Alphascript v1.0

for fMRI preprocessing at CIBSR

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Alphascript is an update to bigascript for fMRI preprocessing at CIBSR. This script is currently SPM5 compatible only and is intended for single sessions. SPM8 and multi-session compatibility will be added in the near future.

Options

1. Median filter
2. Slice time correction
3. Realignment (reslice performed)
4. **ArtDespike (new)**
5. Spatial smoothing (individual)
6. Motion correction
7. ArtRepair
8. **Coregistration (new)**
9. Normalization (reslice performed)
    a. via EPI template
    b. **via custom template & gray matter segmentation (new)**
10. Spatial smoothing (group)
11. **File clean-up (new)**

Additional items

Alphascript will generate a new folder within each subject directory, named ***preproc_data,*** which will be used to consolidate the storage of files that are generated during the preprocessing pipeline. Copies of the following files will be stored in this directory for quick access:

- 10th functional volume of every process performed (.img & .hdr)
- artdespike.jpg
- artglobal.jpg
- ArtifactMask (.img & .hdr)
- ArtRepair/Motion files (e.g. art_dewieghted.txt, art_motion.txt, art_repaired.txt)
- gray matter segmentation (native & normalized)
- SPM graphic files from realignment, coregistration, & normalization

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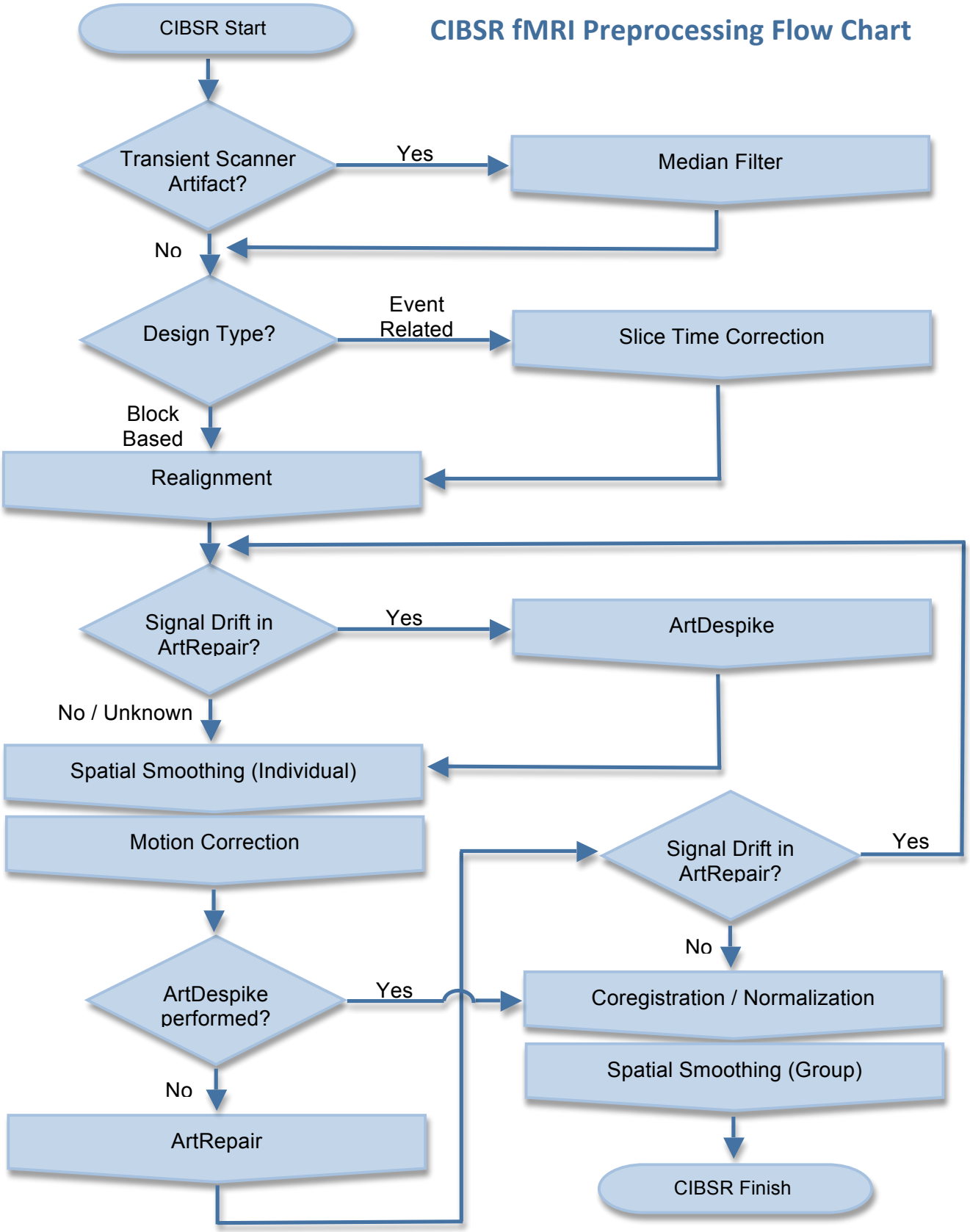

CIBSR fMRI Preprocessing Flow Chart
CIBSR Start
Transient Scanner Artifact?
Yes
Median Filter
No
Design Type?
Event Related
Slice Time Correction
Block Based
Realignment
Signal Drift in ArtRepair?
Yes
ArtDespike
No / Unknown
Spatial Smoothing (Individual)
Motion Correction
Signal Drift in ArtRepair?
Yes
No
ArtDespike performed?
Yes
Coregistration / Normalization
Spatial Smoothing (Group)
No
ArtRepair
CIBSR Finish

Preparing to Run Alphascript

The following variables must be defined in order to run Alphascript:

scriptDir :	The path to the directory containing alphascript.m *e.g. '/fs/TURNER/…/scripts/alphascript/'*
sjDir :	An array in which each element is the path to a new subject *e.g. {'/fs/TURNER/…/CON/111.1/',…* *'/fs/TURNER/…/CON/222.1/'}*
images :	Standard directory name that contains a subject's functional images e.g. *'processed/'*
process :	An 11 element array in which each element corresponds to a unique alphascript option that will either be ignored or performed *i.e. [0 0 1 1 1 1 0 1 1 1 0]*
prefix :	A 10 element array in which each element corresponds to the prefix of the functional files that will be operated on during each of the 10 preprocessing steps. The 11th process (Clean Files) does not require a prefix. *e.g. {'I, 'fI', 'afI', 'rafI', 'srafI', 'msrafI', 'vmsrafI',…* *'dvmsrafI', 'dvmsrafI', 'wdmsrafI'}*

