

# **spm12Batch System for systematically processing BOLD fMRI data.**

This is an ecosystem for processing fMRI data in a coherent, flexible, streamlined, and self-documenting way. This ecosystem is based on bash and in general provides wrapping of **MATLAB** (along with **FSL** utilities, **ANTs**, **AFNI**, and **ANIMA**) to provide a full pipeline of data processing. The pipeline is typically executed in steps.

This system has successfully run on MAC OS X and Linux. Because the system is bash based, it is highly transportable, and as long as the underlying third party executables are accessible, the code should work out of the box after a short configuration.

While the system is called **spm12Batch**, it does leverage functionality from other processing systems to result in a more robust processing pipeline. This includes having the option to use **ANTs** for normalization, and to use **AFNI** for despiking of data. The steps of slice-time correction, motion correction, and co-registration steps are done with **SPM**. There is also an option to use **SPM** to do tissue segmentation to provide for WM and CSF masks that can be used further down for physiological denoising using a process such as COMPCOR. **ANIMA** is used for EPI distortion correction.

The code is written such that you call the code with a list of parameters, if other than default values, and a list of fMRI sessions (subjects/participants). The code will then build the necessary (unique) scripts and launch those into background, providing a log file. The result is a fully logged process of how your data have moved through pre-processing.

The code is such that while session names are unique, file names below that level are not unique, which provides for ease of specification.

A general philosophy of this ecosystem is to keep different functional tasks apart from each other, and to treat each fMRI session as independent for pre-processing, regardless of whether these are multiple visits for a single participant.

One result is that if there are multiple-tasks for a session, then the pipeline is to be run fully by task, this does result in a little bit of size inflation and process inflation as the derivation of normalization to MNI space is done for each task. This is due to the high-resolution image being co-registered to the BOLD data, and not the BOLD data being co-registered to the high-resolution image. Because each task is independently processed, this does provide flexibility that would not otherwise exist if all tasks were being processed in a single pipeline.

Currently this provides minimal QC, limited to motion parameters being plotted to a PNG file for viewing. Future versions will incorporate additionally QC metrics.

# spm12Batch System

## Server Installation - Instructions for System Administrator

In addition to access to **SPM12**, you need in your bash **PATH** accessing **FSL**, **ANTs**, **AFNI**, and **ANIMA**. We leave it up to you to install these packages. You will also need to have the MICCAI labeled data in your Templates directory for ANTs.

Also have the distribution folder for **spm12Batch** (downloadable from GIT) in you **PATH**. This has successfully worked with various version of **FSL** from version 5.x (only using small utilities in FSL for doing s-form and q-form manipulation, etcetera), and **ANTs** 2.3.5, **ANIMA** 4.X, and **AFNI** (21.0.20 “Titus”).

Edit **spm12Batch/spm12Batch\_Global** to point to **MATLAB** and to **SPM12** code.

Once successfully configured, then run the command:

**spm12Batch\_CheckInstall**

to see the list of commands do:

**spm12Batch**

Each command has **built-in** help. To see the help, issue the command without any options.

**To successfully execute a command you must first run the command without any options as to let the command know you have minimally examined the help. If you wish to bypass this, then place a file called “.help.[command]” for each command in your home directory.**

*The system can be configured, via an expert, to allow for jobs to either email or text you on completion. Automated email at conclusion of a job, however, is problematic on some systems that are not configured with a static IP address and IP name in a DNS. The email will also be dependent on what firewall rules exist at your institution. Presently, the automated email is disabled. This has worked before on system using postfix. If you would like to attempt to use the automated email system, contact Robert for some small guidance, but you will need to have expertise in Linux/MAC OS X and a mail system such as postfix.*

# spm12Batch System

## Server Installation - Instructions for System Administrator

Installing the **MICCAI** labeled data in your **Templates/** directory for **ANTs**.

You will need to go to the website:

[http://www.neuromorphometrics.com/2012\\_MICCAI\\_Challenge\\_Data.html](http://www.neuromorphometrics.com/2012_MICCAI_Challenge_Data.html)

and place the resulting templates into the **Templates/** directory which resides in parallel to the **bin/** directory for **ANTs**. You will need to ensure the following images are in the folder **[ANTS]/Templates/MICCAI2012-Multi-Atlas-Challenge-Data/**

```
T_template0.nii.gz
T_template0_BrainCerebellum.nii.gz
T_template0_BrainCerebellumExtractionMask.nii.gz
T_template0_BrainCerebellumMask.nii.gz
T_template0_BrainCerebellumProbabilityMask.nii.gz
T_template0_BrainCerebellumRegistrationMask.nii.gz
T_template0_glm_4labelsJointFusion.nii.gz
T_template0_glm_6labelsJointFusion.nii.gz
```

# spm12Batch System

## Initial usage by users

Make sure to have your **.bashrc** or **.bash\_profile** such that your **PATH** variable has access to **FSL**, **ANTs**, **AFNI**, and **ANIMA**. Ask your sys admin for assistance as needed.

Once successfully configured, then run the command to verify access:

**spm12Batch\_CheckInstall**

To see the list of commands do:

**spm12Batch**

Each command has **built-in** help. To see the help, issue the command without any options.

***To successfully execute a command you must first run the command without any options as to let the command know you have minimally examined the help. If you wish to bypass this, then place a file called “.help.[command]” for each command in your home directory.***

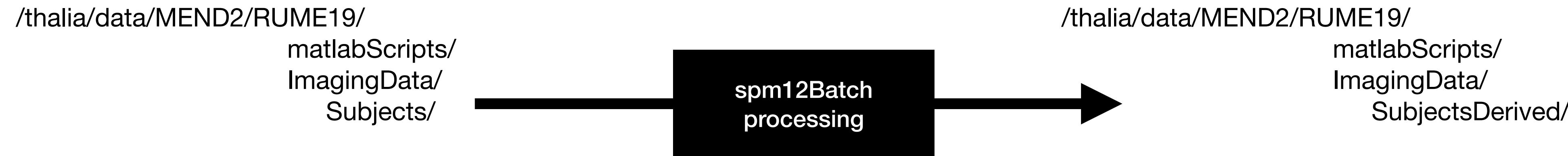
*The system can be configured, via an expert, to allow for jobs to either email or text you on completion. Check with your sys admin if email on the system has been properly configured. Automated email at conclusion of a job, however, is problematic on some systems that are not configured with a static IP address and IP name in a DNS. The email will also be dependent on what firewall rules exist at your institution. Presently, the automated email is disabled. This has worked before on system using postfix. If you would like to attempt to use the automated email system, contact Robert for some small guidance, but you will need to have expertise in Linux/MAC OS X.*

# spm12Batch System

## Usage

The general philosophy of this package is to automate each step of pre-processing, but to not necessarily do a full pipeline on a session *all at once*. The system, however, does have flexibility to allow for full pipeline processing on a session. By allowing each step to be processed on a batch of sessions this allows for visual QC to occur on that batch of sessions prior to moving on to the next step. This is different than some other published processing pipelines. I always encourage people to look at their data and to get close to it, and to do this examination at each step. By having the flexibility to process each step at a time allows for data examination. This permits erroneous issues to be resolved before moving on to the next processing step.

Data is organized such that all MR sessions reside under a master directory, and the scripts are invoked above that directory. The default is for the master directory to be called **ImagingData/Subjects**. The typical usage of the **spm12Batch** system is to process data and have the processed (derivatives) data reside in a separate tree, which typically is called **ImagingData/SubjectsDerived**. The flexibility of the code is such that this can be specified if you so choose to keep all of your original data and processed data the same. I do, however, encourage using the **SubjectsDerived** folder as it permits ease of removing erroneously processed data without needing to be in the original data tree.

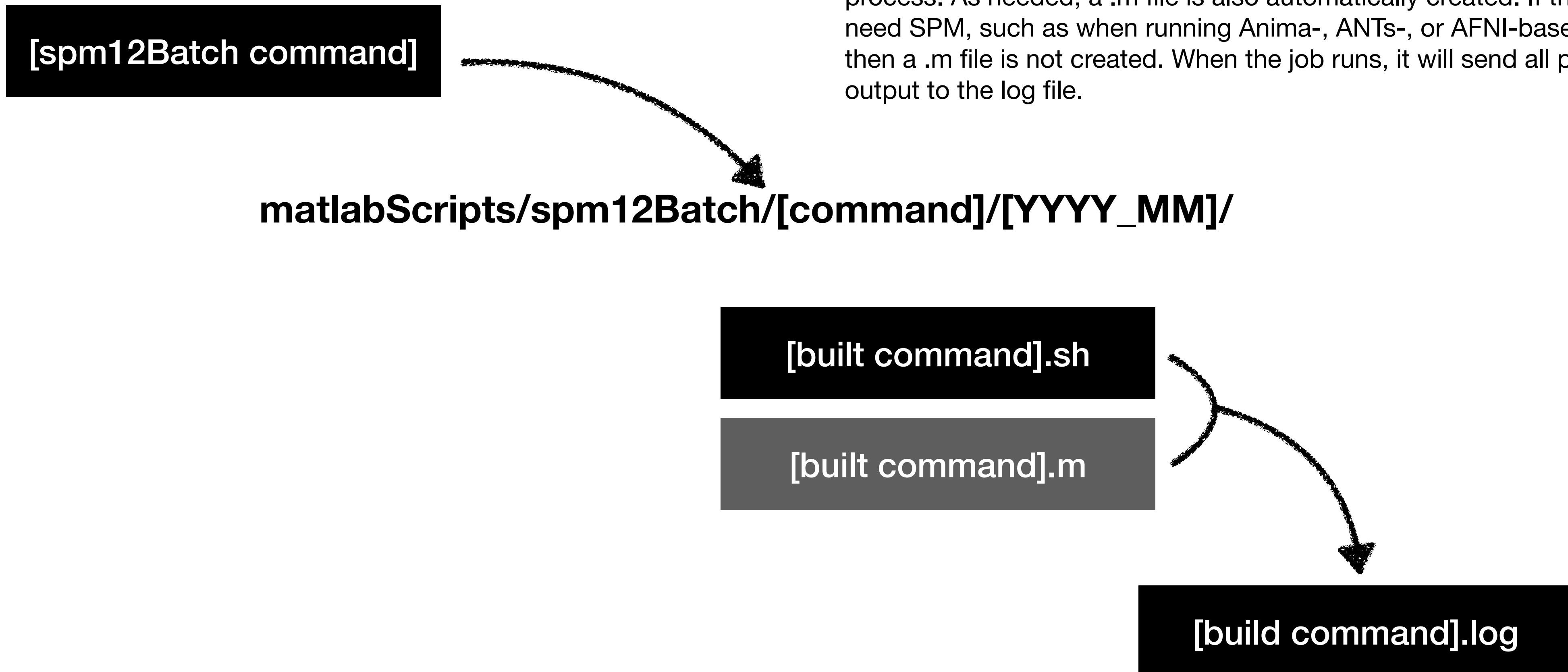


When the commands are invoked, scripts are written to a folder called **matlabScripts/spm12Batch**. Each command (such as **despikeANFI**, **distortionCorrect**, **etcetera**) and the built scripts live in a tree with the year and month of creation. Scripts are fully unique, include the name of the command, the date/time of creation in the name, the user that created, and an abbreviation of the host system. An example for **distortionCorrect** is here:

```
distortionCorrect_210324_00_10_20_201_rcwelsh_mutis.sh  
distortionCorrect_210324_00_10_20_201_rcwelsh_mutis.log
```

# **spm12Batch System**

## **Command building**



# spm12Batch System

## Expected Organization

The general organization is structured, and with generic names as to facilitate file name searches. An example is below. While the code is expecting the anatomy to reside in a folder called “**anatomy/**”, this can be overridden with the “-a” flag. This is the same for task folder organization.

