SPM preprocessing pipeline — v1

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Reference: Thackery (Cognitive Neuroimaging Lab), Mumford videos on youtube, Maureen Ritchey's Github, ArtRepair website, SPM manual etc etc

ritcheym (Github)
https://github.com/ritcheym

Step00: Header Information

Header information contained details on how your data were being stored and some details about data acquisition.
Why correct header is important:

1. Preprocessing softwares may use data acquisition information in header as parameters. For example, nifti header stores information about the timing of an fMRI acquisition, which is represented by a number code. A preprocessing software could use this code to perform slice timing correction.
2. Header information also tells a program how to read in the data. If there is something wrong about it, then you would read in the data wrong. For example, if the orientation information is not correct, it could lead to wrong labeling of the left and right hemispheres.

To check the nifti header:
fslhd displays more information than spm_vol.
Code:
fslhd NAME_OF_THE_VOL
spm_vol(NAME_OF_THE_VOL)

- return a structure
    - fname: file name
    - dim: the x,y, and z dimensions of the volume
    - df: data type
    - mat: affine transformation matrix mapping from voxel coordinates to real world coordinates (see Step01: reorientation for more info)
    - pinfo: plane info for each plane of the volume

Nifti header information
http://brainder.org/2012/09/23/the-nifti-file-format/

Step01: Reorienting

Background:
The NIFTI intensity data is stored on disk as a list of numbers (voxel coordinates). The ordering of these numbers are arbitrary. This depends on how you reconstruct the image. For example, (0,0,0) of this 3D matrix is not necessarily the center of the brain. These voxel coordinates (i,j,k) gives your spatial information of where a voxel locates in this 3D matrix, but this is not relates to anatomical information.

Header information is used to associated spatial and anatomical location information (qform and sform mtr) with these numbers. qform is the scanner coordinate system (the real space inside the scanner bore) and sform is relating to standard space coordinates (e.g. MNI152). One of them is being used to assign anatomical information to voxel coordinates. This is what it meant by mapping from voxel coordinates to real world coordinates. The " real world" coordinates are also called continuous coordinates or mm coordinates (the mm in the SPM display dialog)). You can check whether this mapping is correct by viewing the image via FSL/Mricron. If the orientation labels are not correct (say, anterior and posterior flip), there may be some prob with the mapping process (this could be one potential reasons for it).

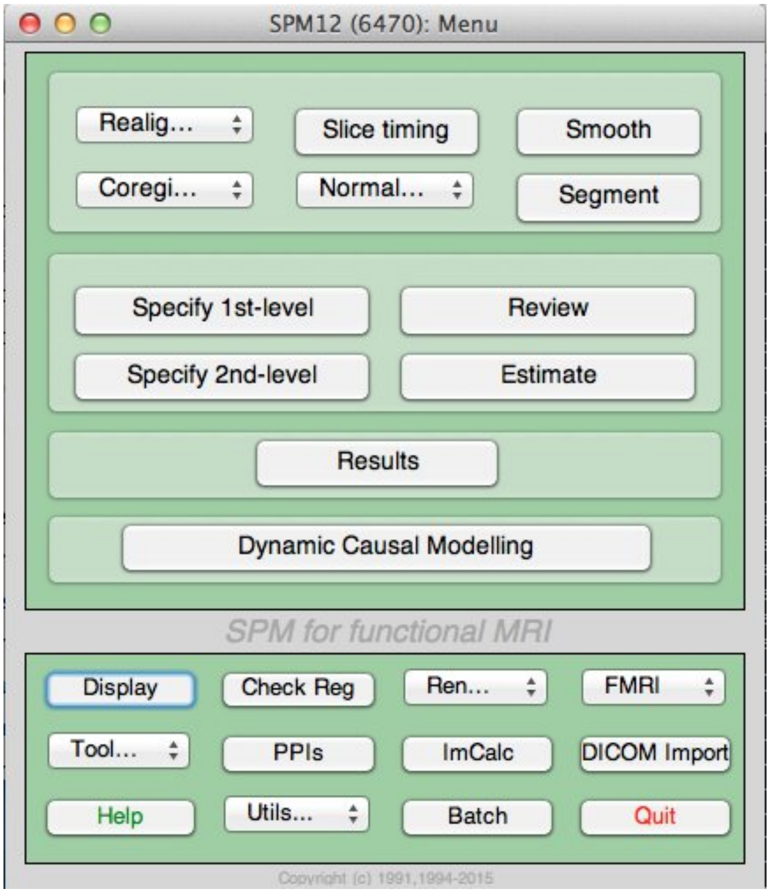
Importance of a "correct" origin:
Setting the origin at AC is important for SPM processing when the procedure has template brain images involved (e.g. normalization and segmentation). The program will match your image and template images according to their origins. Procedures would work fine when your origins are around AC, but the results would be very bad if it is way off (which means your origins do not have to be at the AC spot — high-res). "Origin" is the 0,0,0 of the mm coordinates. Reorigin will set the origin to AC and "label" the origin of mm coordinates in voxel coordinates.

Motion correction and coregistration are using rigid body transformation and therefore, origins do not play an important role in these procedures.

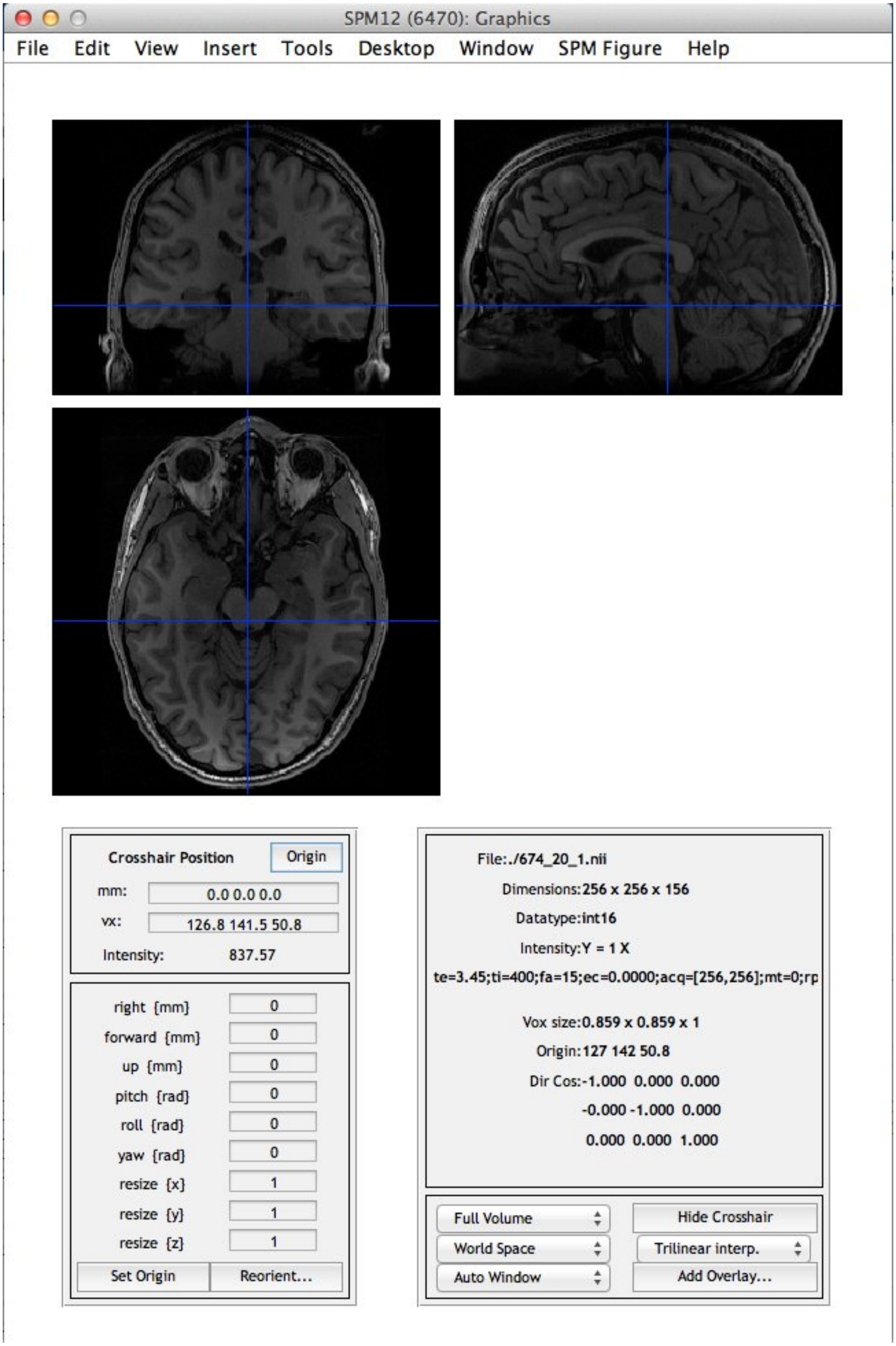
- reorientation: change header sform only
    - sform_name:scanner Anat -> *Aligned Anat*
    - sform code: 1 -> *2*
    - sform mtr

GUI:

1. Display: navigate to a reference structural image (e.g. SPGR) for setting AC-PC line



1. Click “Origin": this will center the crosshair to the initial origin. You MUST do this BEFORE adjusting the coordinates of the crosshair to the anterior commisure. If the origin is already at the anterior commisure, you do not need to change origin! Remember to check all images!! (also header!)



Crosshair Position

mm: 0.0 0.0 0.0

vx: 126.8 141.5 50.8

Intensity: 837.57

right {mm} 0

forward {mm} 0

up {mm} 0

pitch {rad} 0

roll {rad} 0

yaw {rad} 0

resize {x} 1

resize {y} 1

resize {z} 1

File:./674_20_1.nii

Dimensions:256 x 256 x 156

Datatype:int16

Intensity:Y = 1 X

te=3.45;ti=400;fa=15;ec=0.0000;acq=[256,256];mt=0;rp

Vox size:0.859 x 0.859 x 1

Origin:127 142 50.8

Dir Cos:-1.000 0.000 0.000

-0.000 -1.000 0.000

0.000 0.000 1.000

Full Volume

World Space

Trilinear interp.

Auto Window

1. Find AC: move the crosshairs on the anterior commisure
    a. If your functional data do not include AC: find AC and move down ~ 10cm (so that the origin is within functional image's coverage)
2. Set Origin: origin will be set on AC. Make note of the reorienting parameters that are used. (right, forward, and up boxes will have those information) You can just take a screen shot of it.
3. Reorient: select all images
    a. fieldmap, functional images, structural images
4. Use Check Reg to see whether all the images are aligned

- motion effect: because of motions, the origin for one image may be different from the origin for another image. Motion correction is using rigid body transformation, so slightly different origin should not be a concern (motion correction should correct for this).