Prefixes

SPM will attach a standard lettered prefix to each file name after a particular preprocessing step has been performed. The prefixes that you will encounter are as follows:

I: raw image prefix
f: median filtered image prefix
a: slice time corrected image prefix
r: realigned image prefix
d: artifact despiked image prefix
s: individual smoothed image prefix
m: motion corrected image prefix
v: artifact detected and repaired image prefix
: coregistered images do not generate new files and thus have no associated prefix
w: normalized image prefix
s: group smoothed image prefix

Defining Parameters for Selected Options

Option 1: Median Filter (by Paul Mazaika)

Median filter will pass your functional images through a high pass filter. This option is intended to compensate for transient scanner artifacts and is NOT recommended for most data.

There are no CIBSR defined parameters in Alphascript for median filter.

Option 2: Slice Time Correction

Slice time correction will compensate for the time delay that is present between the acquisition of slices within a given functional volume. This option is most useful for event related tasks rather than block-based designs.

The following parameters must be defined when performing slice time correction:

order : The order of slice acquisition within each functional volume.
e.g. 1 (ascending); 2 (descending); 3 (interleaved)

interval : Corresponds to TR, in seconds.
e.g. 2

Option 3: Realignment

Realignment will correct for variation in orientation of your functional volumes within a given time series.

The following parameter must be defined when performing realignment:

source : The n-frame number to which all other functional volumes will be realigned.
e.g. 003

Option 4: ArtDespike (by Paul Mazaika)

ArtDespike will send your data through a high pass filter with the intention of detrending a functional image timeseries by removing low frequency drift from the mean global signal. This option should be reserved for cases in which visual inspection of the ArtGlobal figure (displayed during Option 7) uncovers greater than +/- 1% drift in the mean global signal across the entire timeseries. See the 'Global Signal Drift' section on page 8 for more information.

There are no CIBSR defined parameters in Alphascript for ArtDespike

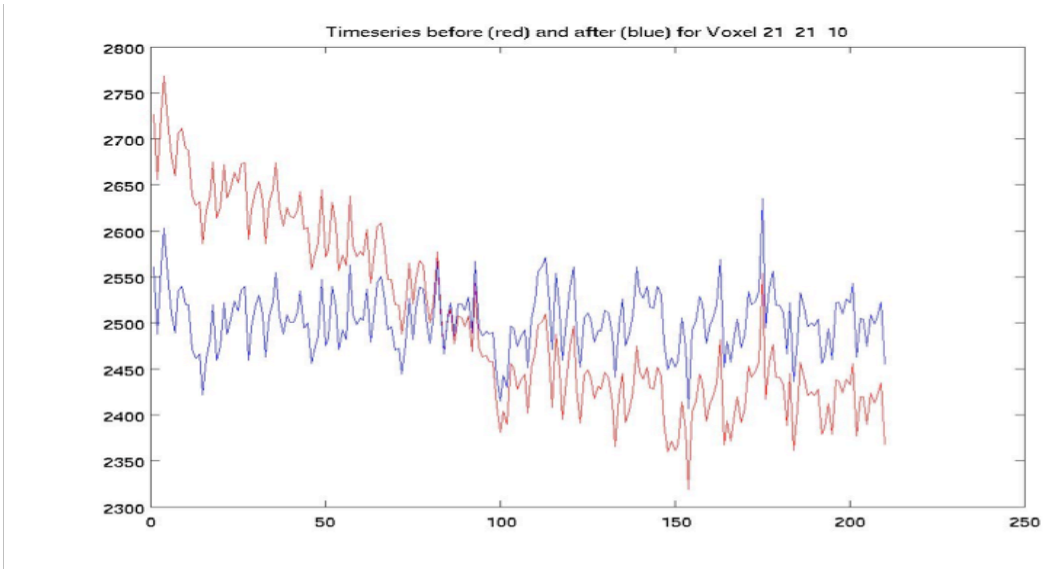


Figure : Global average signal before (red) and after (blue) using ArtDespike.

IMPORTANT: ArtDespike should be performed AFTER realignment but BEFORE individual spatial smoothing and motion correction (See 'CIBSR fMRI Preprocessing Flow Chart' on page 3). Subsequently, ArtRepair should NOT be performed, and deweighting cannot be used during contrast image estimation.

Option 5: Spatial Smoothing (Individual)

Smoothing will reduce the influence of spatial distortions in your data that may have been introduced due to filtering and/or interpolation (during reslicing) in previous preprocessing steps. This is particularly useful to help better estimate motion for each subject during motion correction.

The following parameter must be defined when performing individual spatial smoothing:

indivdualFWHM :	The size of the Gaussian smoothing kernel (mm) that will be applied to the functional images. *e.g. 4* ***(CIBSR default)***

Option 6: Motion Correction (by Paul Mazaika)