The **spm12Batch** system is flexible to file names, as long as they follow a generic pattern, and to folder names, also following a generic pattern. A typical organization is below. Default names are overridden using flags to the **spm12Batch** commands.

[myExpDir]/ImagingData/Subjects/

```
[session]/
    anatomy/
        hiRes.nii           ← as long as this is the same name for all sessions to be processed, it can be anything (no spaces)
        loRes.nii           ← this is for legacy processing when headers in NII are missing orientation.
    func/
        [task]/
            fieldMap/
                forward.nii   ← We use ANIMA for correction, which has a forward and backward image
                backward.nii
            run_01/
                run_01.nii   ← Generic name for a BOLD starts with “run” (default)
            run_02/
```

To get better sense of how the system are used, look at the example calls in **BatchExamples**. I provide additionally functionality in those scripts, which are to be executed in numeric order. Examine these to better understand how to operate within the **spm12Batch** system. The folder **Examples\_wANTS** provided a full pipeline, when there is a high-resolution image, fieldmap files, and EPI BOLD data. An example of processing the full pipeline on a single session is given in **Examples\_DaisyChained**. Daisy chaining is accomplished by indicating to **spm12Batch** to not sent jobs to the background (with **-B** flag). Instead, if you wish to process in the background you would submit a full pipeline command to the background. Processing following the SPM nomenclature of prepending the name of the BOLD data with the processing step. This is a parameter that can be specified with the **-on** flag, but have sensible defaults.

# spm12Batch System

## Note on derivatives folder

Most commands will operate on data and put resulting data back into the same tree. However, the earlier stages can be directed to output data to a new parent tree.

**distortionCorrect** can take input data with **-M** flag and put into a new tree with the **-MO** flag.

**prepDeratives** will copy input data with **-M** flag and put into a new tree with the **-MO** flag. This is good for copying over **anatomy/** folder to the **SubjectsDerived** folder.

**despikeAFNI** will copy input data with **-M** flag and put into a new tree with the **-MO** flag.

If you've used **distortionCorrect** with the **-MO** flag, then for **despikeAFNI** you will need to specify both **-M** and **-MO** with the same parameter since **distortionCorrect** has already put output into new tree, and **despikeAFNI** will need to know that. You have to also specify the **-MO** to ensure you're putting data where you expect it to go. Examine the examples of how this works.

ImagingData/Subjects  
[subject]/  
[subject]/  
...  
...

ImagingData/SubjectsDerived  
[subject]/  
[subject]/  
...  
...

If you are using the **SubjectsDerived** folder tree, then you will want to make sure to specify **ImagingData/SubjectsDerived** with the **-M** flag for all subsequent commands.

# spm12Batch System

## spm12Batch Commands

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Command	Purpose
distortionCorrect	A wrapper to ANIMA to correct EPI BOLD images.
prepDerivatives	A script to move data from canonical data to derived data.
sliceTime12	A wrapper to the SPM12 slice time correction routine.
sliceTimeMB	A wrapper to the SPM12 slice time correction routine. Use this command for multiband data.
realignfMRI12	A wrapper to the SPM12 coregistration for time-series.
despikeAFNI	A bash routine to find bad image slices using AFNI.
coregOverlay	A wrapper to the coregistration routine in SPM12.
coregHiRes	A wrapper to the coregistration routine in SPM12.
antsHiRes	A wrapper to ANTs functionality for doing warping of HIRES.
antsfMRI	A wrapper to ANTs functionality for warping fMRI data.
antsN4SS	A wrapper to ANTs functionality to N4 and skull strip HIRES.
newSeg	A wrapper to do MNI warping of hi-resolution image to MNI the standard normalize function in SPM12.
pcafMRI	A wrapper to calculate COMPOR-like regressors.
erodeMask	A wrapper to FSL/fslmaths to erode masks. Usually auto-called by newSeg/cat12 commands
warpSeg	A wrapper to do MNI warping of functional images to MNI space based on either output of newSeg or cat12HiRes.
smoothfMRI	A wrapper to smooth images using SPM12 routines.

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# spm12Batch System Examples

Following are diagrams illustrating the pipeline steps and different use cases.

The general syntax for calling the **spm12Batch** commands is to first name the command, then list all of your flags with parameters and then the list of subjects. The list should **not** be in quotes. You can use bash to pass a list as well using in-line execution.

**[spm12Batch command] [options] [list of sessions]**

Example of passing a list of subjects assuming you have a plain text file with one session listed per row, and that the file is called **ListOfSubjects.txt**, you use the backward single quote (below the escape key on an extended Mac keyboard).

```
smoothfMRI -M ImagingData/SubjectsDerived -f func/Rest -v w_r12_aMB `cat ListOfSubjects.txt`
```



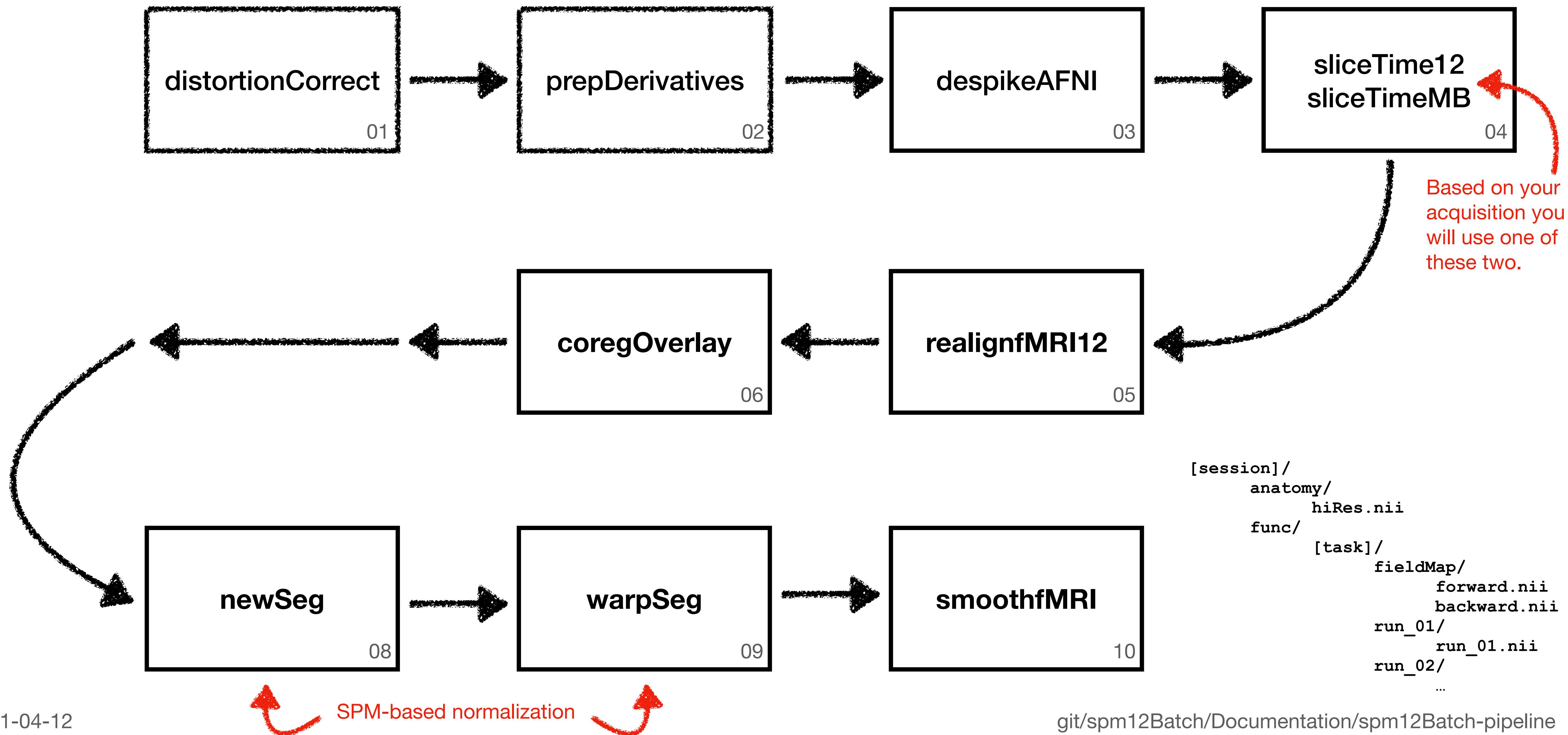
spm12Batch Command      Options      List of sessions

Example Number	Description
1	Have images to do distortion correction, and to use SPM for warping to MNI space.
2	Have images to do distortion correction, and to use ANTs for warping to MNI space.
3	Same at 2), but also use SPM to do segmentation of the bias corrected native image.
4	Same as 2) above, but using also an intermediate lo-res anatomy file called the overlay image.

## Example 1

# spm12Batch System

## spm12Batch processing pipeline without overlay image using SPM normalization



## Example 1

In this example, we start with a set of data that has a high resolution image called **mprage\_noFace.nii** that resides in the **anatomy**/ folder. For the task of interest (**Rest**), which resides under the **func**/ folder, we have two runs, each in their own folder: **run\_01/run\_01.nii** and **run\_02/run\_02.nii**. We also collected a field map, with the phase encode polarity in the **FM\_PA.nii** image matching the phase encode polarity in BOLD data, and the other polarity (backward image) as **FM\_AP.nii**. You can download the TestSubject folder from:

The processing steps we will do are:

```
distortionCorrect -M ImagingData/Subjects -MO ImagingData/SubjectsDerived -bi FM_AP.nii -fi FM_PA.nii -fm fieldMap -f func/Rest -on dc_ -v run TestSubject  
prepDerivatives -M ImagingData/Subjects -MO ImagingData/SubjectsDerived/ -inc anatomy/mprage_noFace.nii TestSubject  
despikeAFNI -M ImagingData/SubjectsDerived -f func/Rest -on ds_ -v dc_run TestSubject  
sliceTimeMB -M ImagingData/SubjectsDerived -f func/Rest -on aMB_ -v ds_dc_run TestSubject  
realignfMRI12 -M ImagingData/SubjectsDerived -f func/Rest -on r12_ -v aMB_ds_dc_run TestSubject  
coregOverlay -M ImagingData/SubjectsDerived -f func/Rest -o mprage_noFace -v r12_aMB_ds_dc_run TestSubject  
newSeg -M ImagingData/SubjectsDerived -a func/Rest/coReg -h mprage_noFace -w func/Rest/coReg/newSeg TestSubject  
warpSeg -M ImagingData/SubjectsDerived -f func/Rest -h mprage_noFace -on ns_ -v r12_aMB_ds_dc_run -w coReg/newSeg TestSubject  
smoothfMRI -M ImagingData/SubjectsDerived -f func/Rest -v ns_r12_aMB testSubject
```

In the **spm12Batch** distribution you will see the folder **BatchExamples/Examples\_Numbered**, look for the file **daisyChange\_example\_01.sh** to see how you can run them all sequentially in a single job by using the “**-B**” flag.