References:
SPM12 manual, Chapter 17 (p145)
http://imaging.mrc-cbu.cam.ac.uk/meg/RepositioningMRIs
Thackery's preprocessing notes from Cognitive Neuroimaging Lab
Background and FSL reorientation:
http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/Orientation%20Explained

Step02: Organize files

This step is setting up your file structure for further analyses. This step will vary across different projects and you can have your own way to meet the purposes:
1. Convert a 4D volume into 3D volume files if needed (My current batch scripts work on 3D files not 4D files. **SPM can work on 4D file**. I just haven't tried it out in my batch scripts. The key point may be in spm_selector: argument *frame* enter number of volumes, for example 1:300, this will read in the first 300 volumes in your 4D file.)

2. Exclude the first few volumes that you save for the scanner to warm up from the following processing steps (My way is to put them into a separate folder). You do want to somehow separate them from other functional volumes because, if you include them in preprocessing pipeline, their signal will propagate to other volumes through any steps that contain interpolation...

Script: Step02_organize_files.m

1. spm_file_split: convert a 4D volume file into a series of 3D volume files (for using batch scripts)
2. put the 4D file into "4D" folder for each run - we are using 3D volume files not the 4D file
3. put the first 5 volumes (varies form projects to projects) into "5v" folder: we are not analyzing the first 5 volumes. Those are for scanner to warm up.

Step03: Check raw data (ArtRepair)

Background:
Repair bad data before preprocessing, otherwise large outliers will propagate to good data through slice timing (interpolation). We will fix bad slices before preprocessing. But, ArtRepair recommends not to repair any bad volumes until after preprocessing.

Software: ArtRepair (Center for Interdisciplinary Brain Sciences Research, Stanford)
ArtRepair software is developed to use with SPM to remove noisy volumes and slices.
http://cibsr.stanford.edu/tools/human-brain-project/artrepair-software.html

Identify artifacts volumes
Script: Step00_check_data
batch_function: 'art_global_raw_sfw'

This is a fast check to get a sense of your data (Run this script to save output image to each run's directory for sanity check. Nothing is being done to the images). This program will identify bad volume based on global signal change and scan-to-scan motion. Because you haven't run motion correction, the program will estimate coarse motion parameters. You can do the same thing within each run. This modified script will save the output image to the directory for each run. All the thresholds are default threshold.

Specified variables at the top of the function script: (You may want to change the figure_name for example)
You do not need to edit anything below these codes.

```
global_type_flag=4;
%which global mean to use:
%1. Regular SPM mask
%4. Auto (generates ArtifactMask and can Calculate
Movement)
%3. User Mask
%2. Every voxel

realignfile = 0;
%Have realignment files? 1: yes 0:no

imgFilter = '.*nii';
%Select functional images

mvmtFilter = '.*txt';
%Select motion parameter file
```

```
repair1_flag = 0;
%Always repair 1st scan of each session? 1: yes 0:no

figure_name = 'art_global_raw_';
out_idx_name = 'outlier_raw_idx_';
```

Bad volumes:

- Detect volume artifacts (threshold for outliers): you can adjust the script to use one of the following threshold
    - Percentage: default 1.3% from the mean. This is an estimate from the Lucas center
    - SD: 3 std from the mean. This is the standard used in lab (also used in art_global_raw_sfw)

Critical codes are here:
It converted the value of 1.3% (or whatever the default percentage is) mean into zscore - created a new "z_thresh" variable

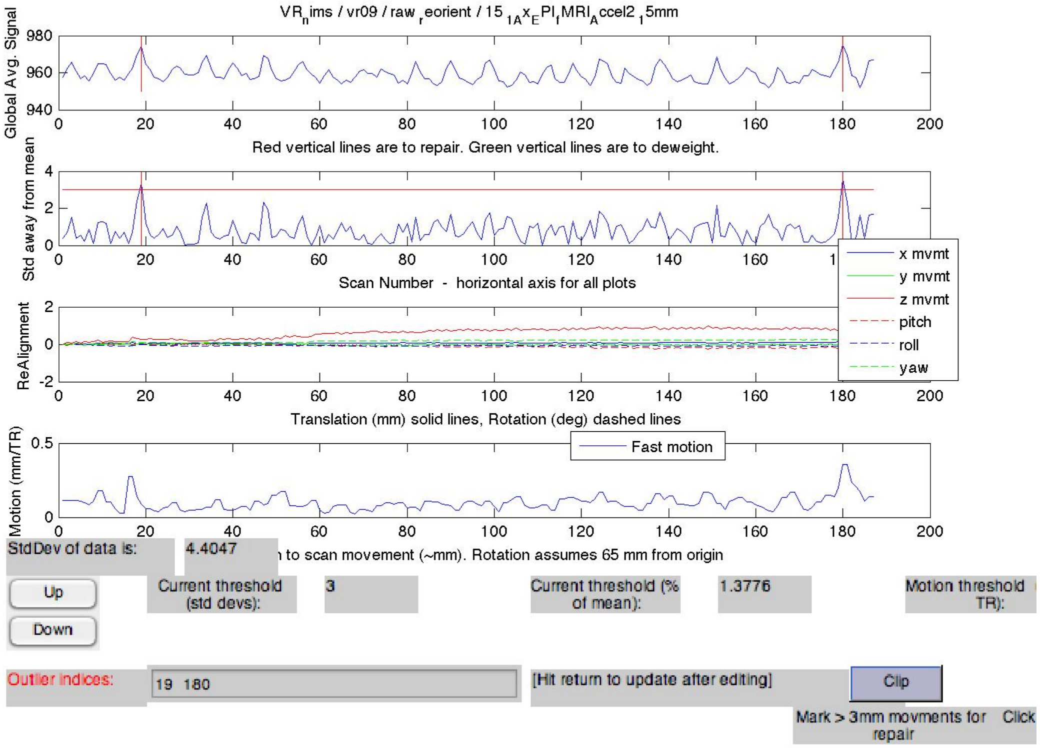
```
gsigma = std(g);
gmean = mean(g);
pctmap = 100*gsigma/gmean;
mincount = Percent_thresh*gmean/100;
%z_thresh = max( z_thresh, mincount/gsigma );
%z_thresh = mincount/gsigma;        % Default value is PercentThresh.
%z_thresh = 0.1*round(z_thresh*10); % Round to nearest 0.1 Z-score value
zscoreA = (g - mean(g))./std(g);  % in case Matlab zscore is not available
glout_idx = (find(abs(zscoreA) > z_thresh))';
```

Bad motion

- default threshold: scan to scan motion: 0.5mm/TR

Output

This is the figure will be saved out after running this script:
The first panel: time history of the mean intensity within the head region
The second panel: the size of the global signal change relative to the mean of the run
The third panel: motion parameter
The forth panel: scan-to-scan motion


VRnims / vr09 / rawreorient / 15 1AxEPIfMRIAccel2 15mm
Global Avg. Signal
980
960
940
0
20
40
60
80
100
120
140
160
180
200
Red vertical lines are to repair. Green vertical lines are to deweight.
Std away from mean
4
2
0
Scan Number - horizontal axis for all plots
ReAlignment
2
0
-2
x mvmt
y mvmt
z mvmt
pitch
roll
yaw
Translation (mm) solid lines, Rotation (deg) dashed lines
Motion (mm/TR)
0.5
0
Fast motion
Up
Down
Clip

StdDev of data is: 4.4047

n to scan movement (~mm). Rotation assumes 65 mm from origin

Current threshold (std devs): 3

Current threshold (% of mean): 1.3776

Motion threshold TR):

Outlier indices: 19 180

[Hit return to update after editing]

Mark > 3mm movments for repair

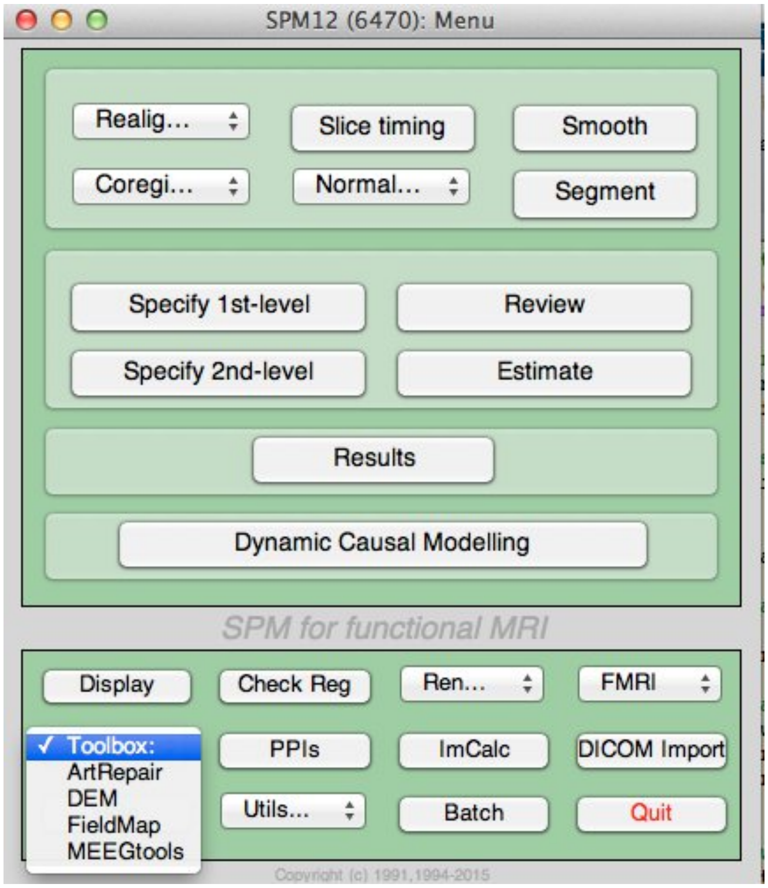
Click

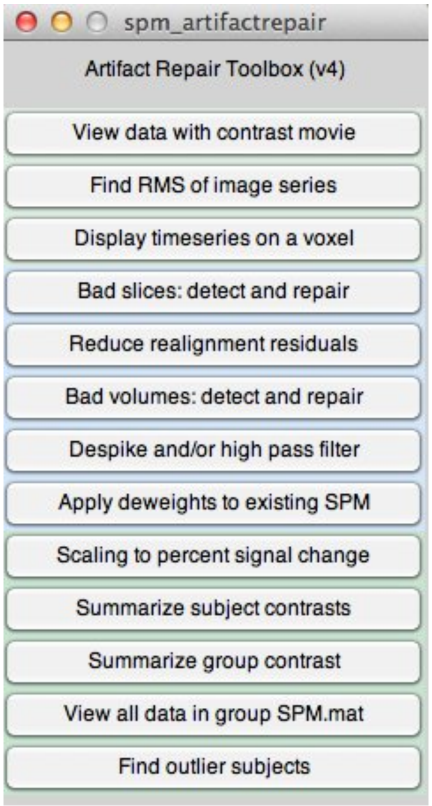
Visual inspect bad volumes
function: **art_movie**

After running the first check, you may want to see what happened to those bad volumes.
This program allows a user to view voxels in a volume.