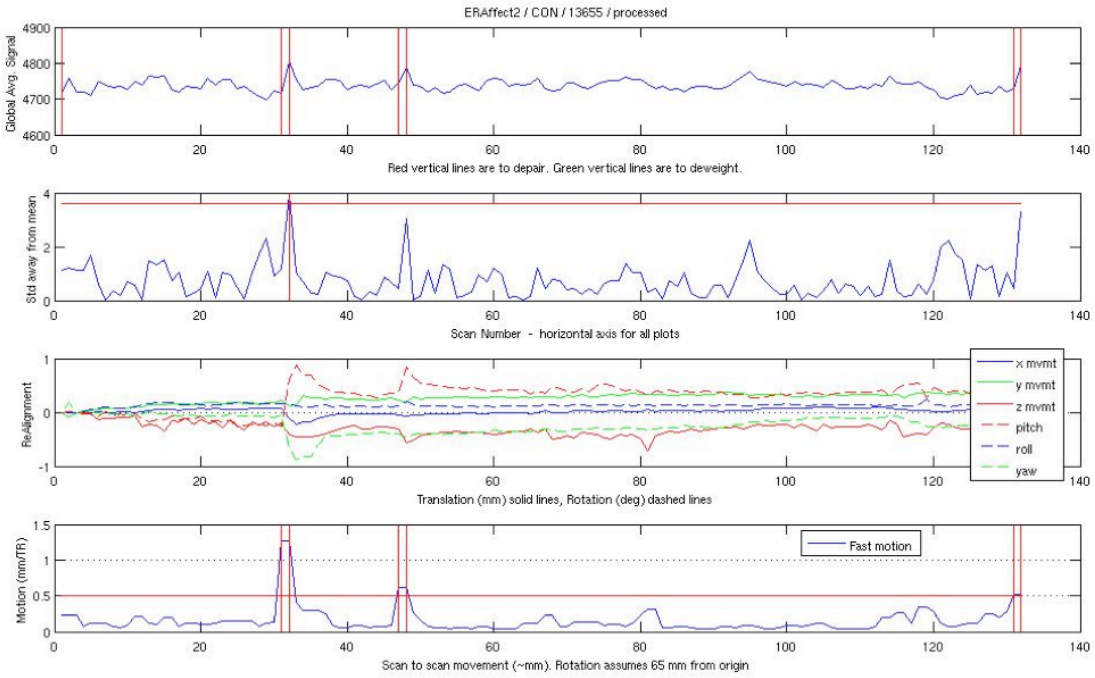
Motion correction will attempt to adjust the voxelwise signal intensities in your functional image volumes to compensate for signal fluctuations that occur as a result of subject motion.

There are no CIBSR defined parameters in Alphascript for motion correction.

Option 7: ArtRepair (by Paul Mazaika)

ArtRepair will estimate global outlier volumes within a functional image timeseries based on global signal fluctuation and scan-to-scan motion. The signal intensities in these outlier scans will then be corrected, and a list of repaired volumes will be generated for [optional] deweighting during the estimation of the General Linear Model.

A figure containing multiple subplots will appear when this step begins (Shown below). These subplots display (1) mean global signal, (2) standard deviation of the mean global signal, (3) absolute scan-to-scan motion, and (4) velocity of scan-to-scan motion. It is important that this figure be inspected for each subject in order to identify any potential issues such as prominent subject motion (i.e. > 20% of the scans repaired due to motion) or global signal drift (i.e. the mean global signal drifts more than +/- 1% over the entire timeseries).



Global Signal Drift

Global average signal drift is a scanner issue that can cause ArtRepair to incorrectly classify a large number of functional image volumes as outliers in need of repair. If the mean global signal appears to steadily drift more than +/- 1% over the course of an entire timeseries, ArtRepair may not be a suitable option. In cases such as these, application of ArtDespike is a more appropriate option and ArtRepair should NOT be performed.

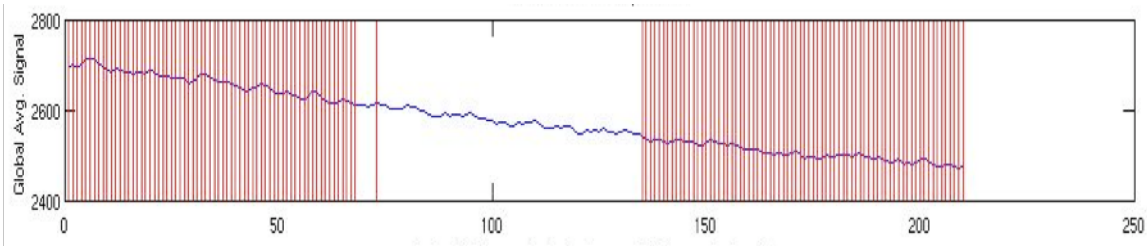


Figure : Global average signal with ~13% negative drift

IMPORTANT: ArtDespike should be performed AFTER realignment but BEFORE individual spatial smoothing and motion correction (See 'CIBSR fMRI Preprocessing Flow Chart' on page 3). Subsequently, ArtRepair should NOT be performed, and deweighting cannot be used during contrast image estimation.

Options 8 & 9: Coregistration & Normalization

Coregistration and normalization will map your functional images into a standard space via linear transformations and nonlinear warps. Alphascript allows you to select from 2 different methods for coregistration & normalization:

1. Normalization via an EPI template in MNI space (coregistration is not applicable).
2. Coregistration and normalization via a custom template and gray matter segmentation of a high res anatomical image for each subject.

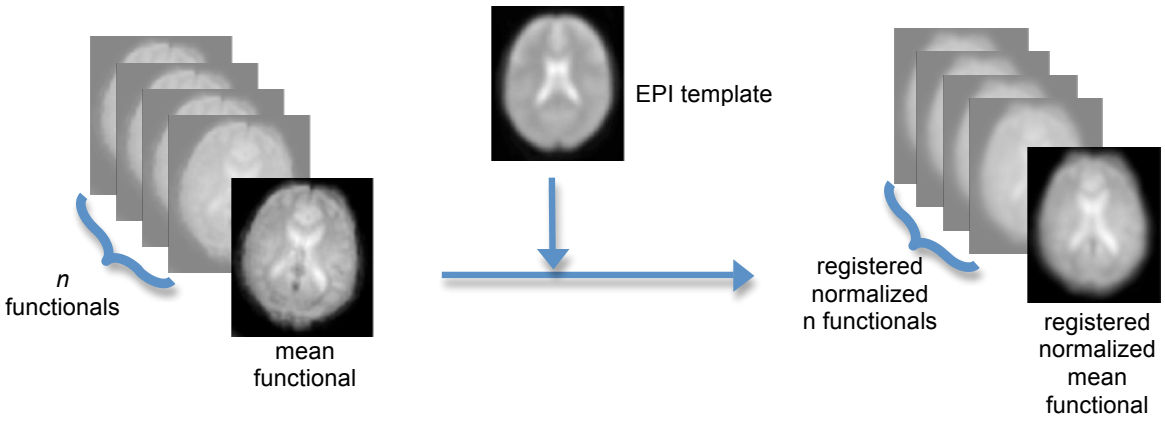
The following parameters must be defined when performing coregistration/normalization:

method :	The coreg/norm method you wish to perform. *e.g. 2*
templateDir :	Directory that contains your template image. *e.g. '/fs/fmrihome/fMRItools/matlab/spm5/templates/'*
templateFile :	The name of your template file(s). *e.g. 'gray.img'*
anatDir :	Standard directory within each subject folder containing anatomicals *e.g. 'anatomical'*
anatPrefix :	A common prefix in the file name of ALL anatomicals. A prefix must be added manually if one does not exist. *e.g. 'abc' for abc_subj#1.img and abc_subj#2.img*

Coregistration & Normalization Method # 1

Step 1: Functional images are registered and normalized directly to a standard EPI template via the mean functional image.

