

SPM Lab II Tuesday, August 16 2005 1-3PM BME 499/Biostat 642

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Name: _____

Group Number: _____

Dataset Used: _____

Goals of this Lab

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After this lab you will...

1. Be able to perform coregistration between the low resolution and high resolution structural images. You will understand the implications for a image to be the "Source" vs the "Target" in terms of the "world space" of each image.
2. Be able to perform spatial normalization, check its success, and apply the transformation to a contrast image.

Coregistration

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SPM's "Coregister" facility is used for registering different types of images from the same subject (it is a "intermodality, intrasubject" registration). To use it you must specify a "Target" or reference image, which does not move, and an "Source" image, which is moved to match the target.

Recall that the rigid body transformation is recorded in the .mat file of the source image. Hence, it is not necessary to write out the transformed image (the Source transformed into the space of the Target), though it is sometimes convenient to do so.

Before coregistering the low- and high- resolution structural images we need to (I) make sure the two images are in the same orientation and not too far from one another, and (II) correct for intensity inhomogeneities in the high-resolution SPGR image.

0. First see how close the hetlooverlay and hetlspgr images are to start with. What button do you use to view more than one image?

Multiple images are displayed in the space of the first image. If they are not previously registered this simply means that their origins are lined up.

Neither image has had their origin set. The default origin is the center of the volume. To see the specific voxel that is defined as the origin, use 'Display' and look in the lower right panel.

1. If the images were very out of register we could try to get the images closer by manually setting the origin to the Anterior Commissure (AC).

- A. On the board will be a diagram of how to find the AC on the midsagittal plane. Sketch it here

- B. Now use the Display button view the hetlooverlay image and locate the location, as best possible of the AC. You should be able to see it on the axial slice.

Hint: Once you are close, it helps to "zoom in". In the display facility, click on the "Full Volume" pop-up menu; select "80x80x80 mm"

What is the location of hetlooverlay's AC in voxels?

_____ Voxels

- C. Use the Display button view the t1spgr image and locate the location, as best possible of the AC.

What is the location of t1spgr's AC in voxels?

_____ Voxels

_____ mm ?

- D. At this point we *could* set each image's origin using "Reorient images..." button in display but we won't. But just for reference...

How to change the origin (again, don't do it now!)

View the image whose origin you want to set, using the 'Display' button. By default, the crosshairs start at the currently-defined origin. (If you've previously been using 'Display' facility, and you're not at the 0,0,0 mm point, click the bar below the title "Crosshair Position".

To change the origin, take the AC location in mm and *multiply* by -1. Enter these three values in the first three boxes on the left ("right {mm}", "forward {mm}", "up {mm}").

See where the crosshairs are located. If they are over AC, then you can continue. Otherwise, you need to adjust the shift values until the crosshairs are over AC

When the crosshairs are right on AC, you've found the correct shifts to move the previous origin to AC. Click "Reorient images...". Select the set of images (any number!) in the same space whose origin you want to change.

We're not changing the origin for two reasons. First, the images *should* already quite close, but there's a more important reason.

By setting the origin on the Target image (hetlovely), we change its "world space"; specifically, the origin of its world space moves from the center of the volume to the AC. Hence it will no longer have the same world space as the functional data *unless* we identically change the origin on all the functional data and any results (beta*, con*, spm_T* etc) we already created.

To summarize, if the images are way off, we can set the origin manually to help the Coregistration. But if we change the origin of the image representing the functional space, we have to similarly change the origin on all functional images.

2. Two processing steps have been performed to the structural images. They have had been scalp-edited and corrected for inhomogeneity.

The t1 images have signal from the scalp and head. Since this extraneous information can throw off subsequent processing steps the image is scalped edited with FSL's BET software. The resulting images are prefixed with an 'e'.

Compare 't1spgr.img' to 'et1spgr.img'. Check the quality of the scalping.

Are there any brain regions accidentally 'scooped-out'? Where?

Are there any nonbrain tissues that should have been excluded? Where are they? (Hint: Check the sagittal sinus).

Anatomical images obtained with high-field magnets (>2T), tend to be brighter in the center of the field of view than at the edge. This inhomogeneity can throw-off subsequent processing steps, especially segmentation. The T1 'e'-images have been corrected for inhomogeneity with a script by Gary Glover and Kalina Kristoff; they resulting images are prefixed with an 'h'.

Compare 'et1spgr.img' to 'het1spgr.img'. Can you see the greater intensity in the center of the et1spgr image? Does the het1spgr image look better? (Use window controls to make the images look similar over all.

3. Coregister!

You will now "Coregister" the high resolution, het1spgr image to the hetoverlay image. The hetoverlay image has the same space as the functionals, and hence this coregistration will set het1spgr's world space to correspond to the functionals.

A. What is your "Target" image?

B. What is your "Source" image?

(Stop! Ask if this is right before you continue.)

C. Click on the Coregister button. You only have one subject and you want to "Coregister & Reslice". You will be asked for the modality of "Target" and "Source" image. What is modality of each? (Circle one)

Target Modality: PET T1 MRI T2 MRI PD MRI EPI Transm SPECT

Source Modality: PET T1 MRI T2 MRI PD MRI EPI Transm SPECT

Select the Target and Source images you identified above.

It asks for "Other images". This would be useful if we had other images that were acquired in the same space as the SPGR. We don't, so just click 'Done'.

Now it will perform the coregistration.

The transformation parameters are written in the .mat file of the source image hetlspgr.img; this sets the world space of hetlspgr to match that of hetlooverlay. Since we asked it to "Reslice", it will also create a rhetslspgr.img, an image with the same dimensions and world space as hetlooverlay.

