notes about each

individual scan (Pfile numbers, etc.).

1 If localizer images aren't displayed, select update to load them.

2 If fallback is not on, then the acquired volume will be centered on the slice that you prescribe from. This can screw up the functional volume position if you copy the inplane Rx while a slice other than that which you prescribed from is displayed! The volume will be the same as the inplanes in two dimensions, but in the third dimension it will be centered on the currently displayed slice. If this is all too confusing, just be sure to turn fallback on for both inplanes and functionals. As long as your subject's head is appropriately landmarked, everything should work fine with fallback on.

3 There are three markers on the bottom slice of the slice prescription. Left mouse button down-pressed on markers will change number of slices and prescription rotation. Left mouse button down-pressed with drag motion will change position of the whole prescription.

4 May be set to either A/P or S/I depending on slice orientation.

5 If images not visible:

* Click on browser icon (the upper-right most of the six icons on the leftof the screen) * Click browser button on left-hand side in middle of screen

* Click on subjects name in left-hand window

* Click on inplane series in right-hand window * Click on selected inplane in bottom window

The differences between the 2 series are the TR (1 or 2s) and the flip angle which differs for different TR. You could use the same series and change the TR value but then you need to update the flip angle according to your new TR. If you are going to use Sprl TR 1 and Sprl TR 2 within one session make sure to copy the slice prescription from the inplanes (either from the graphic RX manager or using the location value). When you switch between the series types the 'move to scan button' may light up. Please ask the subject if the bed has moved. IT SHOULD NOT MOVE. If the bed has moved you probably didn't update the slice prescription properly. Please update it and the bed will move to original location!

Data Transfer; Cleaning Up

First you will want to make sure you have done a successful screen save for this session.

Data Management: moving anatomies and Pfiles to local drives

There are separate instructions for anatomicals and functions. The reason is that anatomicals are created on lucas and the functions are created on mrsic3t.

Checking that you have enough disk space:

Prior to starting, you should have made sure you have enough disk space on your local drive partition.

>> ssh moach -l username [e.g., 'sayres'] password: >> [enter your password]

>> cd /biac1/kgs/mri/ $\frac{11}{1}$ >> df - h.

You will get an output like this:

Used Avail Use% Mounted on **Filesystem** Size

biac1:/u3/kgs 806G 741G 24G 97% /biac1/kgs In this case, Avail=24G, so we have 24 Gigs of free space. There should be at least 4 Gigs of free space, or you're in trouble. (Realistically, a session will take up 1-2 Gigs of space usually, but it's important to leave some buffer space on the RAID.

Transferring Anatomicals:

Transferring from the scanner to lucas

There is a script set up on the heeger@lucas account to set up the session structure nicely, and get all the anatomical data files. Open a C-shell and do the following:

>> ssh lucas -l heeger >> password : v1->mt

>> simptrans3.sh Date:

>> mmddyyXX [XX are subject's initials, e.g., 071302pb -- referred to as a session code] Exam Number:

>> ZZZZ [this is a 4-digit code, which can be found in the preview window in the upper left corner] Localizer series #: (enter the number of the series off of which you prescribed the inplanes--usually 2 if you did a 3-plane plus sag localizer)

>> 2 Inplane series #:

>> 3 Screen save series #:

Now there should be a session directory present in your working directory (/local/heeger/), named after the session code (e.g. 071302pb). This should contain a Raw directory. The Raw directory contains an examNum.txt file, an Anatomy directory, and a Pfiles directory. We want to get the whole thing over to our local drives, and transfer the pfiles there. There are two ways to do this: using FTP and SCP. SCP is preferred.

>> exit

>> 99

The heeger@lucas account generally doesn't exit cleanly (for an unknown reason), so you'll probably need to close the window to close the connection.

Make a tarfile of the anatomies (localizers, inplanes, and screensave) on lucas: Log in as usual.

>> cd /local/heeger/ >> tar cvf .tar >> exit

Now transfer the anatomy files from lucas to moach

To FTP the anatomies to local directories

>> ssh moach -l [username] >> cd mri/raw >> ftp lucas Username: >> heeger Password: >> v1->mt>> cd /local/heeger >> bin >> get mmddyysessiondCode.tar >> bye

>> tar xvf .tar

To SCP the anatomies to local directories

You can also scp files directly to our machines instead of tarring them. For this you ssh to moach.