Step 1: Registration / Normalization



Coregistration & Normalization Method # 2

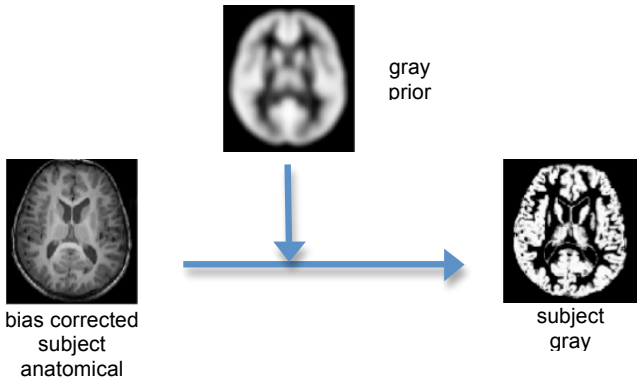
See figure on the next page for a schematic.
NOTE: Subject anatomicals need to be in the same SPM orientation as your template images (See 'Checking SPM Orientation' on page 11 for more information).

Step 1: A high resolution subject anatomical image is first bias corrected followed by segmentation of the gray matter via a custom gray matter prior (white & csf priors are also required in order to perform this step).

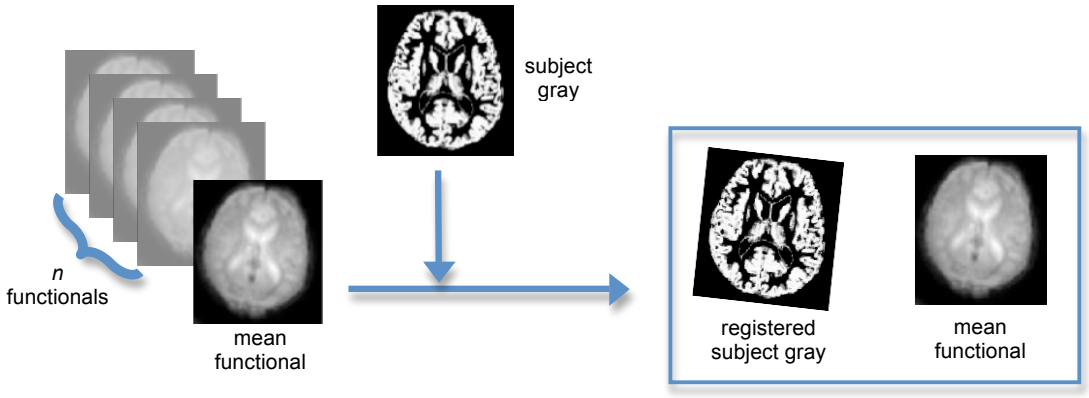
Step 2: The subject's segmented gray matter volume is registered to the mean functional image. Since each functional volume is directly related to the mean functional volume, they are all essentially coregistered to the gray matter segmented volume.

Step 3: The subject's segmented gray matter volume is re-registered to the gray matter prior and is normalized. The resulting transformation matrix is then applied to all of the functional volumes that were in register with the segmented gray matter volume.

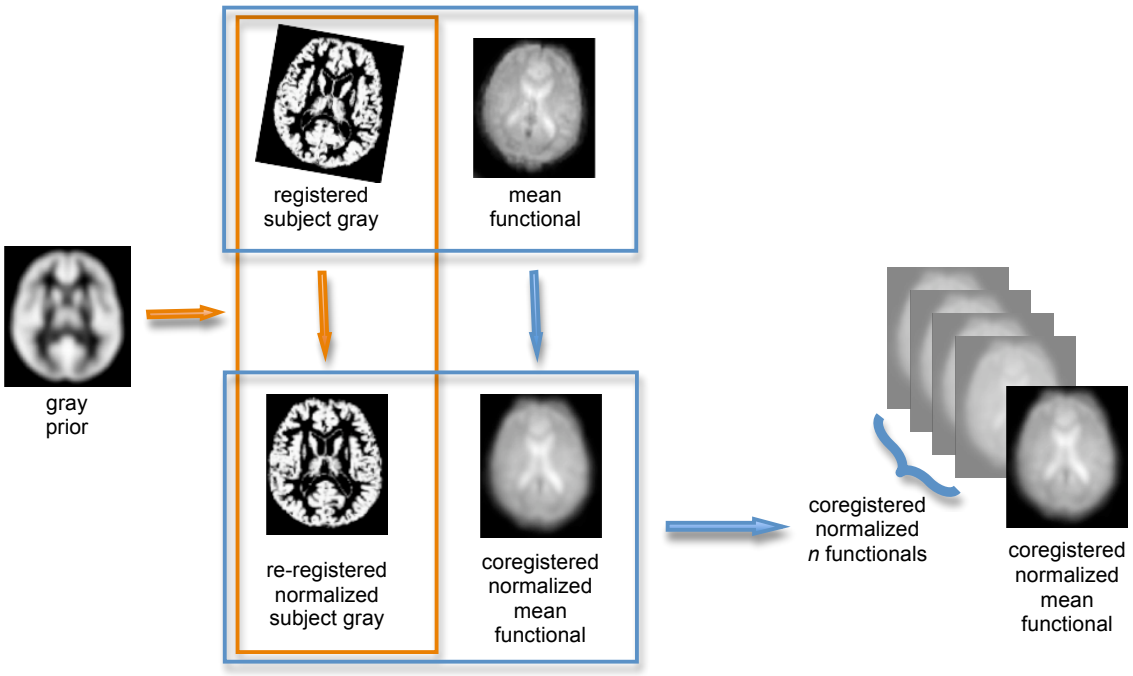
Step 1: Bias Correction / Gray Matter Segmentation