- visual inspection: bad volumes identified by art_global
- visual inspection: bad slices identified by CNI QA

GUI: **view data with contrast movie**


SPM12 (6470): Menu
Realig...
Slice timing
Smooth
Coregi...
Normal...
Segment
Specify 1st-level
Review
Specify 2nd-level
Estimate
Results
Dynamic Causal Modelling
SPM for functional MRI
Display
Check Reg
Ren...
FMRI
✓ Toolbox:
ArtRepair
DEM
FieldMap
MEEGtools
PPIs
ImCalc
DICOM Import
Utils...
Batch
Quit
Copyright (c) 1991,1994-2015


spm_artifactrepair
Artifact Repair Toolbox (v4)
View data with contrast movie
Find RMS of image series
Display timeseries on a voxel
Bad slices: detect and repair
Reduce realignment residuals
Bad volumes: detect and repair
Despike and/or high pass filter
Apply deweights to existing SPM
Scaling to percent signal change
Summarize subject contrasts
Summarize group contrast
View all data in group SPM.mat
Find outlier subjects

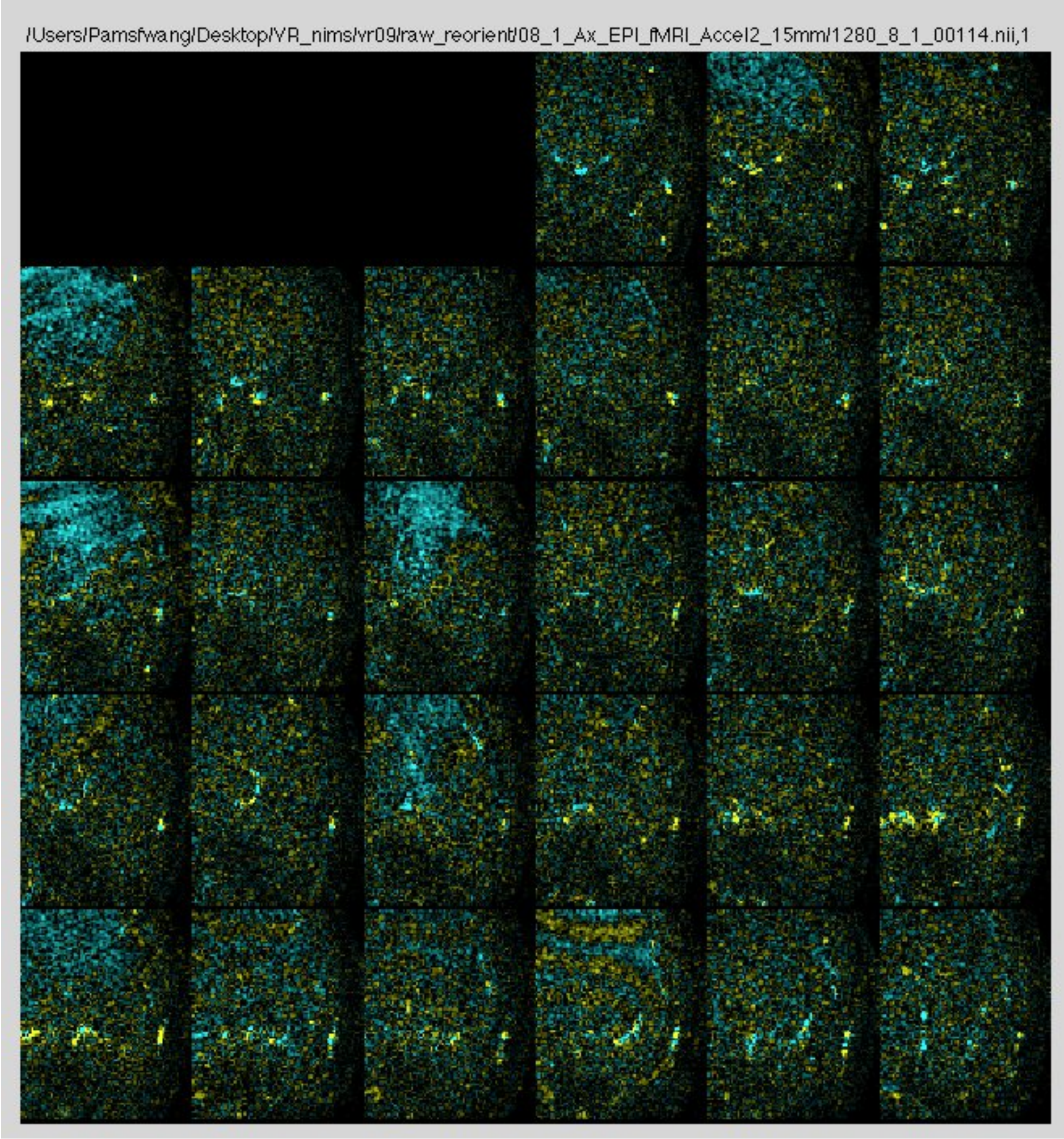
1. Choose Orientation: Transverse, Sagittal, or Coronal
2. Choose a set of images to review (the program can only run up to 86 images)
3. Select Raw/Contrast/ High Contrast display
    a. contrast mode is recommended for identifying artifacts
        i. Contrast: (a volume - a reference volume) * 10 = contrast image
        ii. a good contrast image of good data should be nearly black, which means that no obvious signal change happened between a given volume and the reference volume.
        iii. Colorbar: [-160 160] (contrast scale is 160 counts) . all input images are scaled to this size. +160 correspond to signal increase 16% from the reference image (yellow). Activation sizes are typically 2%, a contrast image of good data should just look dark.
4. Select refernece image: user may choose any image (e.g. a mean image)
5. Select movie or interactive slider

A good volume:

A bad volume:

Bad slices:

Showing contrast images (see below for how the program defines threshold) signal decrease in several slices (blue thing)


/Users/Pamsfwang/Desktop/VR_nims/vr09/raw_reorient/08_1_Ax_EPI_fMRI_Accel2_15mm/1280_8_1_00114.nii,1

Step04: Fix bad slices (ArtRepair)

Identify bad slices

Bad slices: abnormally high or low tSNR of a slice

- increase background signal: ArtRepair
- decrease object signal: CNI QA

- Fix background bad slices via ArtRepair

Script: Step00_check_data.m

batch_function: art_slice_sfw

- Generate whole head mask: the whole head mask is used to select head voxels for calculation (basically, separate head from the background)
    - art_automask: the ArtifactMask (a whole head mask) generated by art_automask will be used in finding bad slice (checking signals outside of the head).
    - Check the ArtifactMask generated by the program: In my case, the auto mask did not cover the entire scalp, and thus, some parts of the scalp were included in "background" noise. This results in a lot of slices were identified as bad slices. To fix this problem, I used SPM segmentation to generate whole head mask for each run and use the mask to separate back ground and the head. This whole head mask is relatively coarse.
- Repair methods
    - Repair Bad Slices and Write BadSliceLog (best choice for TR >2 sec)
        - use linear interpolation of the before and after volumes.
        - Bad slices are detected when the amount of data scattered outside the head is at least T (signal value) above the usual amount for the slice.
            - The usual amount is determined as the average of the best two of the first three volumes. It differs for each slice. Basically, this means that if background signal (area outside of the head) in a slide > threshold, the slide will be identified as a bad slice
            - pq = 0.5*(min(p) + median(p,1)); pq+threshold you defined
                - p: the first 3 volumes you enter to the program
            - This filter removes outliers, but may reduce activations, so it's safest when fewer than 5% of the slices are cleaned up.
        - Adds a prefix "g" to the cleaned output images.
    - Median Filter All Data (Best choice for TR =2 sec or less)
    - Eliminate data outside head
    - Repair Bad Slices and Eliminate data outside head
    - Median Filter All Data and Eliminate data outside head
- Other slices/volumes remained the same!

***visual inspection: CNI QA**
***my CNI QA script**
***manually enter these volumes to art_global and fix them by interpolation**
***keep a log and generate regressors when modeling**

Step05: Slice timing and motion correction

Background:
Slice timing correction:
Correct differences in image acquisition time between slides. If your TR is 2 seconds, the time difference between the first slide and the last slide you collected is 2 seconds! The GLM model assumes slides were collected at the same time. Therefore, you can either fix the model or fix the signal (functional image).

- slice timing differences are worse in event related design
- Short TR would have less slice timing differences (obviously). According to Mumford, if your TR <=2 + interleaved acquisition + spatial smoothing, you can reduce slice timing effects (actually, she does not do slice timing correction for her data)
- Adding temporal derivatives to model would help

Basically, doing slice timing correction in preprocessing is fixing the signal by interpolation. This is also why removing outlier slides or volumes before preprocessing is important. If you do not remove outliers, those "bad" signal will be used in interpolation.

- This is accomplished by a simple shift of the phase of the sines that make up the signal and the correction works by lagging theme-series data on each slice using sinc-interpolation
- each time series having the values that would have been obtained had the slice been acquired at the same time as the reference slice

How to know the slice order?

1. check your scan protocol!
2. The information should be stored in the header (check check check!)

In header:

Slice acquisition information
The fields fields `char slice_code`, `short slice_start`, `short slice_end` and `float slice_duration` are useful to store information about the timing of an fMRI acquisition, and need to be used together with the `char dim_info`, which contains the field`slice_dim`. If, and only if, the `slice_dim` is different than zero, `slice_code` is interpreted as:

	CODE	INTERPRETATION
1	0	Slice order unknown
2	1	Sequential, increasing
3	2	Sequential, decreasing
4	3	Interleaved, increasing, starting at the 1st mri slice

5	4	Interleaved, decreasing, starting at the last mri slice
6	5	Interleaved, increasing, starting at the 2nd mri slice
7	6	Interleaved, decreasing, starting at one before the last mri slice

Motion correction (Realignment)

Align each image in a time series with a reference image. Uses rigid body motion correction (x,y,z, 3 rotations). Register each volume to a reference volume. You will obtain motion parameters (how much a volume is being moved to match the reference) after doing registration. Motion parameters can be used to illustrate the motion over time.