- >> ssh moach -l username
- >> cd /biac1/kgs/mri/ 11 >> scp -r heeger@lucas:/local/heeger/mmddyyXX.

you will be prompted to enter a password (enter the heeger password @ lucas, v1->mt)

Functionals: Pfile transfer

Log into moach and cd to the local partition you're using to store your data (e.g., /biac1/kgs/mri/):

>> cd /Raw/Pfiles >> ftp mrsic3t >> cd /usr/g/mrraw Username: signa Password: 30tlucas >> cd /usr/g/mrraw >> bin >> prompt >> mget P* (repeat for each P* and each P*.mag file) >> mget E* (repeat for each E* header file) >> bye

11 The location on the RAID, /biac1/kgs/mri/, is the current location as of March 1, 2004, but may change. Some other locations to keep data are: The second RAID partiion: /biac2/kgs/mri/ Scratch directories:

/eynaim/scr1/mri /eynaim/scr2/mri

Running a High-Res Volume Anatomy Scan

The purpose of these scans is to aquire a high resolution volume of the brain to reconstruct the cortical surface and flatten the brain. You can do volume anatomicals either on the 3T or 1.5T. The 1.5T has the advantage that there is less inhomgeneity between center and periphery compared to the 3T, which makes the segmentation easier.

The most important parameter that governs the quality of our scans is that the gain/scale factor parameter in the CV window be set to a value of 10.

At the 1.5T, there is a choice of two coils: one large (white coil :"HEAD") and one small ("SMHEAD"). The smaller head coil gets ~50% signal-to-noise. However, not everyone's head fits inside this coil. The large head coil is a GE coil and it is encased in light-colored plastic. The small head coil is encased in dark gray/black plastic. Our protocol is currently set up for "SMHEAD" if you choose the other coil "HEAD", you must make a change to all the series in the protocol to be setup for "HEAD" instead of "SMHEAD. The Wandell lab (and Gary) prefer anatomy collection at the 3T. This uses the "FMRIC" coil. The Wandell lab collects these with the protocol: wandell-helmet-anatomy-mprage-fspgr [old, should be verified/replaced].

The subject's head is stabilized inside the coil with foam pads. There is no display¹ to set up for these scans. Like the functional scans, it is necessary to know the subject's weight and birthday.

Volume Anatomy Scanner Instructions

Set Up

- 1. Enter scanner mode: click scanner icon in upper-leftcorner of display. 2. If exam is in progress, select End Exam in Rx Manager and Confirm.
- 3. Click New Patient.
- 4. In Patient Position area: • Patient ID: kgrillspector xxx (xxx are your initials).
- Patient Name: subject's full name. • Weight: subject's weight.
- Exam description: brain dob mm/dd/yyyy (date of subject's birth) 5. Put subject in scanner. Landmark subject.
- 6. Protocol Selection (schematic representation of human body) • Protocol set to Site (not GE).
- Click the head of the body schematic (protocols will appear).
- On the 1.5T: select kgs-vAnat-smhead-082002 On the 3T select: wandell-helmet-anatomy-mprage-fspgr

Scout

- 1. Select scout series. This series scans in 3 plane : 7slices per plane.
- 2. Save Series 3. Prepare to Scan

• Accept.

- 4. Alert subject that scout is coming.
- 5. Select Scan in Scanner Control area. Scanner will automatically run a prep for about 30 seconds followed by the scout scan. 6. When scanner stops, images should be displayed in miniviewer in upper-right of display, images aren't displayed, select update to load them
- 7. Maximize to enlarge display. Use scroll bar on the right-hand side of the viewer. 8. Adjust brightness and contrast. Press middle mouse button. Drag target up/down to increase/decrease brightness. Drag target left/right to
- increase/decrease contrast. 9. Scroll through localizer images. Choose the longest axial slice. You use this slice to prescribe the coronal slices of the localizer scan.

10.Write slice number of longest axial slice. Localizer

- 1. Select localizer series. Localizers in this case are coronal slices.
- 2. Choose Graphic Rx.

3. Prescribe coronals off the longest axial slice. Slices should cover the whole brain front to back. Try to get middle slice co-aligned with the middle of the brain. Calculate brain length:

slices * (slice thickness + gap)/10.

- This will give you brain length in cm.
- 4. Print screen 5. Save Series
- 6. Prepare to Scan
- 7. Alert subject that localizers are coming.
- 8. Select Scan in Scanner Control area. Scanner will automatically run a prep for about 30 seconds followed by the localizer scan. 9. When scanner stops, images should be displayed in miniviewer in upper-right of display. If localizer images aren't displayed, select update to load them
- 10.Maximize to enlarge display. Use scroll bar on the right-hand side of the viewer. 11.Adjust brightness and contrast Press middle mouse button. Drag target up/down to increase/decrease brightness Drag target left/right to increase/decrease contrast. 12.Scroll through localizer images
- 13.Write down slice number of widest coronal slice.