Step 2: Coregistration



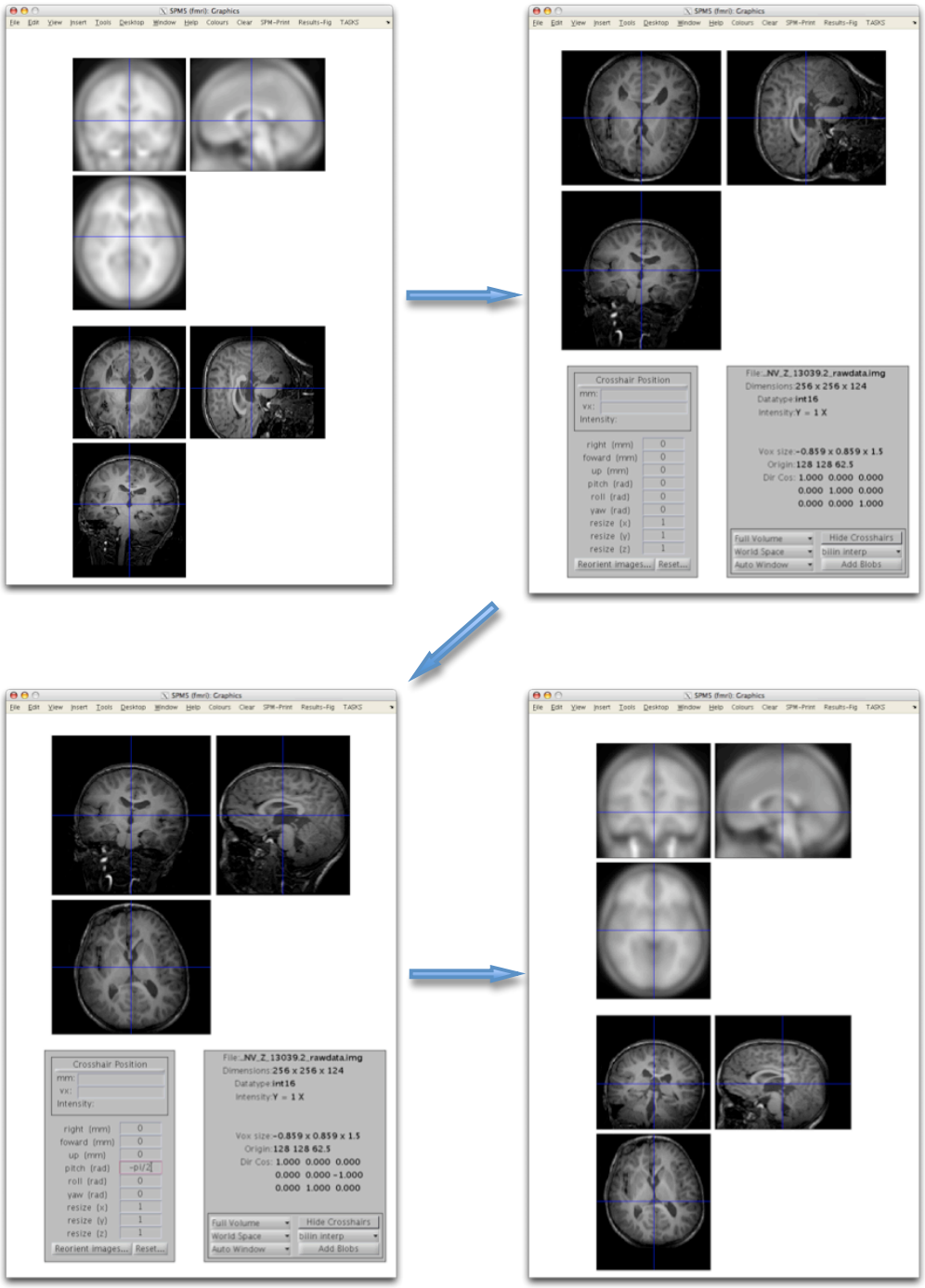
Step 3: Normalization



Checking SPM Orientation

NOTE: This operation can be avoided by using NIfTI format images (.img).

Subject anatomicals (and functionals) need to be in the same SPM orientation as the template file(s) that you are using. Use the 'Check Reg' function in the SPM GUI to compare orientation. If rotation is needed, use the 'Display' function in the SPM GUI to rotate about the 3 axes (Remember to use radians when rotating!). When the orientation is correct, use the 'Reorient Images' button to apply and save your rotation to the appropriate file(s).



Option 10: Spatial Smoothing (Group)

Smoothing will help create activations that overlap from subject to subject. (Recall each subject actually has a different gyral/sulcal pattern, so their normalized brains are not the same.) This is particularly useful to help cluster activation regions across subjects in a group analysis. Group smoothing kernels between 6mm-12mm also help make the group statistics valid.

The following parameter must be defined when performing group spatial smoothing:

groupFWHM :	The size of the Gaussian smoothing kernel (mm) that will be applied to the functional images. *e.g. 7* ***(CIBSR default)***

Option 11: Clean Files

IMPORTANT: Be careful when using this option.

Alphascript adds the additional option to delete intermediate files that were created during the preprocessing pipeline. On average, deleting intermediate files can free up between ~300MB and 1GB of disk space per scan!

The clean up process is divided into two sub options:

purge.images : Performs a clean up in your '*images*' directory

purge.images = 0	All files are saved
purge.images = 1	'I' files, ArtRepair files*, & group smoothed files are saved
purge.images = 2	Only 'I' files are saved

*If ArtRepair was performed, then ArtRepair generated files are saved, such as *v*-files and .txt files. Alternatively, if ArtDespike was performed, then motion corrected (smoothed) files are saved instead. This option can be run independently of all other preprocessing steps and should automatically recognize which files to save.

purge.preproc_data : Deletes the preproc_data directory

purge.preproc_data = 0	preproc_data is not altered
purge.preproc_data = 1	preproc data and all of its contents are deleted

fMRI QC Checklist

These steps help ensure that you have usable fMRI data. Please use this as a guide to check the quality of all your data.

☐ **MAKE A SPREADSHEET FOR LOGGING QUALITY CHECK INFO**
Make an excel spreadsheet to enter each of the following checking points for each subject / scan.

☐ **CONFIRM BX DATA AND DEMOGRAPHICS**
IQ, age, gender, etc…

☐ **DISPLAY RAW IMAGES**
Use the 'display' function in SPM to display I_010.img

WHEN

After you convert the P file into I files (see ~/fmrihome/fMRItools/HowToFiles/HowToPreprocessPfiles3.doc) or when you run through the megascript.