Relative displacement (i.e. how far a volume moved from the last scan) is typically more informative about the change in BOLD signal magnitude.

How to choose the reference volume: the reference volume should be closed to other images on average.

- mean image: you need to calculate the mean! This is an extra step. The image is blurry
- the middle image
- the first image: remember the first few images may have artifact due to scanner warm up. If you do not chop off the first few images, do not use them as reference.

In SPM:

1. align the first scan from each session to the first scan of the first session.
2. The images within each session are aligned to the first image of the session

Script: Step03_preproc.m

- This is a wrapper script that will loop through all subjects and all batch functions (i.e. slice timing correction and realignment)
    - For each subject: perform slice timing correction first, and then motion correction

batch_function: job_slice_timing.m , job_realign.m

- each batch function script contains parameters for SPM to run that specific batch function

- You should adjust those parameters according to your project (e.g. TR, slice order, number of runs,etc.)
- Of course you can add more batch_function scripts! It will be easier to do it on one subject in GUI once and then save it into script. Finally, generalized it. (Please see below!)

project specific script: initialize_vars.m

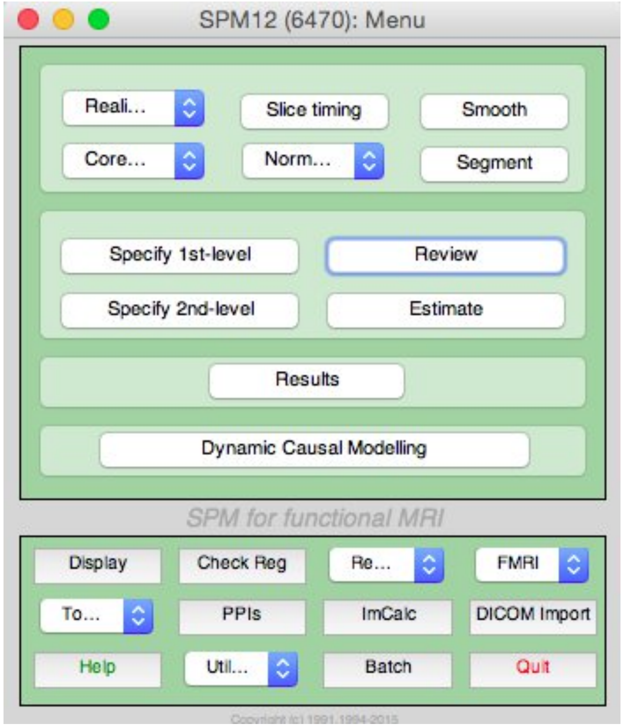
- This script contain subject specific information (e.g. run numbers for each subject, subject directories,etc.)

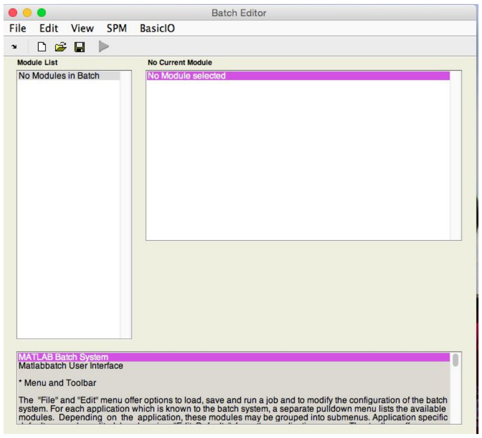
remember to modify --
project specific initialize_vars script, each job script (for file selector, remember to select all BOLD runs and/or field map!)

GUI

Example: Generate one representative job script for performing slice timing correction (start with GUI, then generalize for all subjects and different projects)

Click "Batch"



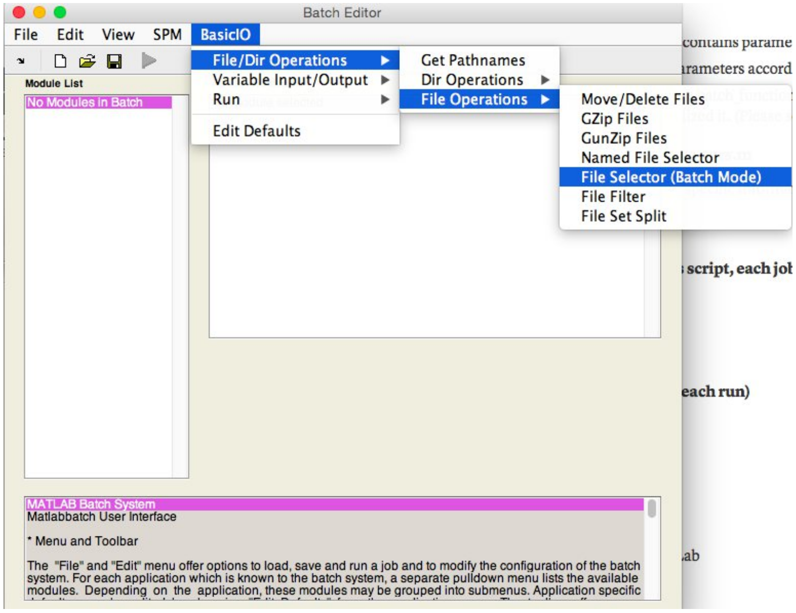


MATLAB Batch System
Matlabbatch User Interface

* Menu and Toolbar

The "File" and "Edit" menu offer options to load, save and run a job and to modify the configuration of the batch system. For each application which is known to the batch system, a separate pulldown menu lists the available modules. Depending on the application, these modules may be grouped into submenus. Application specific

1. The first thing to do is to tell the program what files you want to use! So, go to “BasicIO”, “File/Dir Operations”, “File Operations”, “File Selector”



MATLAB Batch System
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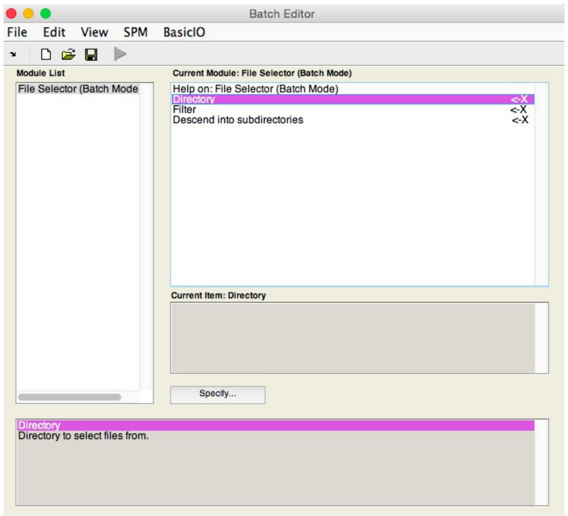
It should looks like this! Then, you just need to fill out the blank. Go to “Directory”, navigate to a directory that contains all images for one run. “Filter”, wildcards for specific file type. For slice timing correction, you will probably select “raw” images — “.*nii”. If you want to do motion correct use slice timing corrected images, you would want to select images with prefix “a”, then type in '^a.*nii” (a is the default predix SPM used for slice-timing correction). Descend into subdirectories (yes or no). Repeat the same procedures for each run till you create a “File Selector” for each run.



Module List

File Selector (Batch Mode

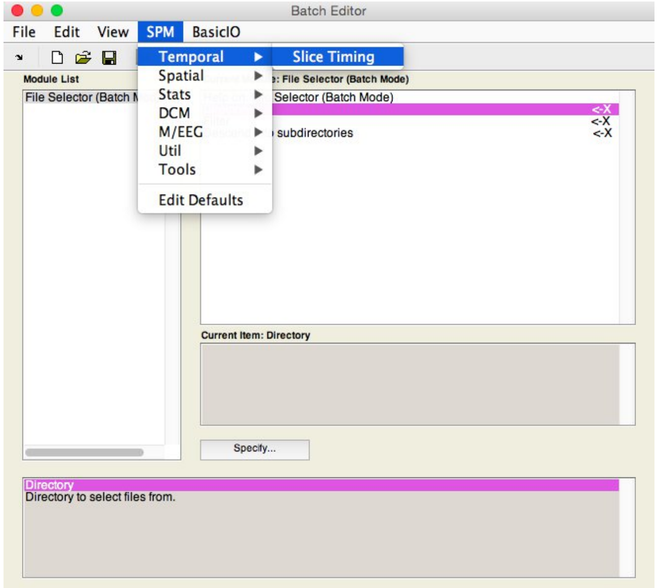
Current Module: File Selector (Batch Mode)

Help on: File Selector (Batch Mode)
Directory <-X
Filter <-X
Descend into subdirectories <-X

Current Item: Directory

Directory
Directory to select files from.

2. After entering all the functional images, you can now select what procedure you want to do on these files. For example, you want to do slice timing correction on these files. It is under "SPM" > "Temporal" > "Slice Timing". Same, if you want to do motion correction, please select Realignment at this step.



Module List

File Selector (Batch M

: File Selector (Batch Mode)

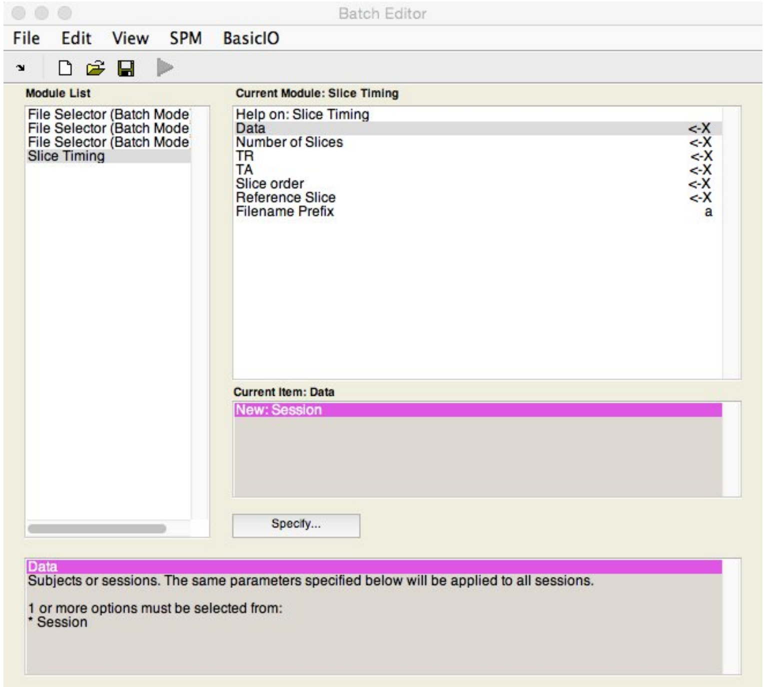
Selector (Batch Mode)
<-X
<-X
subdirectories <-X

Current Item: Directory

Directory
Directory to select files from.