## Example 1

# spm12Batch System

## Details of processing, with flag explanations

```
distortionCorrect -M ImagingData/Subjects -MO ImagingData/SubjectsDerived -bi FM_AP.nii -fi FM_PA.nii -fm fieldMap -f func/Rest -on dc_ --v run TestSubject
```

-M ImagingData/Subjects	input folder specification
-MO ImagingData/SubjectsDerived	output folder specification
-bi FM_AP.nii	backward field map
-fi FM_PA.nii	forward field map
-fm fieldMap	field map directory
-f func/Rest	task folder name
-on dc_	output name prepend to file
-v run	which generic volume name to look for
TestSubject	list of sessions

```
prepDerivatives -M ImagingData/Subjects -MO ImagingData/SubjectsDerived/ -inc anatomy/mprage_noFace.nii TestSubject
```

-M ImagingData/Subjects	input folder specification
-MO ImagingData/SubjectsDerived	output folder specification
-inc anatomy/mprage_noFace.nii	which things to copy to output
TestSubject	list of sessions

## Example 1

```
despikeAFNI -M ImagingData/SubjectsDerived -f func/Rest -on ds_ -v dc_run TestSubject
```

-M ImagingData/SubjectsDerived	input folder specification
-f func/Rest	task folder name
-on ds_	output name prepend to file
-v run	which generic volume name to look for
TestSubject	list of sessions

```
sliceTimeMB -M ImagingData/SubjectsDerived -f func/Rest -on aMB_ -v ds_dc_run TestSubject
```

-M ImagingData/SubjectsDerived	input folder specification
-f func/Rest	task folder name
-on ds_	output name prepend to file
-v ds_dc_run	which generic volume name to look for
TestSubject	list of sessions

## Example 1

```
realignfMRI12 -M ImagingData/SubjectsDerived -f func/Rest -on r12_ -v aMB_ds_dc_run TestSubject
```

-M ImagingData/SubjectsDerived	input folder specification
-f func/Rest	task folder name
-on r12_	output name prepend to file
-v aMB_ds_dc_run	which generic volume name to look for
TestSubject	list of sessions

```
coregOverlay -M ImagingData/SubjectsDerived -f func/Rest -o mprage_noFace -v r12_aMB_ds_dc_run TestSubject
```

-M ImagingData/SubjectsDerived	input folder specification
-f func/Rest	task folder name
-o mprage_noFace	name of high-resolution file to get from anatomy/
-v r12_aMB_ds_dc_run	which generic volume name to look for to co-register to
TestSubject	list of sessions

## Example 1

```
newSeg -M ImagingData/SubjectsDerived -a func/Rest/coReg -h mprage_noFace -w func/Rest/coReg/newSeg TestSubject
```

-M ImagingData/SubjectsDerived	input folder specification
-a func/Rest/coReg	where to find the co-registered anatomy
-h mprage_noFace	name of high-resolution file to get
-w func/Rest/coReg/newSeg	where to put the results of the segmentation and warp calculation
TestSubject	list of sessions

```
warpSeg -M ImagingData/SubjectsDerived -f func/Rest -h mprage_noFace -on w_ -v r12_aMB.ds_dc_run -w coReg/newSeg TestSubject
```

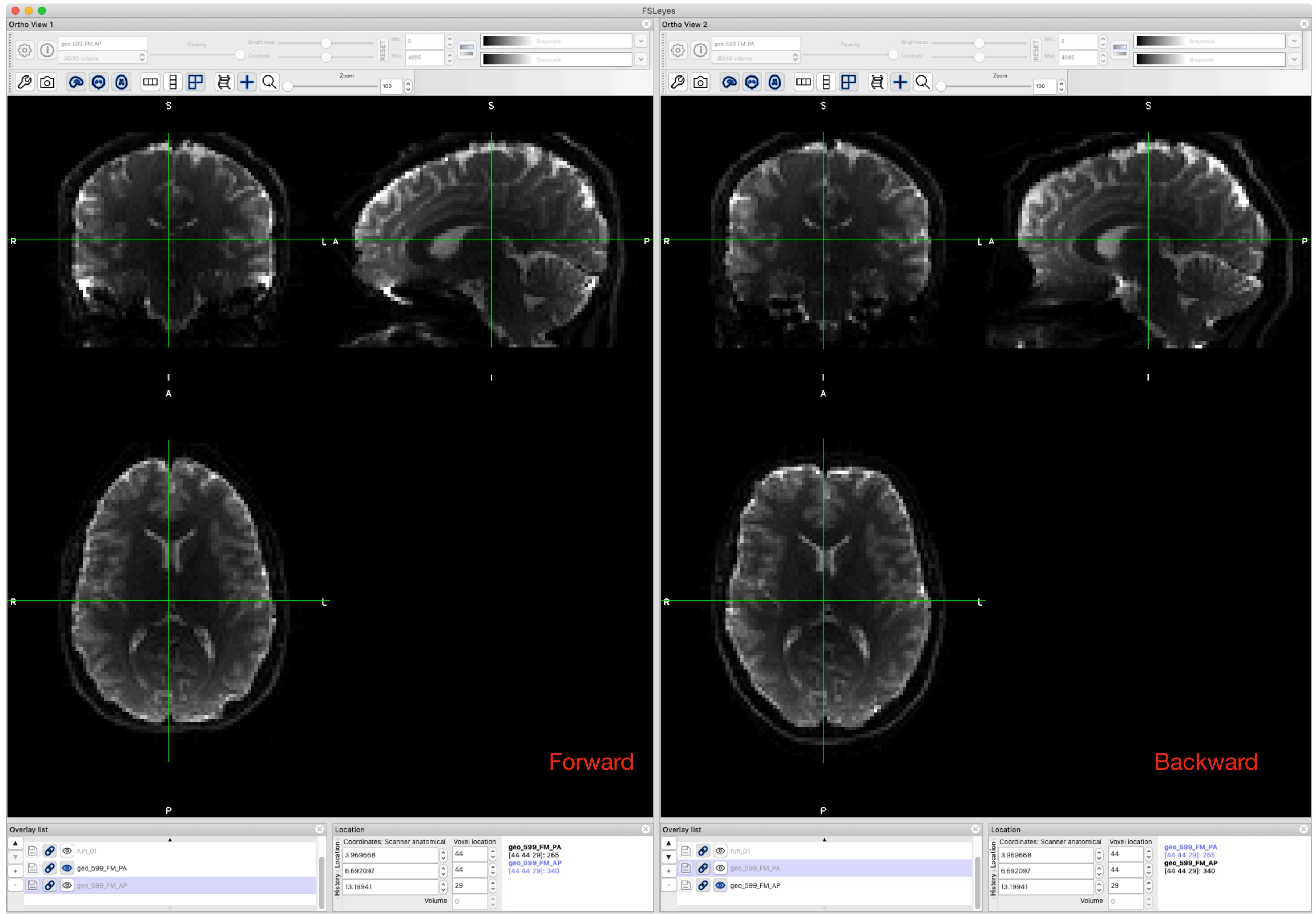
-M ImagingData/SubjectsDerived	input folder specification
-f func/Rest	task folder name
-h mprage_noFace.nii	name of high-resolution file to get from the newSeg folder
-on w_	name to prepend to the output
-v r12_aMB.ds_dc_run	which generic volume name to look for to warp to MNI
-w coReg/newSeg	where to find the warping instructions under the task specified
TestSubject	list of sessions

## Example 1

```
smoothfMRI -M ImagingData/SubjectsDerived -f func/Rest -v w_r12_aMB testSubject  
  
-M ImagingData/SubjectsDerived      input folder specification  
-a func/Rest/coReg                 where to find the co-registered anatomy  
-v r12_aMB_ds_dc_run               which generic volume name to look for smoothing  
  
TestSubject                         list of sessions
```