3D Anatomy

- 1. Hilight 3D Anatomy series in Rx Manager. This scan is ~24 min.
- 2. View/Edit 3. Select Graphic Rx in Scan Parameters.
- 4. Scroll through and select chosen Localizer image using ImageNumber Slider on the left-hand side of display. Adjust brightness and contrast, if necessary 5. Turn-off/deselect Auto W/L. 6. Prescribe slices:
- These are 3D inplanes and are prescribed as such.
 - Drop slab by clicking mouse left-button. • Orient slab so it will cover the brain R/L.
 - If the skull doesn't fit inside the slab, adjust FOV:

view).

- Erase all (in Graphic Rx) • Accept.
- Adjust as necesary:
- FOV in Scanning Range
- Slice Thickness in
- Scanning Range • Return to Graphic Rx.
- Select chosen slice.
- Increase slice thickness in increments of 1/10 (i.e. $1.2 \rightarrow 1.3$).

adjusts the FOV along the coronal and axial directions (the y direction in Graphic Rx

adjusts the FOV along the sagittal directions (the x-direction in Graphic Rx view).

- Drop and orient slab again with one left-click of the mouse. slab should appear wider now.
- 7. Set Fallback to R0. 8. Accept.
- 9. Make sure Freq DIR in Acquisition Timing section below Autoview window is not set to R/L. May be set to either A/P or S/I dependingonslice orientation.
- **10.Save Series**
- 11.Prepare to Scan (wait while inplanes download). 12.Scanner control display (small monitor to the right of scannerinterface) should show timing for the new series.
- 13. Alert subject that he/she will move
- 14. Move to Scan
- 15.Alert subject scan is coming. 16.*Scan*. Prep will run for 30 seconds, followed by Inplane scan.

Screen Save

Can be done only after 3D anatomy is collected. 1. Click browser icon in upper-left. 2. Within image-view window, click browser left-hand side. 3. Select current patient in left-hand window. 4. Select Localizer series in right-hand window. 5. Select chosen slice in bottom-window. 6. Viewer 7. With image slider, select chosen image. 8. In blank area at lower-left of screen, type xr s# (# = inplane series number, '3' in this case) 10. Save Screen

Acquiring hires volumes anatomies on the 3T:

- 128 sagittal slices: 1.2 mm thick
- protocol name: wandell-helmet-anatomy-mprage-fspgr In this protocol you can use of two 3D sequences : mprage or fspgr. Opinions vary as to which type is easier to segment; consult someone in Brian or Kalanit's lab. This protocol is used for acquitting hiresolution brain volumes for reconstruction and flattening. The scanning instrux are the same as for the 1.5t

 - 2. anatomy localizer (coronals)
- Data Management: preparing and anatomies and moving them to local drives

- >> cd /local/heeger b. Run script: If the volume anatomy was collected at the 1.5T, run:
- >> anattrans.sh If the volume anatomy was collected at the 3T, run: >> anattrans3.sh You will be promted with the following: Subject:
- >> mmddyyXX (XX initials) Localizer series #:
- >> 2 (coronals) Inplane series #: >> 3 (sagittals) Screen save series #:
- >> 99 2. When the script is done running, copy over the anatomies to a local disk:
- instructions except that series name are different: 1. anatomy localizer (3pln)

 - 3. fspgr 128 slices; FOV=24; thickness=1.2mm (approximately 24minutes) 4. mprage 128 slices; FOV=24; thickness=1.2mm (approximately 24minutes

- 1. Session Initialization and transferring anatomies 5 a. From Tools window, open shell, login to lucas:
- >> rloginlucas -l heeger Password: >> v1->mt

>> ssh -l username moach enter your password >> cd /biac1/kgs/mri/

From the destination location type: >> scp -r heeger@lucas:/local/heeger/mmddyyXX . Enter 'yes' at warning. Enter password at prompt:

1 Although there's no stimulus to set up, sometimes the operator will set up the display and play a dvd off of a computer to keep the subject occupied.

Other Useful Information

How to...

>> v1->mt

Run Real-time fMRI

This is used to see the results of the functional scans as they happen. This can be quite useful to do several things: for instance, to check for scanner spiking noise, check that localizer reference scans are working, or confirm that the prescribed inplanes contain the functional regions you're interested in. The main instructions for running this are on **David Ress' page**. However, there are a few notes here that may be of relevance to people in Kalanit's lab:

[coming up ... :)] **Do Manual Shimming**

After Scanning...

1. Back Up Your Data 2. Create a link in your project directory 3. <u>Copy Over Stimulus Files</u>

4. Input and Upload Session information

Back Up Your Data

This is of course the first thing you should always do.

Kalanit asks only that you copy the P*.7 files from your scan, but it's probably a good idea to copy the P*.7.mag files too, as data CDs do sometimes fail if they're stored too long, and extra backup is helpful. It might sometimes help to copy over your stimulus code first, but do not forget to burn CDs or DVDs of the MRI data files.