D. Note changes in world spaces.

"Display" hetlooverlay.img and use the "World Space"/"Voxel Space" pop-up button to change between the two spaces.

Does the image move as you flip between the two spaces?

"Display" hetlspgr.img and do the same again.

Does the image move as you flip between the two spaces?

Why does one move and the other doesn't?

D. Check the success of the Coregistration.

Use check reg to check the registration. Check the points mentioned in the last lab:

- i. Frontal pole
- ii. Occipital (posterior) pole
- iii. Left & Right sides (e.g. superior temporal gyrus)
- iv. Corpus collosum: (1) Most anterior, (2) most superior and (3) most posterior extent.

Also try tracing sulci.

Has the coregistration succeeded?

Spatial Normalization

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Spatial Normalization is SPMese for intersubject registration. It is essential for performing intersubject analyses or, for intrasubject analyses, determining Talairach/MNI coordinates of activation foci.

While the "Normalize" button can accept any kind of image (T1, T2, etc), to register your subject into the standard atlas space, it is important to use the highest resolution structural data.

1. For us, that is which image:

(Check your answer before continuing on!)

Spatial normalization (or, with a British accent, normalisation) takes three types of images

(i) "Source images"

These are the high resolution anatomical images from which the spatial transformation is determined. Typically you only specify *one* such image per subject.

(ii) "Images to write normalised"

These are other images *with* *the* *same* *world* *space* as image (i) above. Typical examples would be statistic or contrast images, or whole set of *ra* functional images.

(iii) "Template image(s)"

Images that define the standard atlas space. You get to choose from images that match the type (or "modality") of the image in (i).

It produces a "*_sn.mat*" file, which records the nonlinear transformation *from* the *world* *space* of image (i) *to* the atlas space.

2. Now that we have coregistered, what does the world space of *hetlspgr* correspond to?

3. Thus if we spatially normalize *hetlspgr* the resulting *_sn.mat* file will not just be good for *hetlspgr*, but for...

Click 'Normalize' to start the spatial normalization process.

Select 'Determine Parameters & Write Normalised'.

For "Template images", select scalpedT1.img. This image is an average of 152 subject's T1 images, from the MNI/ICBM, smoothed with an 8mm filter, which was *then* been edited of scalp by folks in the Jonides lab. (ICBM=International Consortium for Brain Mapping).

For "Source image, subj 1", select hetlspgr.img, the homogeneity-corrected, scalp-edited, hi-res anatomical image.

For "Images to write, subj 1", select again hetlspgr.img.

For now, we are only doing 1 subject; so when it asks for "Source image, subj 2", just click 'done'.

After a short while it will finish. This will create a hetlspgr_sn.mat and reslice the requested file, creating a whetlspgr.img.

Check the success of the registration, comparing the normalized image (whetlspgr.img) to the unsmoothed version of the template image, that is avg152T1.img in the spm2/canonical directory.

4. Using the landmarks suggested above, has the spatial normalization succeeded?

Analyzing Event-Related Data

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First! Create a new directory, like G?ER (except replace ? with your group number). Copy the onset data to those directories.

Load these event timing data (here, for group 2; change 2 to your group number)

```
FaceOns = load('G2ER_F.dat');  
HousOns = load('G2ER_H.dat');
```

Look at them with this matlab command (type carefully!)

```
figure  
plot(FaceOns, .9*ones(size(FaceOns)), 'v', ...  
     HousOns, -.9*ones(size(HousOns)), '^')
```

Do they look random? Note how you never have two events at the same time.

First, smooth the data. Click the 'Smooth' button and select all of the run_2 ra*vol.img you will analyze. As yesterday, use a 8mm isotropic smoothing. This creates sra*vol.img's.

Now specify a model. Briefly...

```
"Interscan Interval {secs}"          2
                                     (This is the TR)

"scans per session:"                 192

"specify design in"                  Scans

"Select basis set..."                'hrf'

"model interactions (Volterra)"        'no'
                                     (You'll always say 'no' here)

"Number of conditions"                2

"name for condition/trial 1"          Faces

"vector of onsets - Faces"            FacesOns
                                     (Crucially, this depends on
                                     you having defined a
                                     'FacesOns' variable in the
                                     Matlab workspace before starting.)

"duration[s] (events = 0)"            0
                                     (Since these are events, we
                                     specify zero duration).

"parametric modulation"              'none'

"name for condition/trial 1"          Houses

"vector of onsets - Faces"            HousOns
                                     (Again, this will fail if
                                     'HousOns' isn't defined.)

"duration[s] (events = 0)"            0
                                     (Since these are events, we
                                     specify zero duration).

"parametric modulation"              'none'

Other regressors
"user specified"                       0
```

SPM has just saved a SPM.mat file with all of the specifications you just gave it.

2. Second, review the model.

In the lower-left window, select
'Explore fMRI design' -> 'Session 1' -> 'Faces'

Does this look different from the block design? How is the
power spectrum different?

3. Assign data to this design

Click 'fMRI and select the 'data' option.

A file selection dialog will appear: 'Select SPM.mat'

"Select scans for session 1"	Select the scans in your study (run_2, event-related design)
"remove Global effects"	'Scale' (Global scaling accounts for random, image-wide fluctuations)
"High Pass filter"	Specify
"cutoff period (sec)"	128 (All drifts with sinusoidal periodicity of 128 seconds or greater will be modeled.)
"Correct for serial correlations?"	'AR(1)'

After a pause, SPM has will update you SPM.mat file with the
information just supplied. The delay is because SPM must
compute the global average for each image.

Create contrasts and examine the results. Compare to the block
results.

Does it seem like the event-related design more or less sensitive?