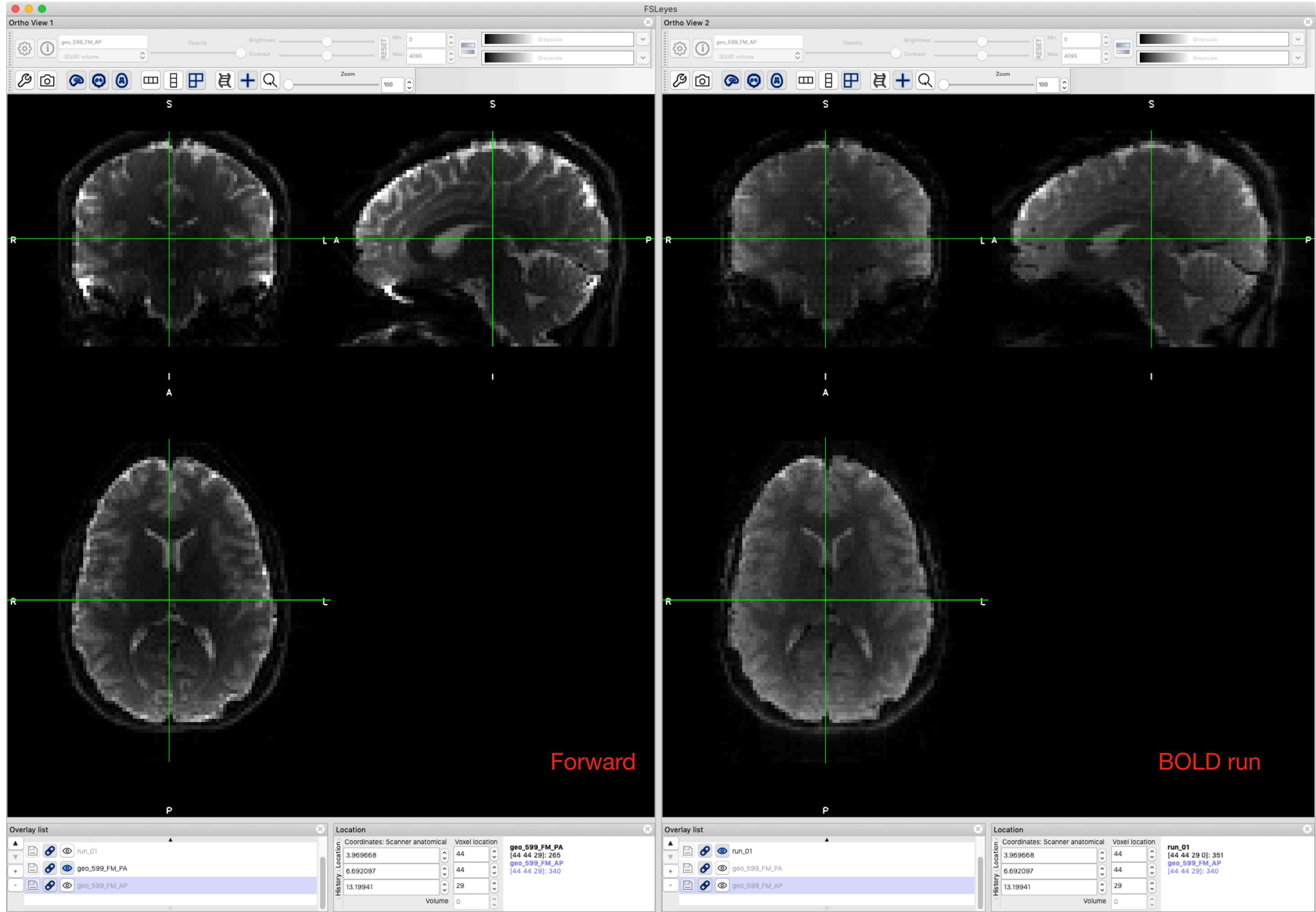
## Example 1

### Field Map Images



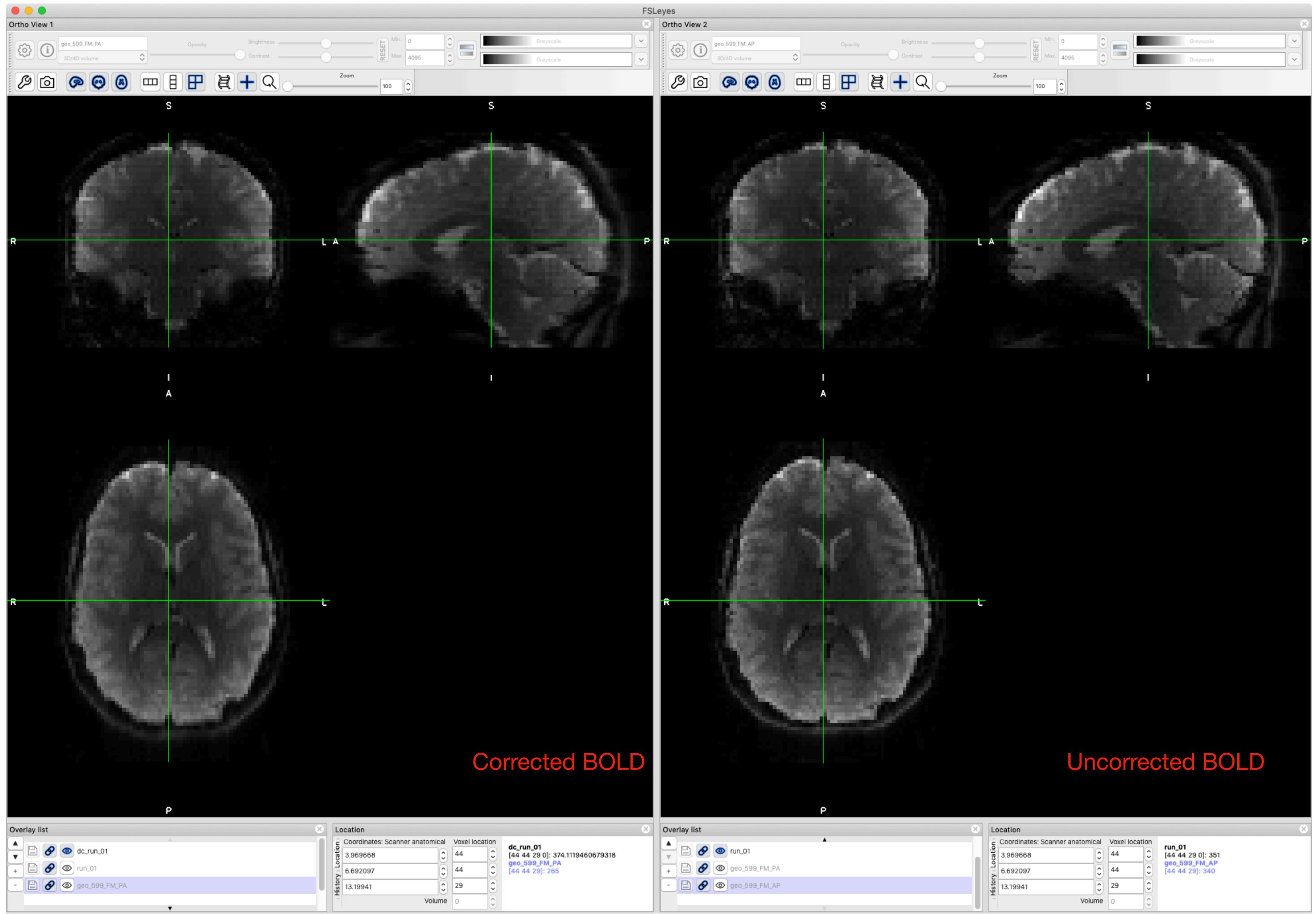
## Example 1

### Forward Field Map Image and Uncorrected BOLD run



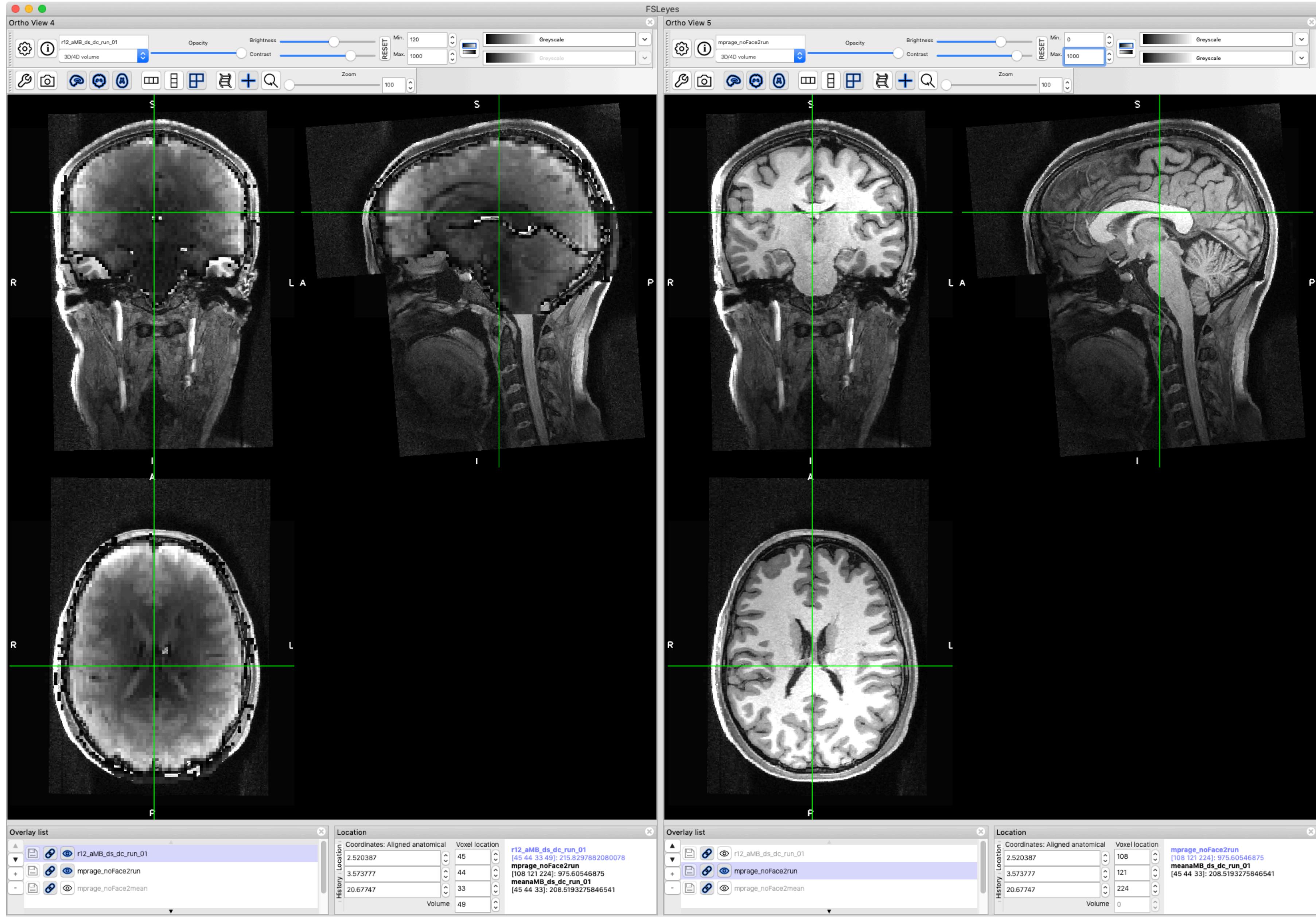
## Example 1

### Corrected BOLD run and Uncorrected BOLD run



## Example 1

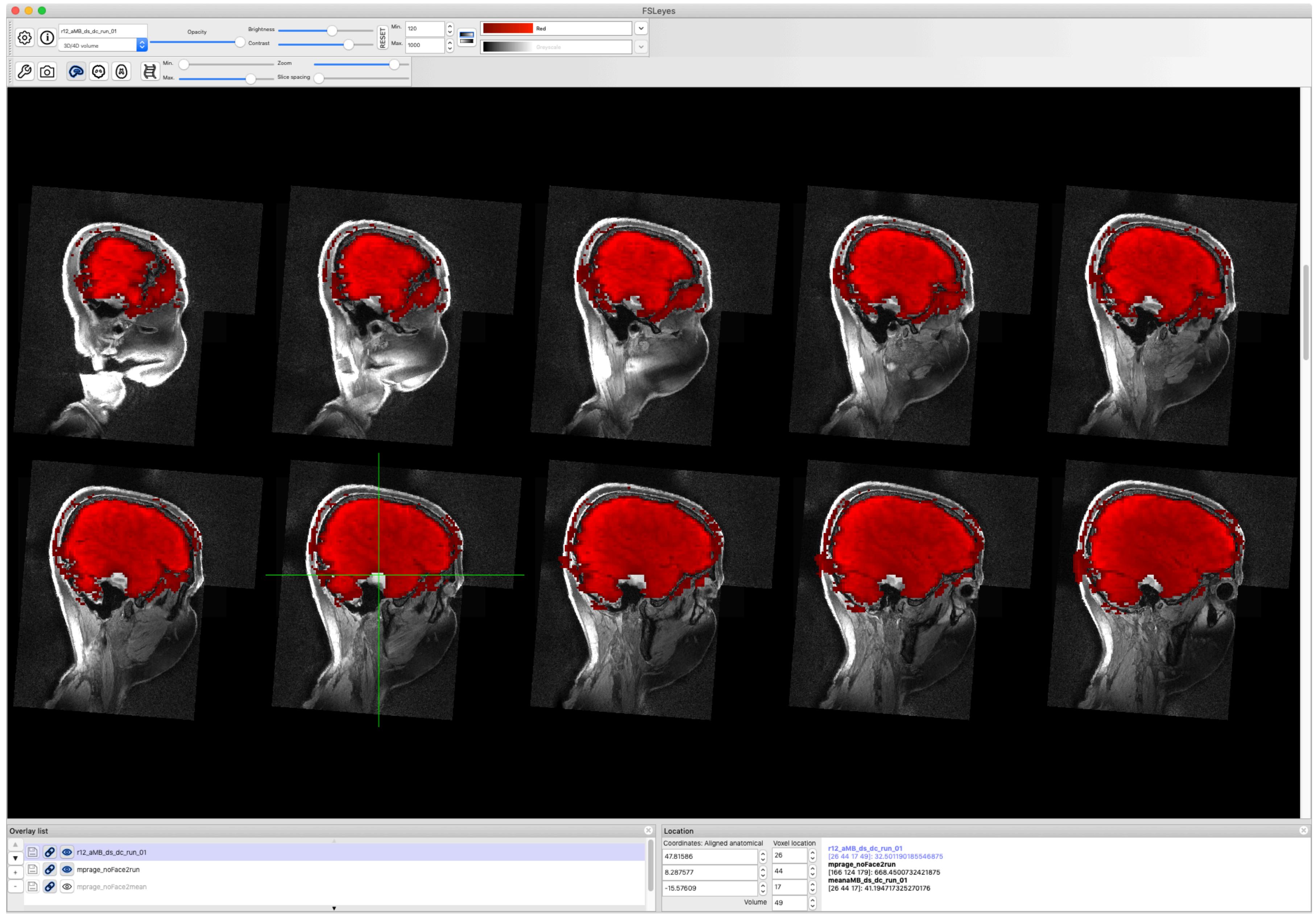
### Checking co-registration of high resolution image



Results of co-registration of high-resolution image (mprage) to the realigned BOLD data.