It should look like this. Then, under "Data" , you need to tell the program what data you want to work on. Remember you already select them by "File Selector"! Here is an example of three runs. Click on "Data" and create three "Session".

- Under 'Current Item: Data'
- Click on '**New "Session**' - Create a new session for **each** BOLD run to be analyzed



Module List

File Selector (Batch Mode
File Selector (Batch Mode
File Selector (Batch Mode
Slice Timing

Current Module: Slice Timing

```
Help on: Slice Timing
Data                 <-X
Number of Slices     <-X
TR                   <-X
TA                   <-X
Slice order          <-X
Reference Slice      <-X
Filename Prefix        a
```

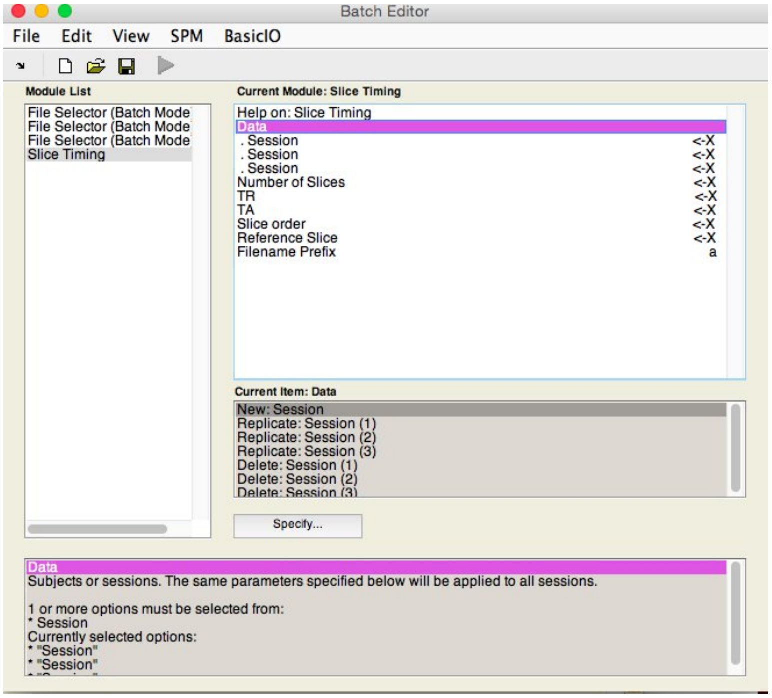
Current Item: Data

New: Session

Data

Subjects or sessions. The same parameters specified below will be applied to all sessions.

1 or more options must be selected from:
* Session



Module List

File Selector (Batch Mode
File Selector (Batch Mode
File Selector (Batch Mode
Slice Timing

Current Module: Slice Timing

```
Help on: Slice Timing
Data
 . Session           <-X
 . Session           <-X
 . Session           <-X
Number of Slices     <-X
TR                   <-X
TA                   <-X
Slice order          <-X
Reference Slice      <-X
Filename Prefix        a
```

Current Item: Data

New: Session
Replicate: Session (1)
Replicate: Session (2)
Replicate: Session (3)
Delete: Session (1)
Delete: Session (2)
Delete: Session (3)

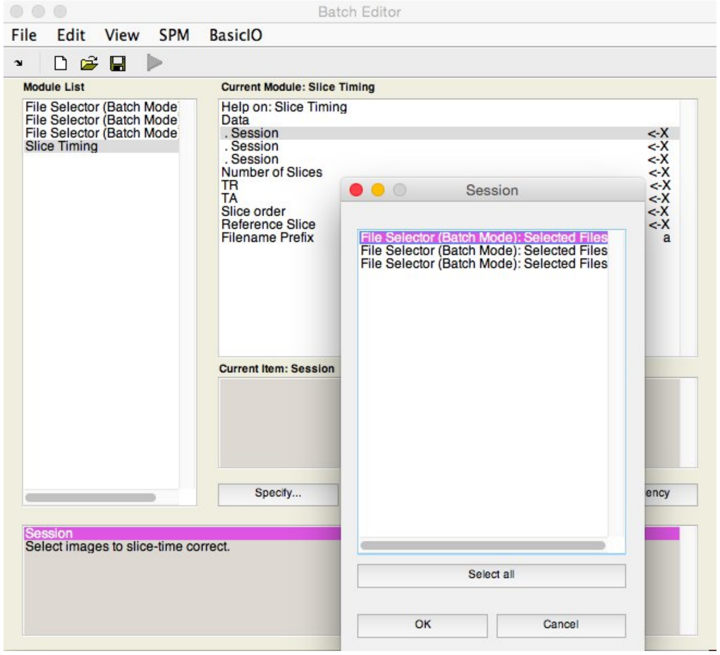
Data

Subjects or sessions. The same parameters specified below will be applied to all sessions.

1 or more options must be selected from:
* Session
Currently selected options:
* "Session"
* "Session"

Click on the first “Session”. Click “Dependency”. Select the first “File Selector (Batch Mode)....”. This represents the first File Selector you enter (i.e. images for the first run). Do the same procedure for all Sessions.

1. For each BOLD run, Click on its ‘**Session ←X**’
2. Click on “Dependency”
3. Select the corresponded “File Selector”
4. Repeat this for each session, selecting run #2's BOLD images for session 2, and so on.



Session
Select images to slice-time correct.

Here is how it looks like when you finished entering “Session” through “Dependency”.

The next values will depend on your slice prescription! Check your parameters to see how many slices you have and the order of acquisition!
Click on ‘**Number of Slices ←X**’ → Click on ‘**Edit Value**’
In the text box, enter total number of slices for one volume

Click on ‘**TR ←X**’ → Click on ‘**Edit Value**’
In the text box, enter TR (sec)

Click on ‘**TA ←X**’ → Click on ‘**Edit Value**’
In the text box, enter the number you obtain for TR- (TR/#slices)
(If 33 slices and TR=2sec, enter ‘**2-(2/33)**’ (This should result in ‘1.9393’))

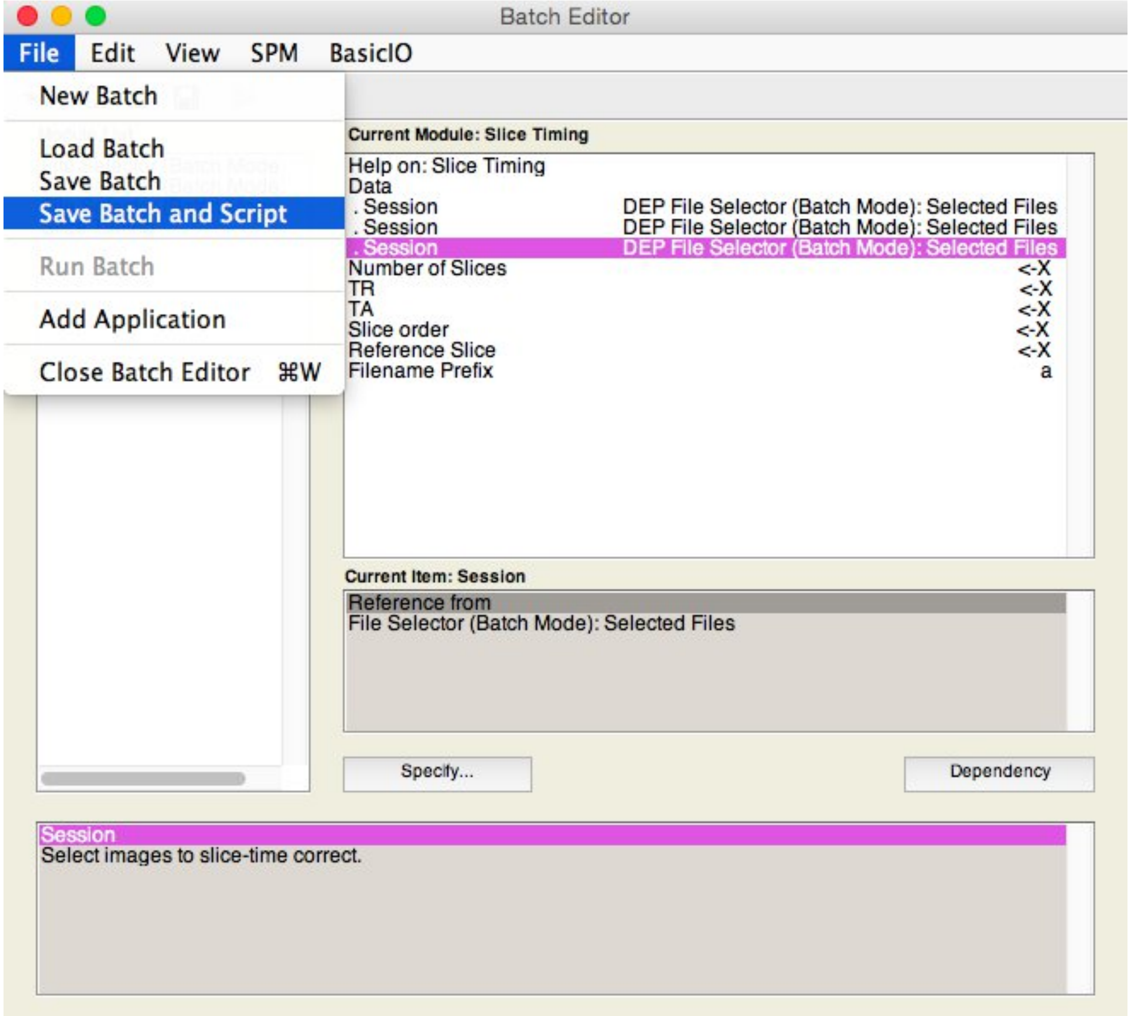
Click on '**Slice Order** ←X' → Click on '**Edit Value**'
In the text box, enter "YOUR SLICE ACQUISITION ORDER"'
A vector of N numbers. Each number refers to the position of a slice within the image file and the order of numbers within the vector is the temporal order in which those slices were acquired
(For example: slice oder interleaved — If 33 slices in total, enter '**1:2:33 2:2:32**')

Click on '**Reference Slice ←X**' → Click on '**Edit Value**'
In the text box, enter a slice number.
This depends on your slice order and which one you want to use as a reference slice in terms of time. As in the "background", slices in a volume were collected at different times. To correct for this time differences, we do slice timing correction. Which time point within a TR? Usually people use middle time point, which will correspond to the slice you collect at the middle of the volume. If your slice order is 1:2:33 2:2:32, then, the middle slice is 2. So, the reference slice is 2. If you want it to be the first slice acquired in time, then the reference slice is 1.