Create a link in your project directory

1. Logon to a linux machine (e.g., moach, white, eynaim) • Windows machines: use an SSH program like putty.

- Mac OSX: Open a Terminal window; type 'ssh moach -l [myaccount]'. • Linux: You're there.
- 2. cd /biac1/kgs/projects/
- 3. If this is the first session of a new project, create a new directory for that project. For instance, we'll use a sample session from a study on distance representation, 10/06/03 js: we'll make a distance project directory: [sayres@moach projects]> mkdir distance

and cd into the directory for that project:

[sayres@moach projects]> cd distance

Note also I can nest these, so if this session is a 'track hybrid' experiment within the distance experiment, I could also make:

[sayres@moach distance]> mkdir trackhybird [sayres@moach distance]> cd trackhybrid

- 4. At the same time as making the project directory, you'll also want to input some information about your project by going to this web page and filling in the fields (ask Rory if you have any questions). 5. Check that the project is in the /biac1/kgs/mri/ directory after the scan:
 - [sayres@moach trackhybrid]>ls /biac1/kgs/mri/

Look for the directory entry, e.g. '031006js'. 6. Make a link to the mri directory in your projects directory:

[sayres@moach trackhybrid]>ln -s /biac1/kgs/mri/031006js/ js031006

(Note that I named this link by subject--is031006--because I like it that way; you can actually name your link however you like)

Copy over stimulus files (optional)

This is a helpful thing to do for a few reasons. One, it lets you have a copy of whatever stimuli you used on that particular session. So if you update your stimulus code or scripts, you don't lose track of those changes. Two, if the stim directory is set up a certain way, setup scripts can automatically upload all your stimulus information onto the database, making it easier for anyone to e.g. get or make .prt files of a given stimulus/scan. Also, it's helpful to have any behavioral data you collect right by the MRI data.

From your display computer, upload your matlab or other stimulus files to the RAID. Make a directory within your session directory named 'stim':

[sayres@moach js031006]> mkdir stim

Then upload your data from the stimulus computer to the stim directory. On a MacOS 9 Mac, you can use NiftyTelnet SSH and use the 'SCP' option to do this. You can put anything in the stim directory, but to get maximal usefulness out of this, it helps to have things a certain way.

Here's an illustration. The parfiles and prtfiles directories contain .par and .prt files for this session's stimuli, respectively. The scripts directory contains the original scripts used. The contents of all of these files are automatically uploaded to the database when session information is entered. Also, any .m files within the main stim/ directory are automatically uploaded for safekeeping.

Input and Upload Session information

First, you'll need...

· A machine with access to the RAID

A copy of MATLAB 6.5 or greater on your machine • The username (vista) and password (ask Rory or Bob Dougherty) to get on to the mrData web page

Windows machines

Before you begin, you'll also need to copy a system file to your machine so that it can automatically access the online database. The file is located at:

/biac1/kgs/dataTools/VISTASOFT/mrData/libMysql.dll

and you need to copy it to:

C:\WINNT\system32\ or C:\WINDOWS\system32

(depending on your version of windows, and assuming C:\ is your main partition.) Contact Rory if this is at all unclear.

Okay, we're almost done ...

- 1. Open MATLAB
- 2. cd to where you have the RAID located 3. >> cd dataTools
 - 4. >> addpath pwd

5. cd to where the session is. E.g.:

>> cd(RAID);>> cd projects\distance\trackhybrid\js031006

6. >> SetupSession

The code will take a few seconds to check your paths, then show you a set of the following four dialogs:

The second	Contractory
	. p.a
	and the second sec
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(800.)		4
a les che c	reserves along the roand	ALC: N
Contraction	26nd were small	Hanest Carmer 7

Fill out whatever is applicable in each of the dialogs. This will generate, among other things, a 'Readme.txt' file in the directory summarizing this session:

17124 55113

Last modifie

7. The code will then try to upload all the information about this scan to the database. First, it will try to log in to the mrData database. Enter the password for vista, plus your username to log in. Then, depending on how things are set up, it may ask you to clarify a few things about the session. For instance, it may ask you to pick the subject from a list of subjects in the database, or choose what kind of display was used (most KGS sessions use the 3T front bore projector). Then it will give a bunch of text indicating upload progress. 8. You're done! Have a cigar.

Okay, but how do I actually look stuff up in the database?

That part's coming up. But you can check here to see the results of your diligent uploading work, and see what else is in the database.

Name_	<u>Birthday</u>	<u>Height</u>	<u>Weight, lbs.</u>
Rory Sayres	11-24-1977	5'9"	150
Kalanit Grill-Spector	???	5'8"	120
Junjie Liu	05-06-1981	5'9"	150
David Andersen	??????	5'9"	185
Janelle Weaver	09-12-1977	5'4"	120
Sven Heinrich	????	???	???
Hyejean Suh	????	???	???
Joakim Vinberg	????	???	???
4-Mar-19 05:28 GMT.			