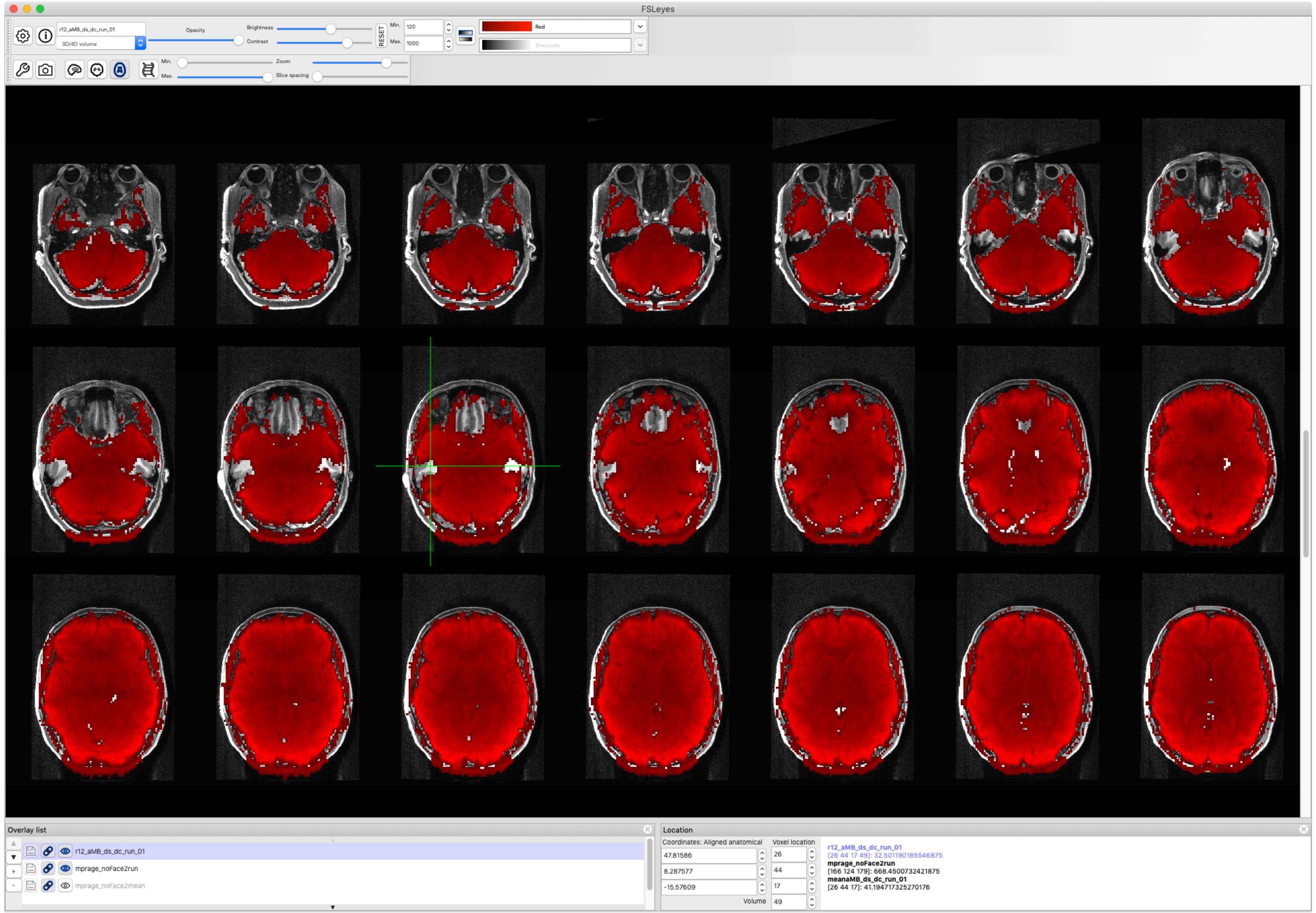
## Example 1

### Checking signal dropout



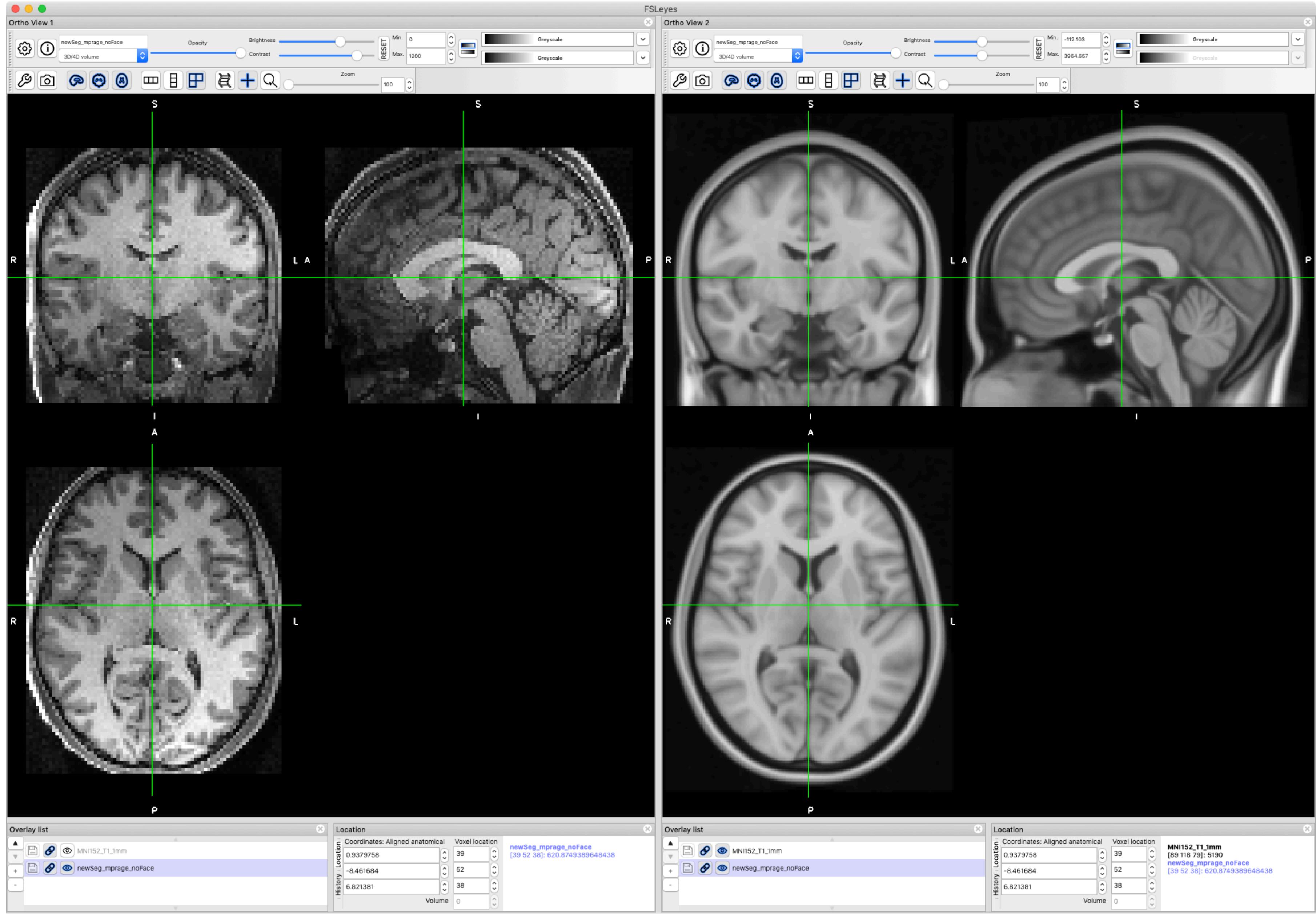
## Example 1

### Checking signal dropout



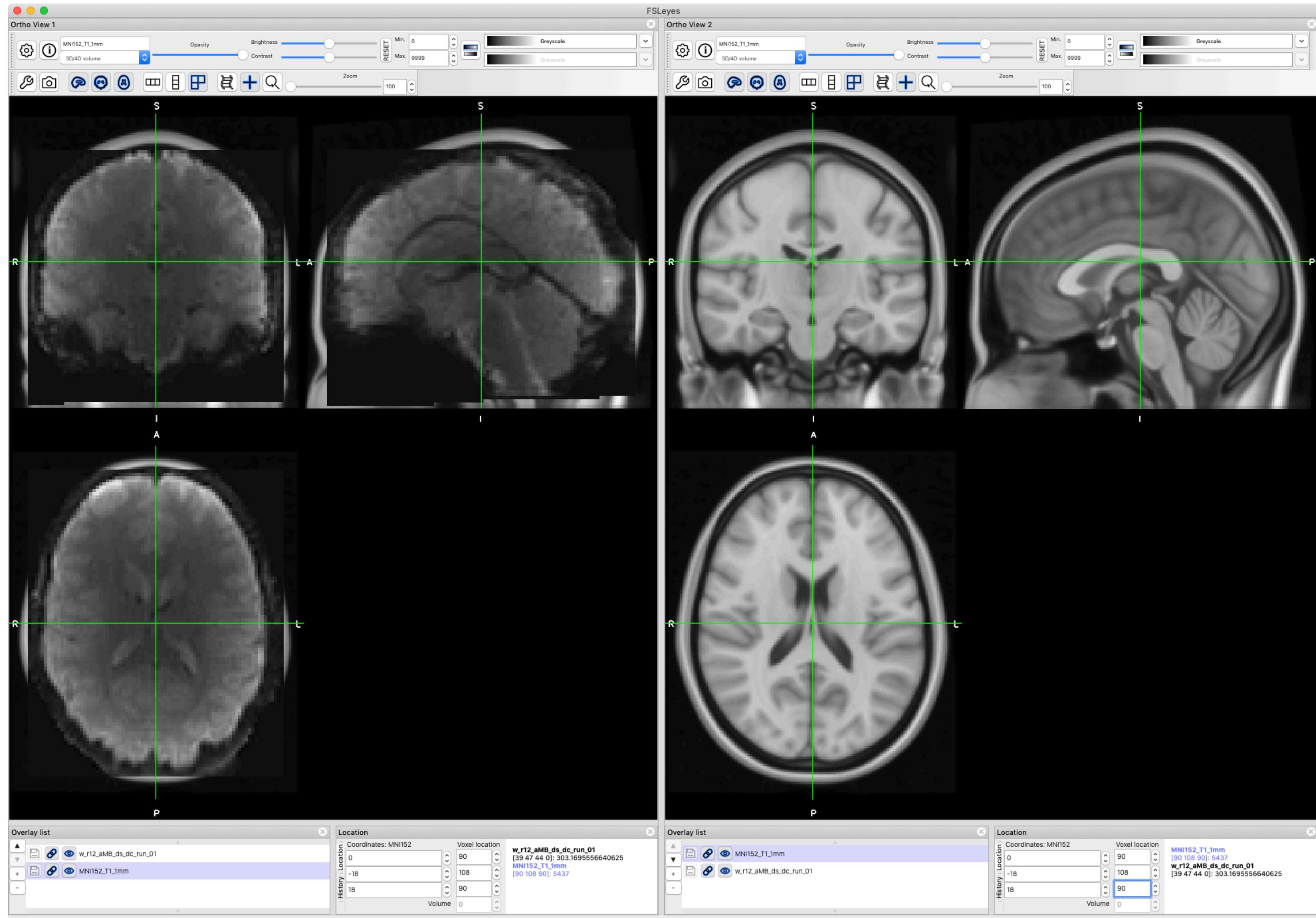
## Example 1

### Checking warping to MNI based on SPM



## Example 1

### Checking warping to MNI based on SPM



## Example 1

# spm12Batch System spm12Batch processing pipeline without overlay image using SPM normalization

Input data in the **Subjects/** folder

```
[session]/  
    anatomy/  
        hiRes.nii  
    func/  
        MyTask/  
            fieldMap/  
                forward.nii  
                backward.nii  
            run_01/  
                run_01.nii  
            run_02/  
                . . .
```