Click on '**RUN**'.

Check in the Matlab window that matlab identifies your TR correctly: **"Your TR is 2.0"**. Note that matlab is now busy running the slice-timing correction even though you cannot see this at first in the SPM8 progress window.

Save Batch and Script: you will have a job script for future use. You can later modify this job script into a function for the wrapper script to use — automatically run all the preprocessing for the entire dataset!



Current Module: Slice Timing

```
Help on: Slice Timing
Data
 . Session                       DEP File Selector (Batch Mode): Selected Files
 . Session                       DEP File Selector (Batch Mode): Selected Files
 . Session                       DEP File Selector (Batch Mode): Selected Files
Number of Slices                                                            <-X
TR                                                                          <-X
TA                                                                          <-X
Slice order                                                                 <-X
Reference Slice                                                             <-X
Filename Prefix                                                               a
```

Current Item: Session

```
Reference from
File Selector (Batch Mode): Selected Files
```

```
Session
Select images to slice-time correct.
```

Motion Correction
Modified from Cognitive Neuroimaging Lab
In the ‘Batch Editor’
Select SPM > Spatial > '**Realign' > “Realign: Estimate & Reslice”**

Click on ‘**Data ←X**’ → Click on '**New Session**' - Create a new session for each BOLD run to be analyzed
Click “Dependency”. Select the first “File Selector (Batch Mode)....”. This represents the first File Selector you enter (i.e. images for the first run). Do the same procedure for all Sessions.

1. For each BOLD run, Click on its ‘**Session ←X**’
2. Click on “Dependency”
3. Select the corresponded “File Selector”
4. Repeat this for each session, selecting run #2's BOLD images for session 2, and so on.

Check SPM manual for the following parameters. Default should be fine!
Under **Estimation Options**
Change the “Quality” value from **0.9** to **1** (maximum quality)
Change the “Separation” value from **4mm** to **2mm**
Reduce smoothing kernel from **5mm** to **4mm** (This is not smoothing your data)
Change the "Interpolation" value from **2nd** to **7th-degree** B-Spline

Under '**Reslices Images (Unwarp)?**'
Change the "Interpolation" value from **4th** to **7th-degree** B-Spline
Make sure **'All images + Mean Image'** is selected (this should be the default).
Leave everything else at 'default'.

Press the '**RUN**' button. This will start the job. New files will be created with the prefix 'r'.

- When done, using **‘Check Reg’** or **‘DISPLAY’**, look at the first and last ‘ra.*nii’ file of the first ‘bold_reorient’ directory.

Step06: Fix bad volumes

Background:
Outlier volumes may be caused by exceeeding the intensity variation threshold or exceeding the scan-to-scan motion threshold, or by user selection (manually entered the volumes).

motion — motion across runs is easier to fix. motion within each run is harder to fix. You can see the effect by Check Reg in SPM.

1. Raw image: check realigment between the first image in the first run and the first image in the last run — you may see motions!
2. Realigned images: check realigment among motion corrected first image in the first run, first image in the last run, motion points within first run and last run. You will see that, after motion correction, the first image of the first and last run aligned pretty well (well, they should!). However, say, in run 1, when compare image at the motion time point with the first image, they may not be aligned!!

Check and repair artifacts volumes
Script: Step00_check_data.m
batch_function: art_global_sfw_zscore_thre
This program will identify bad volume based on global signal change and scan-to-scan motion and repair outliers. Outlier volume will be saved in the same directory for you to include in the GLM. This script also save output image into the same directory.

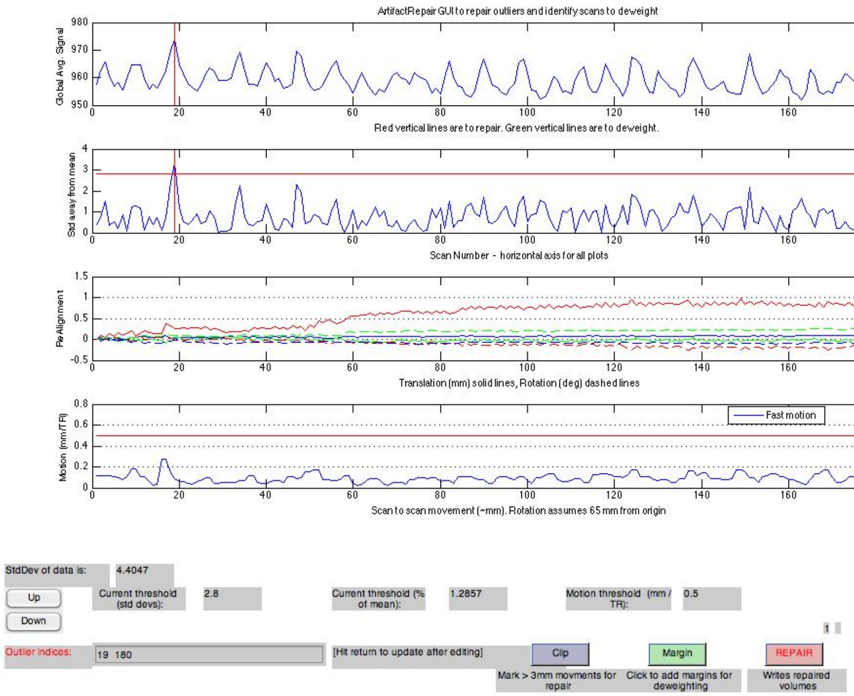
To run this script, set up variables:

```
%% FOr running art_global_sfw_zscore_thre
%Auto or GUI collect files
```

```
GUI = 0; %0==auto, 1==GUI
%Define zscore threshold
zscore_threshold = 3;
per_thresh = 0;
GoRepair=1; % repair volumes =1 (yes), 2 (deweighted), 0
(no)
```

Output

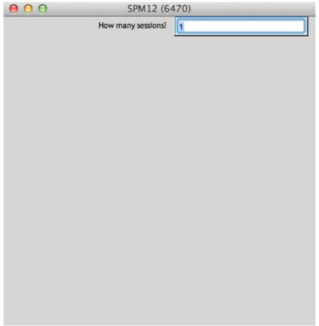
repaired volumes: art_reparied.txt (You can change the file name)
output figure:


ArtifactRepair GUI to repair outliers and identify scans to deweight
Global Avg. Signal
980
970
960
950
Red vertical lines are to repair. Green vertical lines are to deweight.
Std away from mean
Scan Number - horizontal axis for all plots
Re Alignment
x mvmt
y mvmt
z mvmt
pitch
roll
yaw
Translation (mm) solid lines, Rotation (deg) dashed lines
Motion (mm/TR)
Fast motion
Scan to scan movement (~mm). Rotation assumes 65 mm from origin
0
20
40
60
80
100
120
140
160
180
200
Up
Down
Clip
Margin
REPAIR
[Hit return to update after editing]
Mark > 3mm movments for repair
Click to add margins for deweighting
Writes repaired volumes

StdDev of data is: 4.4047
Current threshold (std devs): 2.8
Current threshold (% of mean): 1.2857
Motion threshold (mm / TR): 0.5
Outlier indices: 19 180

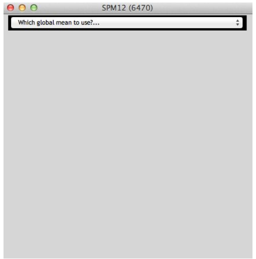
GUI

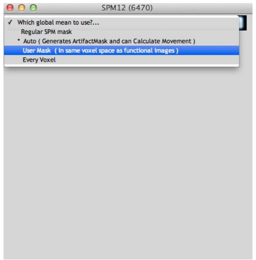
Function: art_global
Number of session: 1 (it is recommended to do within run)

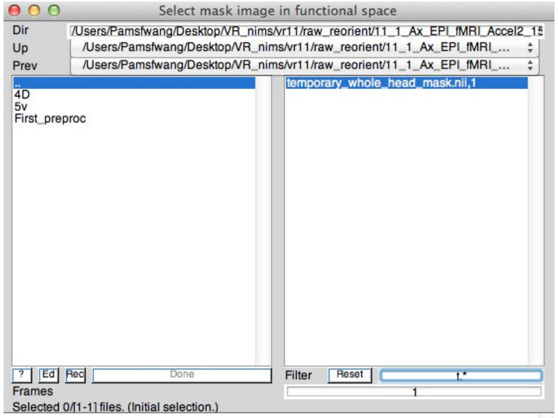


How many sessions? 1

Mask: users mask — Select the whole head mask you generated




SPM12 (6470)
✓ Which global mean to use?...
Regular SPM mask
* Auto (Generates ArtifactMask and can Calculate Movement)
User Mask (in same voxel space as functional images)
Every Voxel



Dir /Users/Pamsfwang/Desktop/VR_nims/vr11/raw_reorient/11_1_Ax_EPI_fMRI_Accel2_15
Up /Users/Pamsfwang/Desktop/VR_nims/vr11/raw_reorient/11_1_Ax_EPI_fMRI_...
Prev /Users/Pamsfwang/Desktop/VR_nims/vr11/raw_reorient/11_1_Ax_EPI_fMRI_...