HOWTO

1. Type 'ml7spm5' in a terminal window followed by 'spm fmri'.
2. Click on 'Display', then choose I_010.img and click 'done'.
3. Select File > Save As > and save file as SID#_raw*.jpg file.
4. Log in the excel spreadsheet after inspecting images.

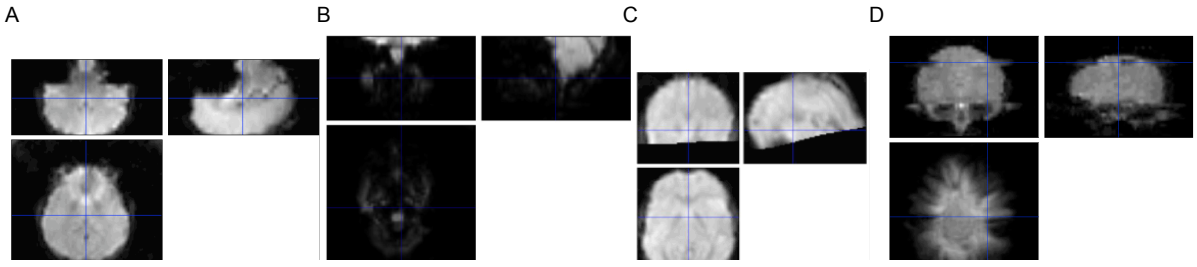
WHAT TO LOOK FOR

Inverted images (correctable, see A below), chopped off brains (uncorrectable, see B & C below), severely tilted brains (correctable), slices in the image that diverge (uncorrectable artifact, see D below).

IMPORTANT: If your images require that they be flipped to become upright (see A below), you MUST also distinguish left from right so that you do not inadvertently introduce a left/right flip. This will most likely occur with Analyze images and not with Nifti images.

WHAT TO DO

For tilted and inverted images, enter appropriate values for pitch, roll, yaw, resize x, y or z and click on 'reorient images' (experiment with this until it looks right, but be careful with right/left inversions). It will then ask which images to apply these parameters to and, generally, choose all functional raw I*.img files to apply to all of the images. Make a note in your spreadsheet that images were reoriented. ***NOTE: If any reorientation or modification of I*.img files is done at this stage, alphascript should be re-run on these new images.***



☐ **ART MOVIE** (use the 'art_movie' function to display raw images)

WHEN

After you convert P files to I files or when you run through megascript.

HOWTO

1. Type 'ml7spm5' in the terminal, then type '**art_movie'**.
2. Choose all I_*.img files (if you do not have time you can choose first 30), then click done.
3. Select orientation that the data was collected (typically **Axial**)
4. Select range (i.e. type 1:186 if you have 186 images)
5. Select data magnification (Contrast)
6. Choose a reference image (select User Specified, then choose the 10th image)
7. Select viewing mode (Slider).

*Images will take approximately 20-60 seconds to load.

8. Check results: save b/w image as 'SID#_bw.jpg'
9. Check contrast results: a yellow/blue image will appear. Scroll through all images and save the worst (brightest) image (excluding the 1st image) as 'SID#_artmovie.jpg'.
10. Log in the excel spreadsheet that art_movie has been completed, and note any observed artifacts.

WHAT TO LOOK FOR

Good images are shown in Fig E (b/w) and Fig F (contrast). In contrast images, darker images are better. Sometimes the images will become brighter as they increase in number. In the absence of other artifacts, this is probably ok.

Fig E

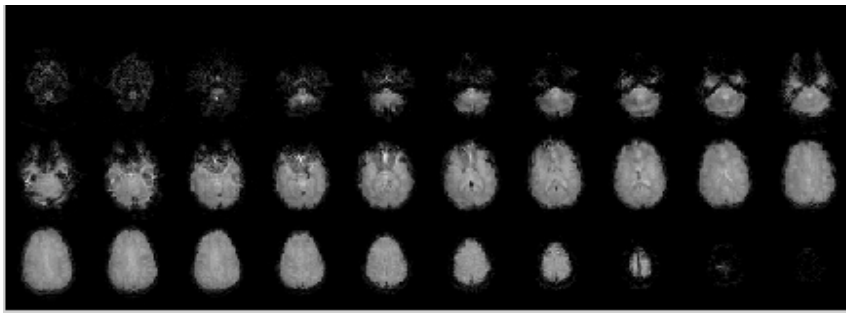
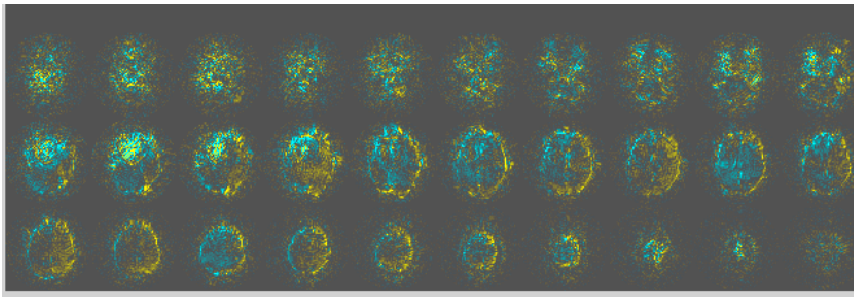
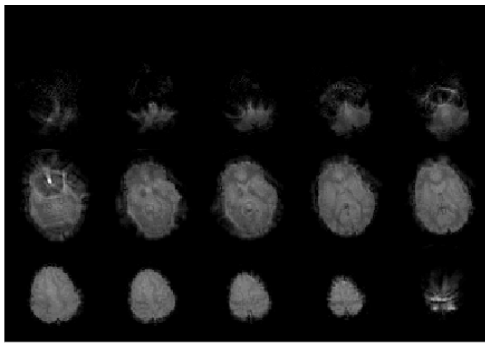
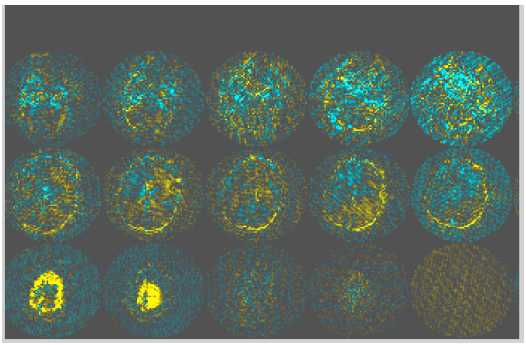