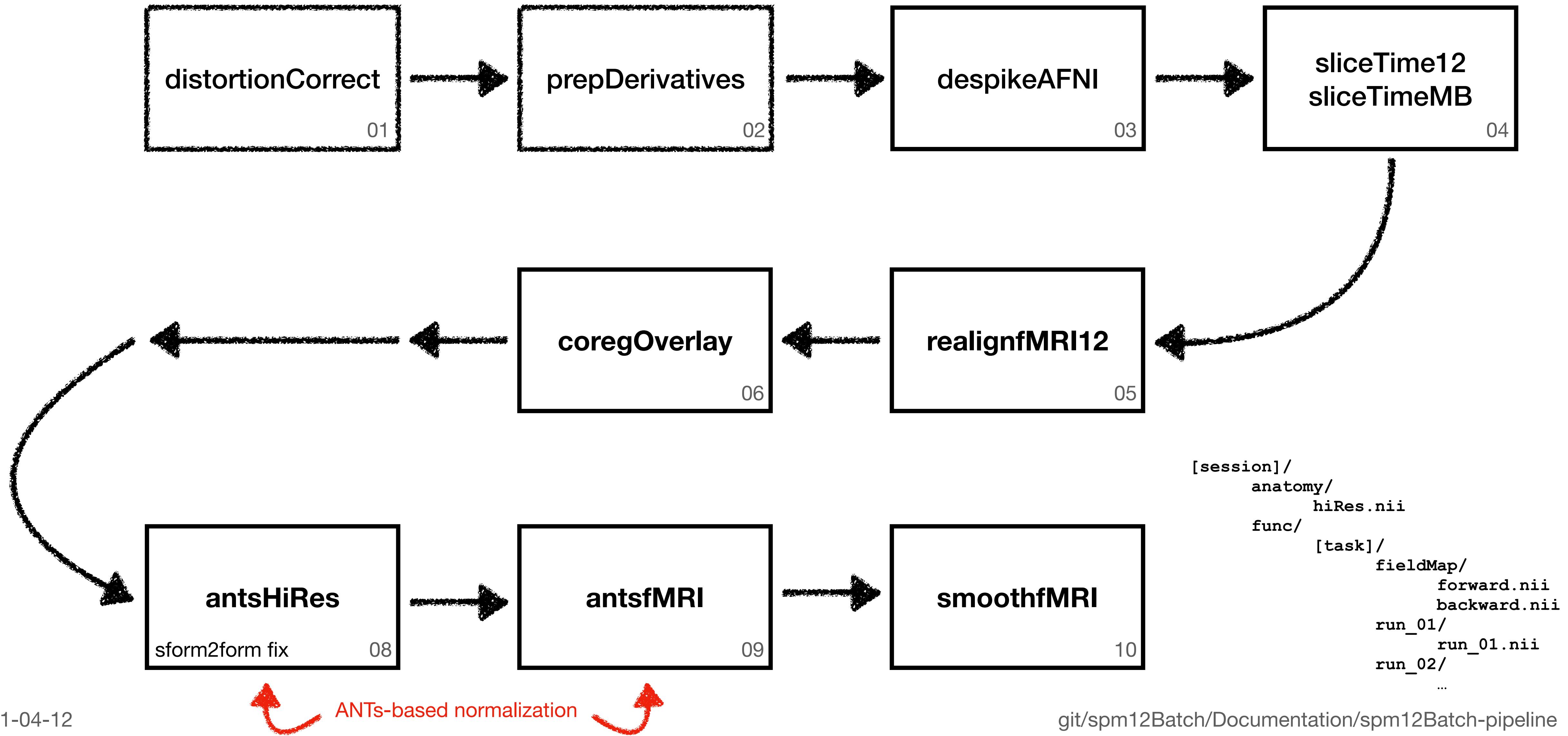
intermediate distortion correction files to ensure  
geometry truly matches without rounding error  
  
output of distortion correction  
output of despiking  
output of slice time correction (non multi-band)  
output of motion correction  
output of warp to MNI  
output of smoothing

Output data in the **SubjectsDerived/** folder

```
[session]/  
    anatomy/  
        hiRes.nii  
    func/  
        MyTask/  
            coReg/  
                mprage.nii  
                newSeg/  
                (. . . lots of output . . )  
            fieldMap/  
                geo_forward.nii  
                geo_backward.nii  
            run_01/  
                dc_run_01.nii  
                ds_dc_run_01.nii  
                a12_ds_dc_run_01.nii  
                r12_a12_ds_dc_run_01.nii  
                ns_r12_a12_ds_dc_run_01.nii  
                sns_r12_a12_ds_dc_run_01.nii  
            run_02/  
                . . .
```

## Example 2

# spm12Batch System spm12Batch processing pipeline without overlay image using ANTs normalization



## Example 2

# spm12Batch System

## spm12Batch processing pipeline without overlay image using ANTs normalization

In this example, we start with a set of data that has a high resolution image called **mprage\_noFace.nii** that resides in the **anatomy**/ folder. For the task of interest (**Rest/**), which resides under the **func/** folder, we have two runs, each in their own folder: **run\_01/run\_01.nii** and **run\_02/run\_02.nii**. We also collected a field map, with the phase encode polarity in the **FM\_PA.nii** image matching the phase encode polarity in BOLD data, and the other polarity (backward image) as **FM\_AP.nii**. The TestSubject can be downloaded from:

The processing steps we will do are (everything up to and including **coregOverlay** is the same as before) the following:

```
distortionCorrect -M ImagingData/Subjects -MO ImagingData/SubjectsDerived -bi FM_AP.nii -fi FM_PA.nii -fm fieldMap -f func/Rest -on dc_ -v run TestSubject  
prepDerivatives -M ImagingData/Subjects -MO ImagingData/SubjectsDerived/ -inc anatomy/mprage_noFace.nii TestSubject  
despikeAFNI -M ImagingData/SubjectsDerived -f func/Rest -on ds_ -v dc_run TestSubject  
sliceTimeMB -M ImagingData/SubjectsDerived -f func/Rest -on aMB_ -v ds_dc_run TestSubject  
realignfMRI12 -M ImagingData/SubjectsDerived -f func/Rest -on r12_ -v aMB_ds_dc_run TestSubject  
coregOverlay -M ImagingData/SubjectsDerived -f func/Rest -o mprage_noFace -v r12_aMB_ds_dc_run TestSubject  
antsHiRes -M ImagingData/SubjectsDerived -a func/Rest/coReg -h mprage_noFace -w func/Rest/coReg/ANTs TestSubject  
antsfMRI -M ImagingData/SubjectsDerived -f func/Rest -h mprage_noFace.nii -on ants_ -v r12_aMB_ds_dc_run -w coReg/ANTs TestSubject  
smoothfMRI -M ImagingData/SubjectsDerived -f func/Rest -v ants_r12_aMB testSubject
```

In the **spm12Batch** distribution you will see the folder **BatchExamples/Examples\_Numbered**, look for the file **daisyChange\_example\_02.sh** to see how you can run them all sequentially in a single job by using the “**-B**” flag.

## Example 2

# spm12Batch System Details of ANTs processing, with flag explanations

```
antsHiRes -M ImagingData/SubjectsDerived -a func/Rest/coReg -h mprage_noFace -w func/Rest/coReg/ANTs TestSubject
```

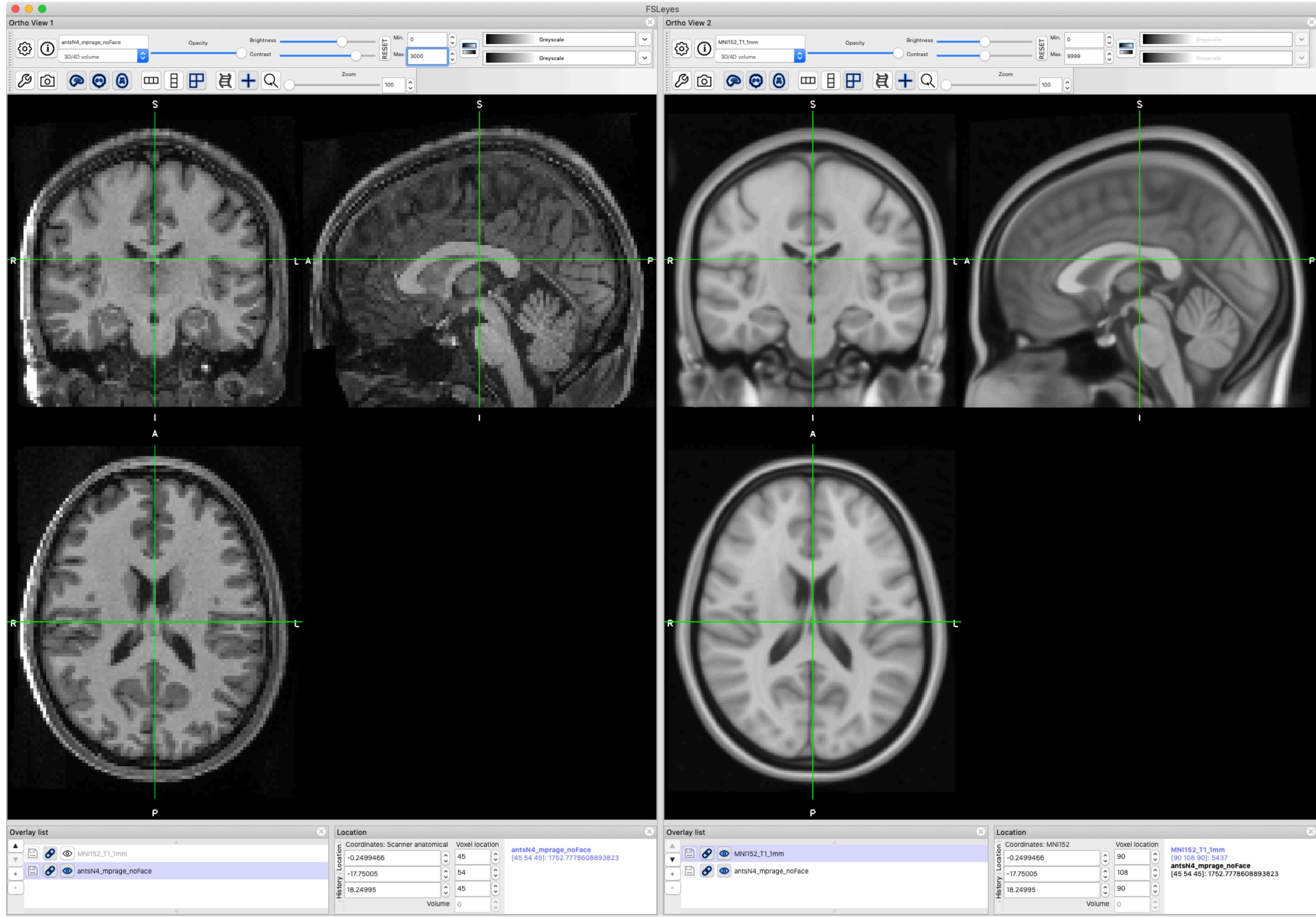
-M ImagingData/SubjectsDerived	input folder specification
-a func/Rest/coReg	where to find the co-registered anatomy
-h mprage_noFace	name of high-resolution file to get
-w func/Rest/coReg/ANTs	where to put the results of the segmentation and warp calculation
TestSubject	list of sessions

```
antsfMRI -M ImagingData/SubjectsDerived -f func/Rest -h mprage_noFace.nii -on ants_ -v r12_aMB_ds_dc_run -w coReg/ANTs TestSubject
```

-M ImagingData/SubjectsDerived	input folder specification
-f func/Rest	task folder name
-h mprage_noFace.nii	name of high-resolution file to get from the newSeg folder
-on ants_	name to prepend to the output
-v r12_aMB_ds_dc_run	which generic volume name to look to warp to MNI
-w coReg/ANTs	where to find the warping instructions under the task specified
TestSubject	list of sessions

## Example 2

### Checking warping to MNI based on ANTs



## Example 2

# spm12Batch System spm12Batch processing pipeline without overlay image using ANTs normalization

Input data in the **Subjects/** folder

```
[session]/  
    anatomy/  
        hiRes.nii  
    func/  
        MyTask/  
            fieldMap/  
                forward.nii  
                backward.nii  
        run_01/  
            run_01.nii  
        run_02/  
            . . .
```

intermediate distortion correction files to ensure  
geometry truly matches without rounding error  
  
output of distortion correction  
output of despiking  
output of slice time correction (non multi-band)  
output of motion correction  
output of warp to MNI  
output of smoothing