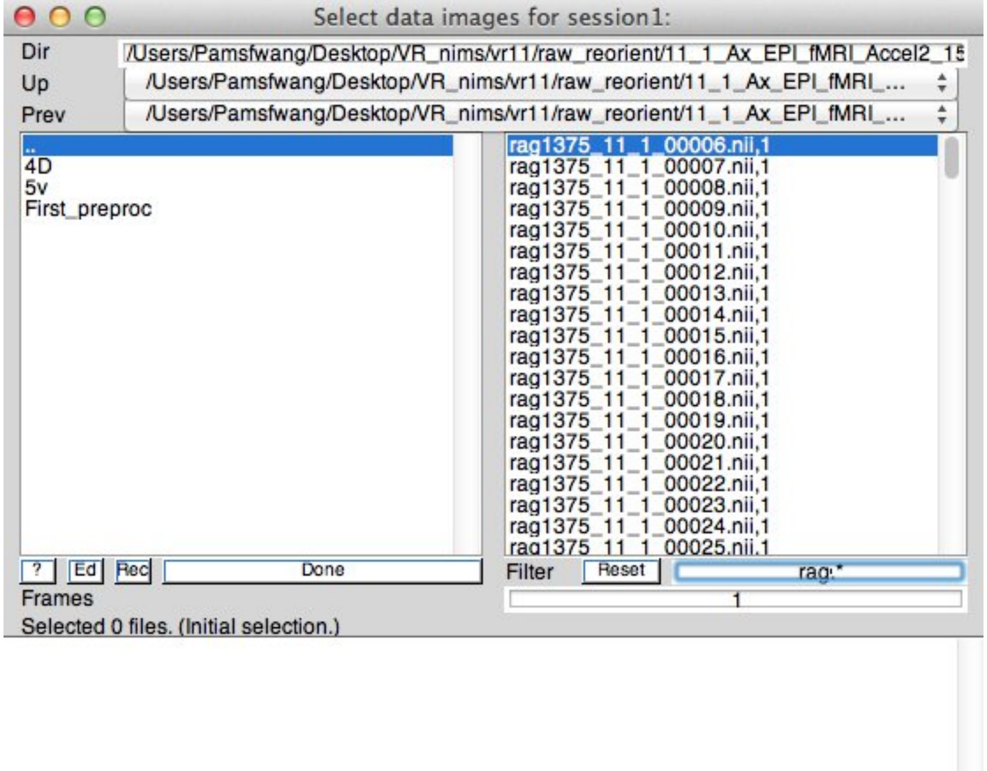
..
4D
5v
First_preproc

temporary_whole_head_mask.nii,1

Filter t.*
Frames 1
Selected 0/[1-1] files. (Initial selection.)

Functional images: select motion corrected images
SPM prefix:

r: realignment
a: slice timing
g: slice repair (by ArtRepair, prefix depends on what repair method you used)



Select data images for session1:

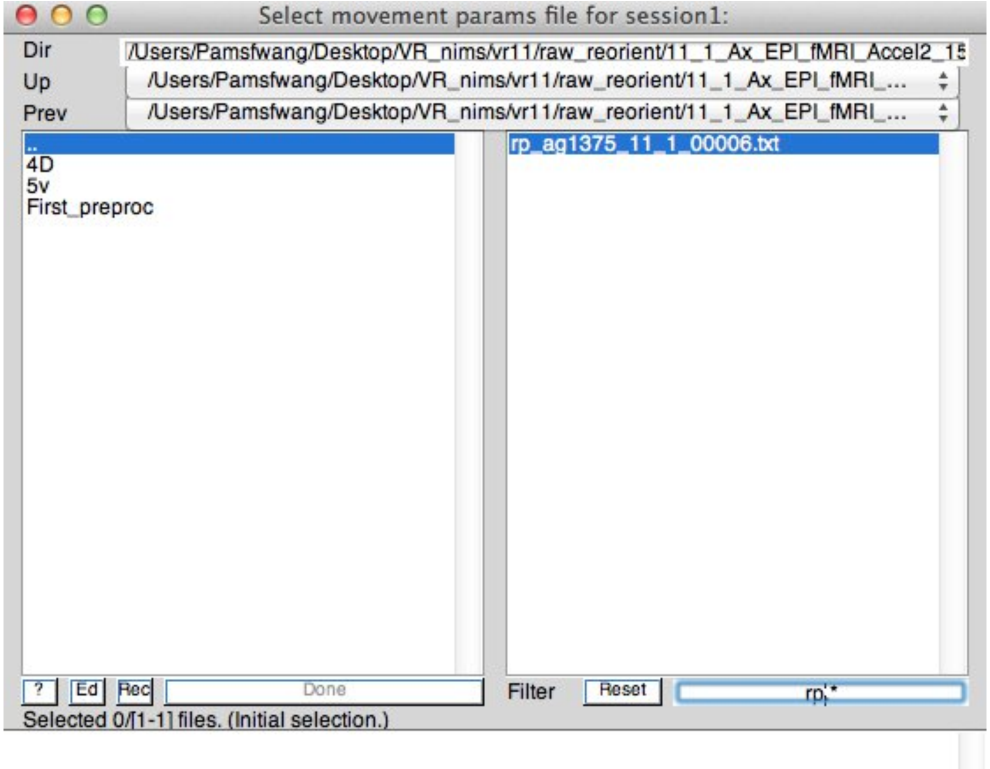
Dir /Users/Pamsfwang/Desktop/VR_nims/vr11/raw_reorient/11_1_Ax_EPI_fMRI_Accel2_15
Up /Users/Pamsfwang/Desktop/VR_nims/vr11/raw_reorient/11_1_Ax_EPI_fMRI_...
Prev /Users/Pamsfwang/Desktop/VR_nims/vr11/raw_reorient/11_1_Ax_EPI_fMRI_...

```
..
4D
5v
First_preproc
```

```
rag1375_11_1_00006.nii,1
rag1375_11_1_00007.nii,1
rag1375_11_1_00008.nii,1
rag1375_11_1_00009.nii,1
rag1375_11_1_00010.nii,1
rag1375_11_1_00011.nii,1
rag1375_11_1_00012.nii,1
rag1375_11_1_00013.nii,1
rag1375_11_1_00014.nii,1
rag1375_11_1_00015.nii,1
rag1375_11_1_00016.nii,1
rag1375_11_1_00017.nii,1
rag1375_11_1_00018.nii,1
rag1375_11_1_00019.nii,1
rag1375_11_1_00020.nii,1
rag1375_11_1_00021.nii,1
rag1375_11_1_00022.nii,1
rag1375_11_1_00023.nii,1
rag1375_11_1_00024.nii,1
rag1375_11_1_00025.nii,1
```

Filter rag.*
Frames 1
Selected 0 files. (Initial selection.)

Motion parameters: rp*.txt


Select movement params file for session1:

Dir /Users/Pamsfwang/Desktop/VR_nims/vr11/raw_reorient/11_1_Ax_EPI_fMRI_Accel2_15

Up /Users/Pamsfwang/Desktop/VR_nims/vr11/raw_reorient/11_1_Ax_EPI_fMRI_...

Prev /Users/Pamsfwang/Desktop/VR_nims/vr11/raw_reorient/11_1_Ax_EPI_fMRI_...

..
4D
5v
First_preproc

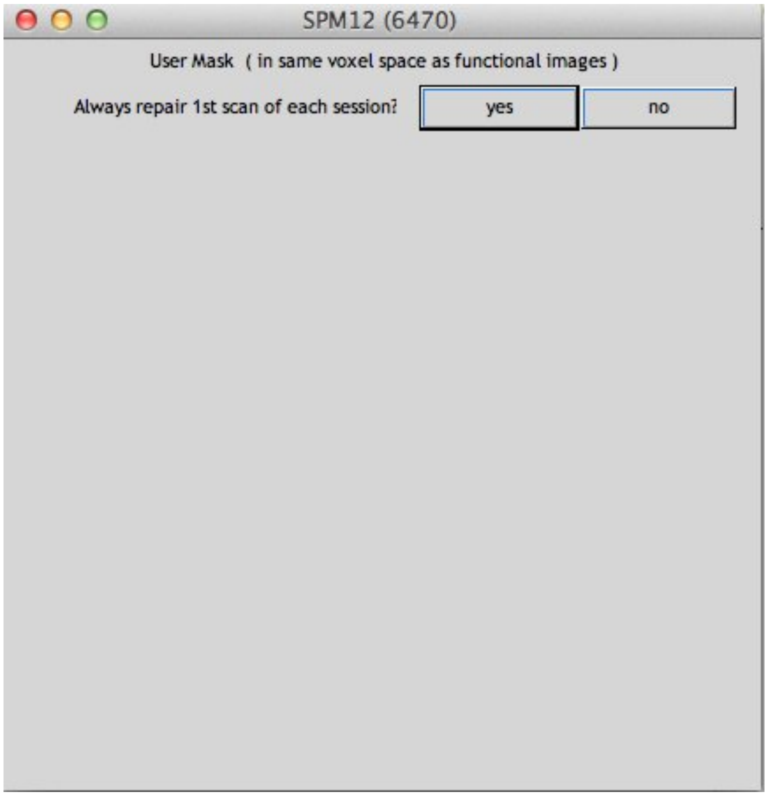
rp_ag1375_11_1_00006.txt

Filter rp.*

Selected 0/[1-1] files. (Initial selection.)

Always repair 1st scan?

- No (if you already removed the first few scans from analyses)
- Yes (if the first image was the first image you collected for the run)



User Mask (in same voxel space as functional images)

Always repair 1st scan of each session?

Repair artifact volumes: interpolation
repairted voluem log .txt — used in creating regressors

Global summary figure
You will obtain a global summary figure. You can adjust threshold and manually add outlier volumes. You can only adjust the z-score threshold and all other thresholds are linked and automatically adjust to your new threshold. To set up your own threshold, you need to modify it in the art_global script. Once you have done adjusting thresholds, Click repair. It will automatically fix the outlier volumes (three options of methods). A list of outlier scans will be saved in the same directory in the file art_repaired.txt and a list of scans to deweight will be saved in the same directory
in the file art_deweighted.txt.

Click: "**repair**" (repair even if there is no outlier — it will do nothing to the data but adding "v" to the file as new prefix)

No changes are made until the Repair button is pressed. The repaired volumes are listed in the text file art_repaired.txt.
Repair methods:

- Recommend to use linear interpolation as the best method of Repair. This function fills values using linear itnerpolation from the nearest unrepaired scans.
- Mean fills values with the mean scan of the run.
- Despike fills values as a linear interpolation of the immediately preceding and following scans, whether they are repaired or not.

ArtRepair suggestions:
Red vertical lines are outlier volumes (volumes with intensity above global mean threshold and/or with rapid motion). All repaired volumes are recommended for deweighting. Deweighted volumes are specified by green vertical lines. These volumes will be close to large discontinuities in global intensity or movement even after repair, and so may degrade the accuracy of SPM estimation. If the data has lots of motion, use motion regressors. Then, no additional deweighted scans are necessary.