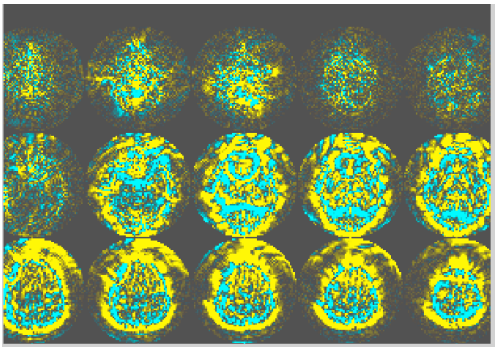
Fig F

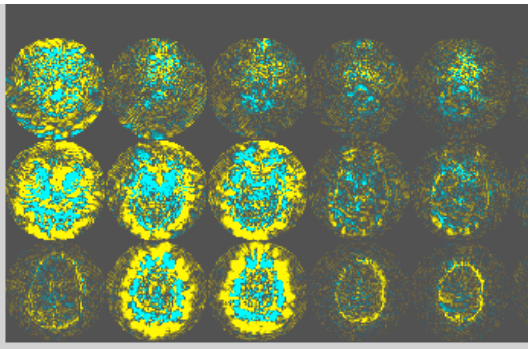


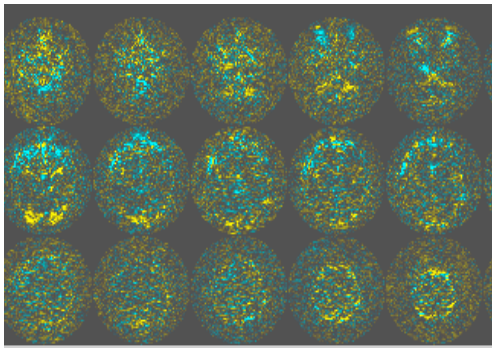
Possible artifacts to look for: blurred b/w images (G), bright yellow/blue corduroy stripes or checkers in image (H), bright areas outside brain (I), certain bright slices while others look ok (J), pixilation (K), images that no longer resemble brains (L, M).

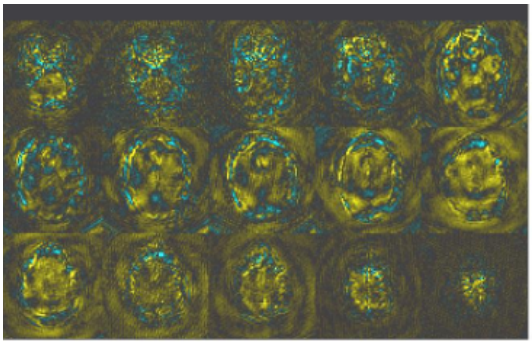
G 

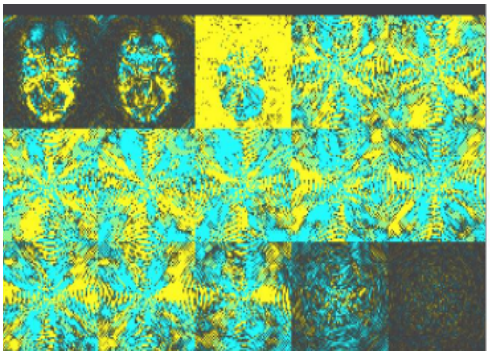
H 

I 

J 

K 

L 

M 

☐ **CHECK GLOBAL SIGNAL AND MOTION PLOTS**

Check artglobalprocessed.jpg located in the preproc_data directory.

WHEN

After you run through alphascript with **'v'** (art_repair) and **'m'** (motion correction) options specified.

HOWTO

Open artglobalprocessed.jpg from the preproc_data directory and check all four plots.

WHAT TO LOOK FOR

Look for scans with excessive repairs, excessive motion, sudden shifts in motion, and global change in signal. If a scan has more than one of these issues, it will probably be unusable.

1. Global Average Signal: count # of red vertical lines, or count # of entries in art_repaired.txt file (also located in preproc_data. Log # and % in excel spreadsheet. Make a note if repaired scans exceed 20% of total nframes. **Also note if Global Average Signal appears to exhibit a significant linear drift (Fig O).**
2. Standard Deviation Plot: Check maximum std dev. Any values > 4 are probably unusable. Log in excel spreadsheet.
3. Realignment Plot: Check motion. Consistent motion > 3mm probably unusable. Log in excel spreadsheet.
4. Motion (mm/TR) Plot: Check for scans flagged for fast motion. If these exceed 25% of total nframes, probably unusable. Log in excel spreadsheet.