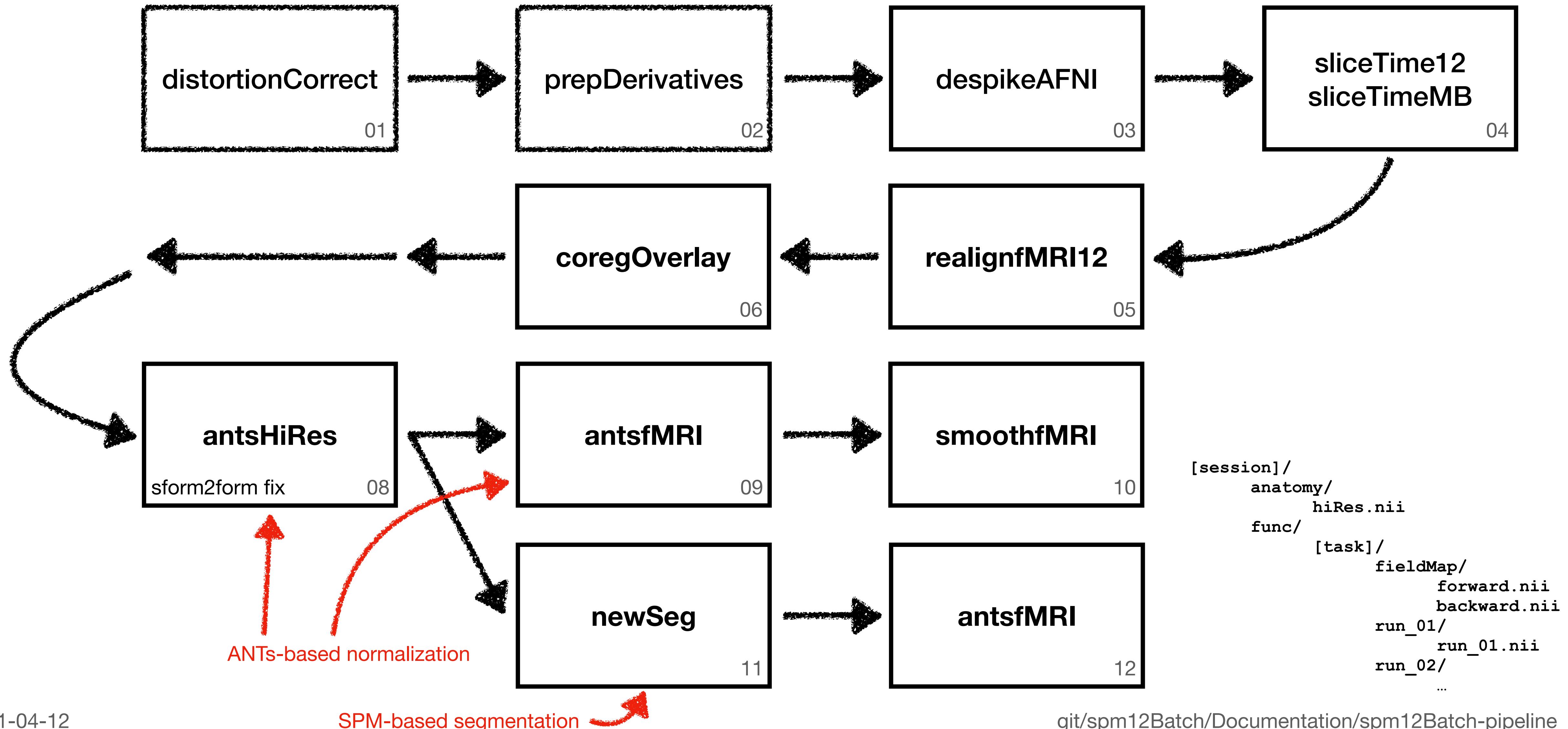
Output data in the **SubjectsDerived/** folder

```
[session]/  
    anatomy/  
        hiRes.nii  
    func/  
        MyTask/  
            coReg/  
                mprage.nii  
                ANTs/  
                    (. . . lots of output . . )  
            fieldMap/  
                geo_forward.nii  
                geo_backward.nii  
        run_01/  
            dc_run_01.nii  
            ds_dc_run_01.nii  
            a12_ds_dc_run_01.nii  
            r12_a12_ds_dc_run_01.nii  
            ants_r12_a12_ds_dc_run_01.nii  
            sants_r12_a12_ds_dc_run_01.nii  
        run_02/  
            . . .
```

### Example 3

## spm12Batch System

### spm12Batch processing pipeline without overlay image using ANTs normalization and SPM segmentation for CSF/WM



## Example 3

# spm12Batch System

## spm12Batch processing pipeline without overlay image using ANTs normalization and SPM segmentation for CSF/WM

In this example, we start with a set of data that has a high resolution image called **mprage\_noFace.nii** that resides in the **anatomy/** folder. For the task of interest (**Rest/**), which resides under the **func/** folder, we have two runs, each in their own folder: **run\_01/run\_01.nii** and **run\_02/run\_02.nii**. We also collected a field map, with the phase encode polarity in the **FM\_PA.nii** image matching the phase encode polarity in BOLD data, and the other polarity (backward image) as **FM\_AP.nii**. This test subject can be copied from **spm12Batch/BatchExamples/TestSubject**

The processing steps we will do are (everything up to and including **smoothfMRI** is the same as before):

```
distortionCorrect -M ImagingData/Subjects -MO ImagingData/SubjectsDerived -bi FM_AP.nii -fi FM_PA.nii -fm fieldMap -f func/Rest -on dc_ -v run TestSubject  
prepDerivatives -M ImagingData/Subjects -MO ImagingData/SubjectsDerived/ -inc anatomy/mprage_noFace.nii TestSubject  
despikeAFNI -M ImagingData/SubjectsDerived -f func/Rest -on ds_ -v dc_run TestSubject  
sliceTimeMB -M ImagingData/SubjectsDerived -f func/Rest -on aMB_ -v ds_dc_run TestSubject  
realignfMRI12 -M ImagingData/SubjectsDerived -f func/Rest -on r12_ -v aMB_ds_dc_run TestSubject  
coregOverlay -M ImagingData/SubjectsDerived -f func/Rest -o mprage_noFace -v r12_aMB_ds_dc_run TestSubject  
antsHiRes -M ImagingData/SubjectsDerived -a func/Rest/coReg -h mprage_noFace -w func/Rest/coReg/ANTs TestSubject  
antsfMRI -M ImagingData/SubjectsDerived -f func/Rest -h mprage_noFace.nii -on ants_ -v r12_aMB_ds_dc_run -w coReg/ANTs TestSubject  
smoothfMRI -M ImagingData/SubjectsDerived -f func/Rest -v ants_r12_aMB testSubject  
newSeg -M ImagingData/SubjectsDerived -a func/Rest/coReg/ANTs -h N4_mprage_noFace -w func/Rest/coReg/ANTs/newSeg TestSubject  
antsfMRI -M ImagingData/SubjectsDerived -f func/Rest -h N4_mprage_noFace.nii -on WM_ -v c2N4_mprage_noFace -w coReg/ANTs TestSubject  
antsfMRI -M ImagingData/SubjectsDerived -f func/Rest -h N4_mprage_noFace.nii -on CSF_ -v c3N4_mprage_noFace -w coReg/ANTs TestSubject
```

In the **spm12Batch** distribution you will see the folder **BatchExamples/Examples\_Numbered**, look for the file **daisyChange\_example\_04.sh** to see how you can run them all sequentially in a single job by using the “**-B**” flag.

## Example 3

# spm12Batch System Details processing

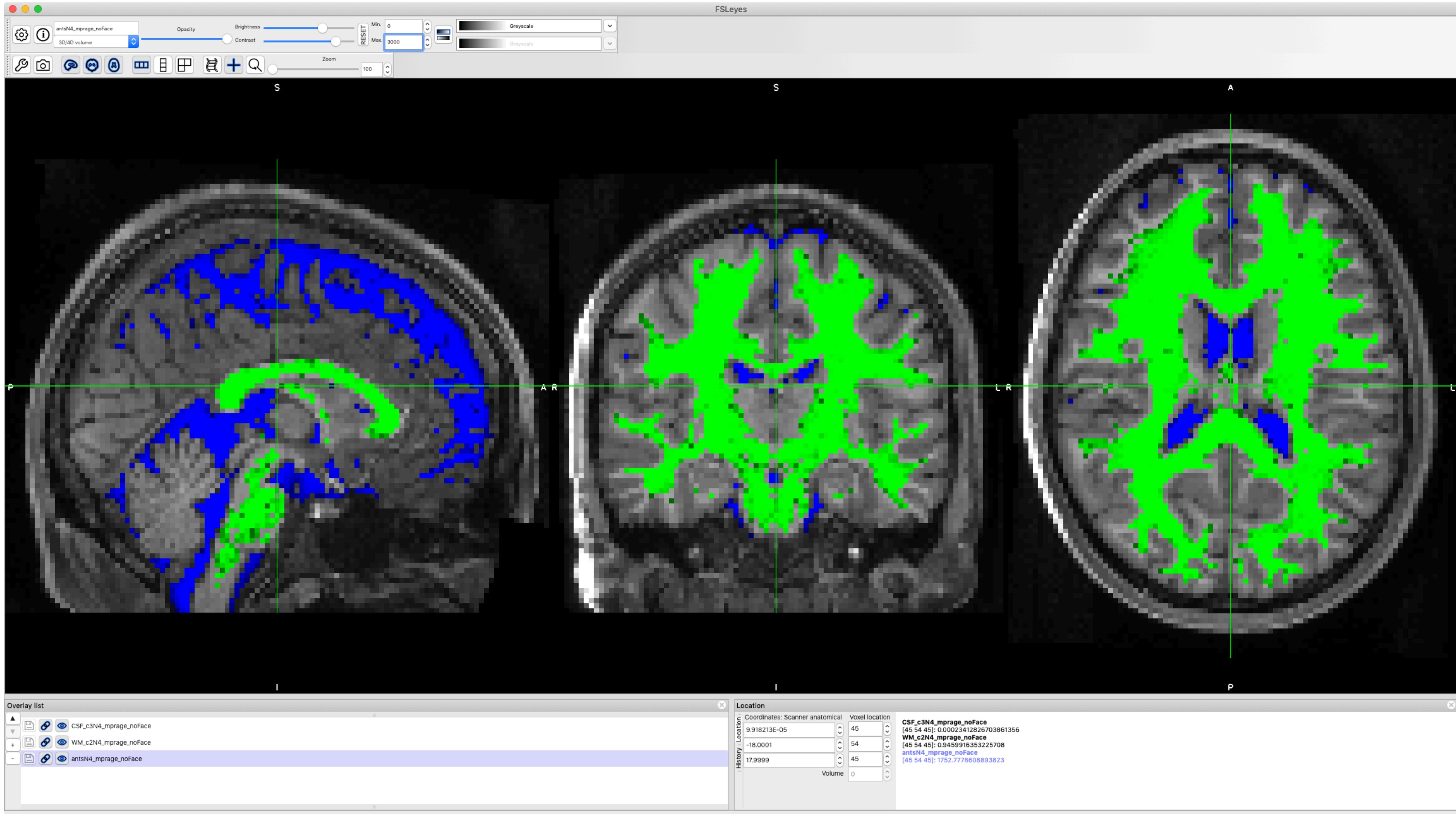
```
newSeg -M ImagingData/SubjectsDerived -a func/Rest/coReg/ANTs -h N4_mprage_noFace -w func/Rest/coReg/ANTs/newSeg TestSubject
```