- The first graph: time history of the mean intensity within the head region.
    - default threshold: 1.3% of the mean signal. (This threshold was set for images from Lucas scanner, details on the website)
- The second graph: the size of the global signal change relative to the mean of the run. (std away from the mean)
    - default threshold: this is calculated according to 1.3% of the mean signal. Therefore, this threshold changes from run to run.
- The third graph shows the six SPM realignment parameters

- The fourth graph shows the scan-to-scan movement.
    - default threshold: 0.5mm/TR

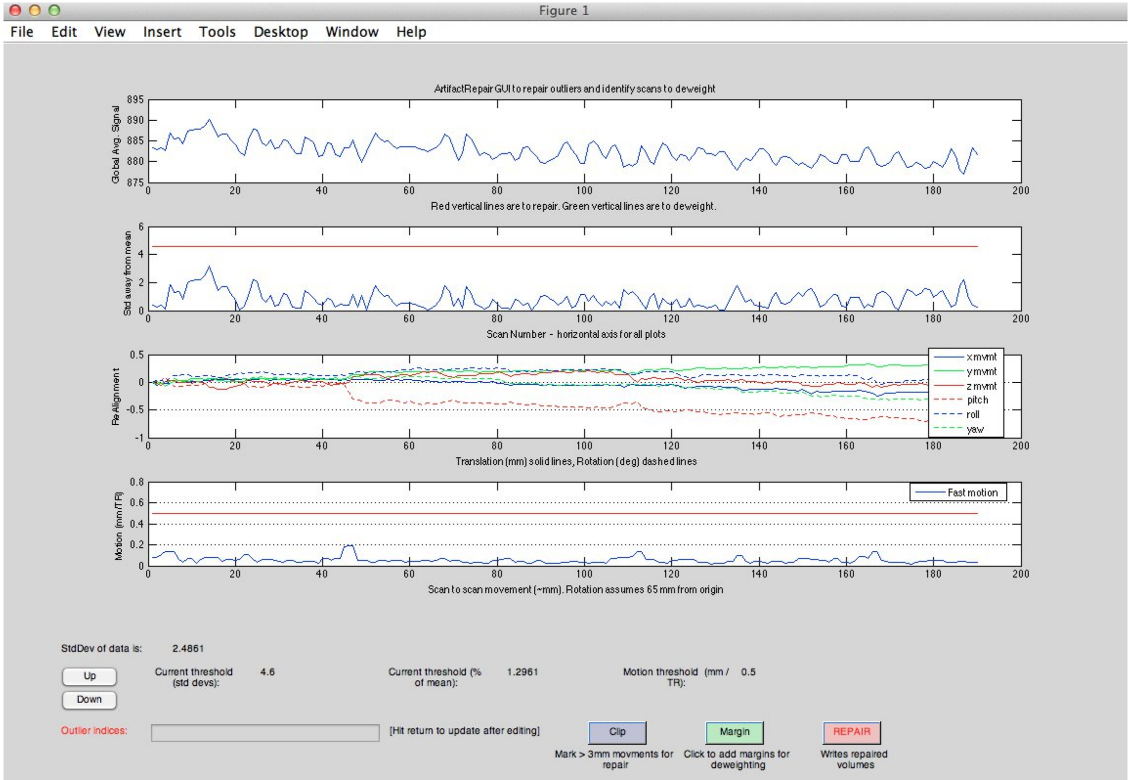


Figure 1
File
Edit
View
Insert
Tools
Desktop
Window
Help
ArtifactRepair GUI to repair outliers and identify scans to deweight
Global Avg. Signal
895
890
885
880
875
0
20
40
60
80
100
120
140
160
180
200
Red vertical lines are to repair. Green vertical lines are to deweight.
Std away from mean
6
4
2
0
Scan Number - horizontal axis for all plots
Realignment
0.5
0
-0.5
-1
x mvmt
y mvmt
z mvmt
pitch
roll
yaw
Translation (mm) solid lines, Rotation (deg) dashed lines
Motion (mm/TR)
0.8
0.6
0.4
0.2
0
Fast motion
Scan to scan movement (~mm). Rotation assumes 65 mm from origin
Up
Down
Outlier indices:
[Hit return to update after editing]
Clip
Mark > 3mm movments for repair
Margin
Click to add margins for deweighting
REPAIR
Writes repaired volumes

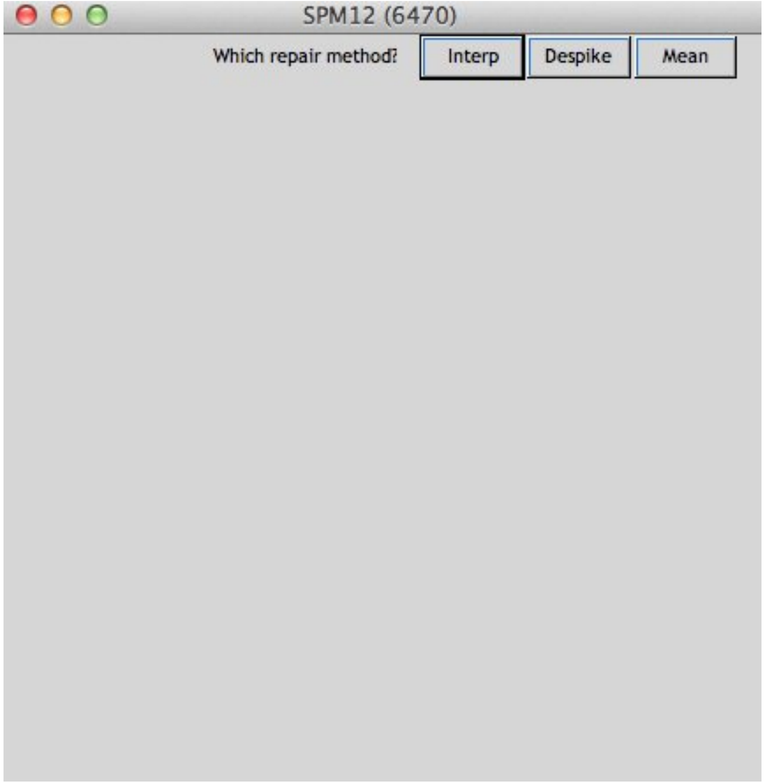
StdDev of data is: 2.4861

Current threshold (std devs): 4.6

Current threshold (% of mean): 1.2961

Motion threshold (mm / TR): 0.5

click interp (linear interpolation)



differences: scan-to-scan differences
absolute
Three graphs:

1. the top graph is the global brain activation mean as a function of time: outliers
2. the second graph is the time series derived from the global BOLD signal: this is used to identify outlier scans — either absolute or scan-to-scan differences (z-scores)
3. The third graph is the time series derived from the subject motion parameters (either absolute or scan-to-scan differences)

```
 By default art generates the following output
files:%  Regressor files (one per session, stored in the
same folders as the%   functional volumes, and named
art_regression_outliers_*.mat
and %   art_regression_outliers_and_movement_*.mat). This
files can be entered%   as covariates in the first-level
analyses in order to effectively%   remove the identified
outlier scans from further analyses%  Analysis mask (one
file named art_mask.img defining the analysis mask%   after
disregarding outlier scans). This file can be entered as
an%   explicit analysis mask in the first-level analyses in
order to%   avoid any influences of the outlier scans on
the implicit analysis mask%   computation (on SPM you will
also need to modify the defaults in order%   to skip the
implicit masking operation, e.g. set defaults.mask.thresh =
%   -inf)
```

Dartel: Use group template to do realignment —> better across subjects realignment
Realignment and unwrap
can be down without field map to correct for drop out
separation: sampling space
smoothing: smooth before calculating motion parameters

COSPAL Coregistration

From Cognitive Neuroimaging Lab

COREGISTRATION OF THE STRUCTURAL IMAGE TO THE MEAN FUNCTIONAL IMAGE

Takes ~2 min to run
The reason why we want to co-register the structural image to the mean functional image is because we would like to display the subjects SPMs on their own anatomical image.
We need to create an accurate average of the two anatomical images. To do this, run the exact same Realign and Unwarp process above, only with one session containing 3danat1.nii and 3danat2.nii selected from their respective folders under 3danat_reorient. This process will account for any motion or subtle distortions between the two images prior to automatically creating an average anatomical image called meanu3danat1.nii.
Press the '**Coregister**' button.
Click on '**Reference Image <-X**'
Click on 'S**elect Files**', and select the mean functional image: meanuarun1.nii, 1 (located in the first ‘bold_reorient’ subdirectory.
Click on '**Source Image <-**X'
Click on '**Select Files**', and select the avg structural image, meanu3danat1.nii, 1 from the 1st folder in the ‘3danat_reorient’ directory.
Default "Histogram Smoothing is fine at 7mm. If you choose to, you can change the value from **7mm** to **6mm**
Press the '**Save'** button and save the job as 'coreg_3danat’ in your subject's job directory (this will create a file called ‘coreg_3danat.mat’.
Press the '**Run**' button.

- When done, use 'Check Reg' to critically inspect the co-registration of the meanuarun1_.nii image file with the meanu3danat1.nii image.
-

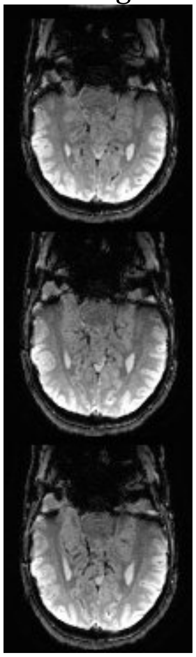
Optional: distortion correction

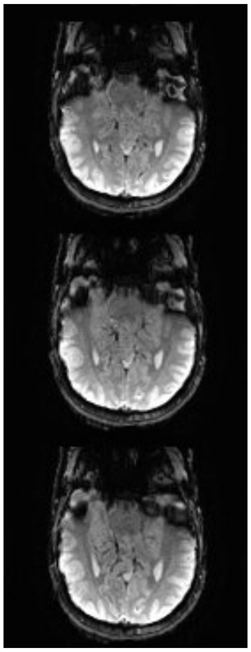
1. when to do distortion correction? raw data? motion corrected data?
2. whether to do it or not??
   a. for my current project I did not do it because the result images look weird (see below)

distortion correction
use Kendrick’s script
needs: a 4D file
I used SPM to split 4D file into 3D files for all the processing…..but using kendricks’ distortion script, we need to use 4D file. After file split, header “description” part was rewrote. But, Kendrick’s script need those info (preprocessfmri_CNI.m). So, we should provide those information.

10/06: used vr13 to try out distortion correction.
order: distortion correction -> remove bad slices -> slice timing -> motion

subject vr03:
raw image





undistorted image