Fig N

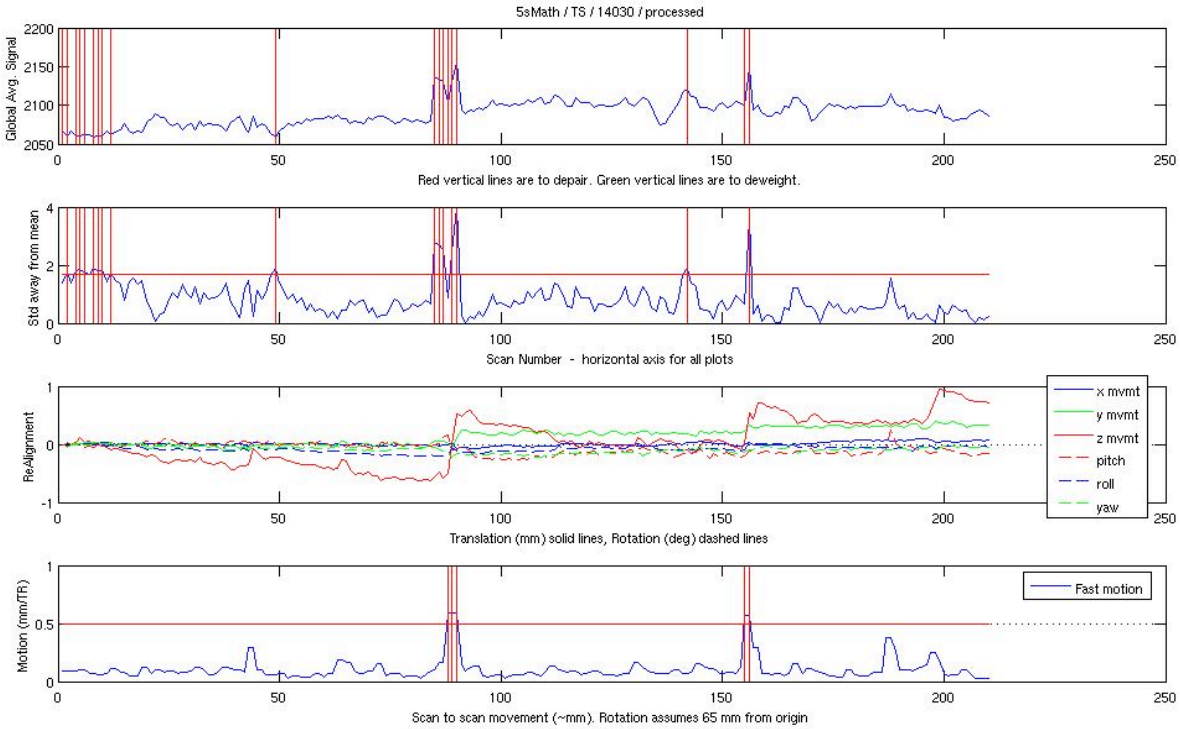
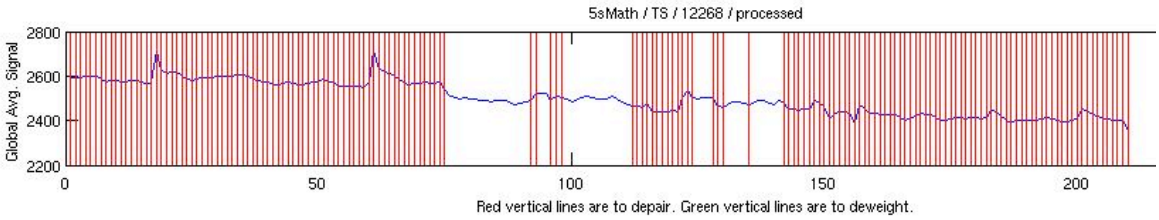


Fig O



WHAT TO DO

If the Global Avg Signal plot displays a significant linear drift, you will probably need to reprocess the scans without the **art_repair** option, or replacing this with **art_despike** option.

☐ **DISPLAY NORMALIZED IMAGES**

First look at the *normalized.ps* file that is created in the preproc_data directory. Then use the 'check reg' function in SPM and select both 'w*I_010.img' and your template image.

WHEN

After you run through the alphascript or do normalization.

HOWTO

1. Briefly check the normalized.ps file the preproc_data directory. Log in your excel sheet if brains clearly do not match.
2. Start SPM by typing 'ml7spm5' in a terminal window followed by 'spm fmri'.
3. Click on 'CheckReg' and select both w*I_010.img and the template image that was used (either EPI or custom gray template).
4. Click around the brains and make sure that the top, front, and back of the brains align nicely with the template. Also check the boundaries of the ventricles and corpus callosum.
5. Right click and insert text (subject ID for example), then right click again and save file as *.jpg file. Log in the excel spreadsheet after inspecting images.

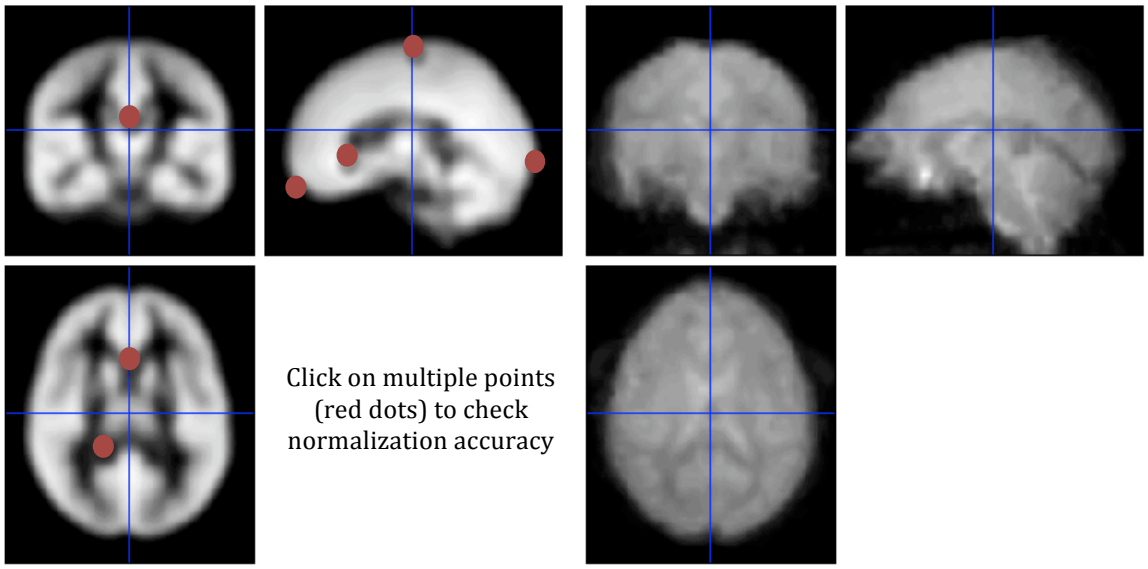
WHAT TO LOOK FOR

Move around the brains and make sure that the top, front, and back of the brain align nicely with the template brain (Fig P).

WHAT TO DO

If the brain does not align nicely with the template, try re-running normalization and check the results again. If you still obtain a poor result, consider reprocessing your images from an earlier step.

Fig P



☐ **DISPLAY STAT RELATED IMAGES** (use 'check reg' in SPM to display mask.img, resMS.img, con_0002.img with template)

WHEN

After you run through individual stats (estiscript or manually).

HOWTO

1. Start SPM by typing 'ml7spm5' in a terminal window followed by 'spm fmri'.
2. Click on 'CheckReg', then choose mask.img, resMS.img, and con_0002.img, and your template image, then click 'done'. Save file as SID#_statimg.jpg file.
3. Log in the excel spreadsheet after inspecting images.

WHAT TO LOOK FOR

Make sure the mask.img looks like a brain, not chopping off any major regions and the size fits the template. Make sure that the resMS.img looks dark and you can hardly see the brain. Make sure that the con_0002.img files do not have stripes or anything that looks mechanical.