-M ImagingData/SubjectsDerived	input folder specification
-a func/Rest/coReg/ANTs	where to find the co-registered anatomy
-h N4_mprage_noFace	name of high-resolution file to get
-w func/Rest/coReg/ANTs/newSeg	where to put the results of the segmentation and warp calculation
TestSubject	list of sessions

```
antsfMRI -M ImagingData/SubjectsDerived -f func/Rest -h N4_mprage_noFace.nii -on WM_ -v c2N4_mprage_noFace -w coReg/ANTs TestSubject
```

-M ImagingData/SubjectsDerived	input folder specification
-f func/Rest	task folder name
-h N4_mprage_noFace.nii	name of high-resolution file to get from the ANTs folder
-on WM_	name to prepend to the output
-v c2N4_mprage_noFace	which generic volume name to warp (the WM segment here)
-w coReg/ANTs	where to find the warping instructions under the task specified
TestSubject	list of sessions

# SPM based segmentation with ANTs normalization to MNI space



## Example 2

# spm12Batch System spm12Batch processing pipeline without overlay image using ANTs normalization

Input data in the **Subjects/** folder

```
[session]/  
    anatomy/  
        hiRes.nii  
    func/  
        MyTask/  
            fieldMap/  
                forward.nii  
                backward.nii  
            run_01/  
                run_01.nii  
            run_02/  
                . . .
```

intermediate distortion correction files to ensure  
geometry truly matches without rounding error  
  
output of distortion correction  
output of despiking  
output of slice time correction (non multi-band)  
output of motion correction  
output of warp to MNI  
output of smoothing

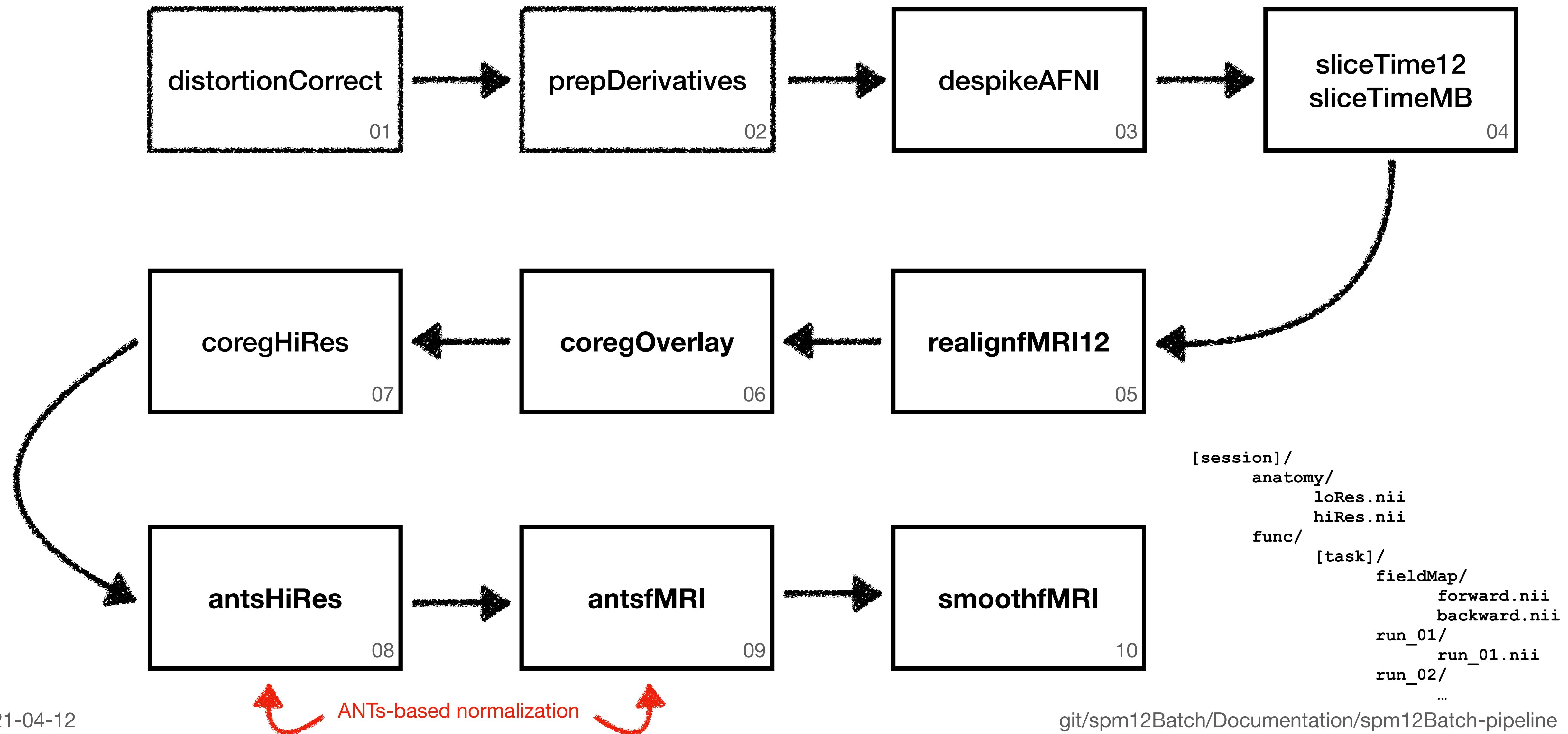
Output data in the **SubjectsDerived/** folder

```
[session]/  
    anatomy/  
        hiRes.nii  
    func/  
        MyTask/  
            coReg/  
                mprage.nii  
                ANTs/  
                    newSeg/  
            fieldMap/  
                geo_forward.nii  
                geo_backward.nii  
        run_01/  
            dc_run_01.nii  
            ds_dc_run_01.nii  
            a12_ds_dc_run_01.nii  
            r12_a12_ds_dc_run_01.nii  
            ants_r12_a12_ds_dc_run_01.nii  
            s_ants_r12_a12_ds_dc_run_01.nii  
        run_02/  
            . . .
```

## Example 4

# spm12Batch System

## spm12Batch processing pipeline with overlay image using ANTs normalization



## Example 4

# spm12Batch System

## spm12Batch processing pipeline with overlay image using ANTs normalization

In this example, we start with a set of data that has a high resolution image called **mprage\_noFace.nii** that resides in the **anatomy/** folder. For the task of interest (**Rest/**), which resides under the **func/** folder, we have two runs, each in their own folder: **run\_01/run\_01.nii** and **run\_02/run\_02.nii**. We also collected a field map, with the phase encode polarity in the **FM\_PA.nii** image matching the phase encode polarity in BOLD data, and the other polarity (backward image) as **FM\_AP.nii**. This test subject can be copied from **spm12Batch/BatchExamples/TestSubject**

The processing steps we will do are (everything up to and including **coregOverlay** is the same as before):

```
distortionCorrect -M ImagingData/Subjects -MO ImagingData/SubjectsDerived -bi FM_AP.nii -fi FM_PA.nii -fm fieldMap -f func/Rest -on dc_ --v run TestSubject  
prepDerivatives -M ImagingData/Subjects -MO ImagingData/SubjectsDerived/ -inc anatomy/mprage_noFace.nii TestSubject  
despikeAFNI -M ImagingData/SubjectsDerived -f func/Rest -on ds_ -v dc_run TestSubject  
sliceTimeMB -M ImagingData/SubjectsDerived -f func/Rest -on aMB_ -v ds_dc_run TestSubject  
realignfMRI12 -M ImagingData/SubjectsDerived -f func/Rest -on r12_ -v aMB_ds_dc_run TestSubject  
coregOverlay -M ImagingData/SubjectsDerived -f func/Rest -o loRes -v r12_aMB_ds_dc_run TestSubject  
coregHiRes -M ImagingData/SubjectsDerived -f func/Rest h mprage_noFace -o loRes TestSubject  
antsHiRes -M ImagingData/SubjectsDerived -a func/Rest/coReg -h mprage_noFace -w func/Rest/coReg/ANTs TestSubject  
antsfMRI -M ImagingData/SubjectsDerived -f func/Rest -h mprage_noFace.nii -on ants_ -v r12_aMB_ds_dc_run -w coReg/ANTs TestSubject  
smoothfMRI -M ImagingData/SubjectsDerived -f func/Rest -v ants_r12_aMB testSubject
```

# spm12Batch System

## Daisy chained example

```
#!/bin/bash

DATEStart=`date`
DATE=date
echo ${DATE} Step 01
distortionCorrect -B -MO ImagingData/SubjectsDerived -bi FM_AP -fi FM_PA -fm fieldMap12 -f func/Rest -v run_01 5502_02
DATE=date
echo ${DATE} Step 01
distortionCorrect -B -MO ImagingData/SubjectsDerived -bi FM_AP -fi FM_PA -fm fieldMap12 -f func/Rest -v run_02 5502_02
DATE=date
echo ${DATE} Step 02
prepDerivatives -B -MO ImagingData/SubjectsDerived -inc anatomy 5502_02
DATE=date
echo ${DATE} Step 03
despikeAFNI -B -M ImagingData/SubjectsDerived -MO ImagingData/SubjectsDerived -f func/Rest -on ds_ -v dc_run 5502_02
DATE=date
echo ${DATE} Step 04
sliceTimeMB -B -M ImagingData/SubjectsDerived -v ds_dc_run -f func/Rest 5502_02
DATE=date
echo ${DATE} Step 05
realignfMRI12 -B -M ImagingData/SubjectsDerived -v aMBds_dc_run -f func/Rest 5502_02
DATE=date
echo ${DATE} Step 06
coregOverlay -B -M ImagingData/SubjectsDerived/ -o mpimage -f func/rest -v r12aMBds_dc_run 5502_02
DATE=date
echo ${DATE} Step 07
antsHiRes -a func/Rest/coReg -B -h mpimage -w func/Rest/coReg/ANTs_New -M ImagingData/SubjectsDerived/ 5502_02
DATE=date
echo ${DATE} Step 08
antsfMRI -B -f func/Rest -h mpimage -M ImagingData/SubjectsDerived -on ants -v r12aMBds_dc_ -w coReg/ANTs_New 5502_02
DATE=date
echo ${DATE} Step 09
smoothfMRI -B -f func/Rest -M ImagingData/SubjectsDerived -v ants12aMBds_dc_ 5502_02
DATE=date
echo ${DATE} Step 10
newSeg -B -a func/Rest/coReg/ANTs_New -h N4_mpimage -w func/Rest/coReg/ANTs_New/newSeg -M ImagingData/SubjectsDerived/ 5502_02
DATE=date
echo ${DATE} Step 11
antsfMRI -B -h mpimage -M ImagingData/SubjectsDerived -f func/Rest -w coReg/ANTs_New -v c2N4_mpimage -in ants -on WM_ants_ 5502_02
DATE=date
echo ${DATE} Step 12
antsfMRI -B -h mpimage -M ImagingData/SubjectsDerived -f func/Rest -w coReg/ANTs_New -v c3N4_mpimage -in ants -on CSF_ants_ 5502_02
DATEStop=date

echo
echo Process is all completed and ran from

echo ${DATEStart}
echo ${DATEStop}
```

Tells spm12Batch to run the command to negate running in the background and to run in the foreground instead. The job is still built the same, but stays attached to your terminal. You might not see any output since that has all be directed to a log file. When you get the command prompt back is when know the job has finished.

because the 4 runs of resting state are under “Rest/”, but have different field maps, then the runs my be explicitly corrected one at a time.

copy the anatomy over to the SubjectsDerived/ tree

despike the data

slice time correct the data

motion correct the data

coregister the mpimage to the motion corrected data.

using ANTs to calculate the warp to normalized space

using ANTs to take the BOLD data to normal space

smooth the data

use SPM to do a segmentation, but in the ANTs tree

use ANTs to normalize the WM segment from SPM

use ANTs to normalize the CSF segment from SPM