

# LLN fMRI Workshop Tutorial

November 2019

## Contributors:

- Mohamed Rezk
- Ane Gurtubay
- Rémi Gau
- Jyothirmayi Vadlamudi
- Stefania Mattioni
- Ceren Battal
- Marco Barilari
- Robeta Pia Calce



# Table of contents

Contributors:	1
Needed for this tutorial	4
Glossary	4
Getting and browsing the data	5
Opening an anatomical image	5
Opening a functional image	6
What is in this data set?	9
How to read JSON files	9
How to read TSV files	9
Preprocessing	10
Slice timing	11
ADVANCED TIP	16
Realign (Estimate and Reslice)	18
ADVANCED TIP	20
Coregister (Estimate)	22
QUALITY CONTROL TIP	24
Segment	27
Normalize (Write)	31
Anatomical image	31
Functional, mean functional and tissue probability maps	33
NOTE	35
Smoothing	36
Statistical analysis - Subject level (First-level)	39
Model specification	40
Model estimation	46
Review your model	47
QUALITY CONTROL TIP	49
QUESTION	49
NOTE	49

Contrast manager	50
Another way to compute the contrasts:	52
NOTE	53
QUESTION	53
Statistical analysis - Group level (Second-level)	54
Getting and browsing the group data	55
Smooth con images	57
Image calculator	61
Creating a mean anatomical image	61
Creating a mean mask image	62
Factorial design	64
Model estimation	69
Contrast manager	71
Explore the results	75
Display statistical results	75
Display results on the average brain	77
Understanding the statistical results	78
Render results on a surface	79
NOTE	80
Use batch to output results	80
NOTE	81
How to script	82
Creating your first script	82
Using the CPP pipeline	83
Preprocessing and subject level analysis	85
Group level analysis and exporting results	87
Where to find help	89
Books	89
List of resources	89
On the web	89
For SPM	90



## Needed for this tutorial

- Matlab
- [SPM12](#) (see [here](#) for more details for setup)
- Install the [atom text editor](#)
- Get data from [zenodo](#)
- Get the [analysis pipeline code](#)
- Install [MRIcron](#) and [MRIcroGL](#)
- Make sure you have at least 5 GB of free space on your computer
- Use this [invitation](#) to join the slack workspace of the workshop

## Glossary

BIDS	<a href="#">Brain Imaging Data Structure</a> . A standardized way to organize your imaging and other metadata (non-imaging data like behavioral or physiological parameters recorded during the experiment).
FFX:	fixed effect analysis
First level analysis :	in SPM this usually refers to an analysis at the subject level, but for other software (e.g FSL) this could mean an analysis at the run level.
Functional MRI localizer:	fMRI experiment designed to localize specific spatial networks related to functional tasks
GLM :	general linear model
Image	Typically refers to an MRI slice
MRI Slice	2D matrix that represents one “cut” from the MRI volume, in any arbitrary direction (axial, coronal, sagittal, or oblique)
MRI Volume	3D matrix that represents an image, in our case a brain or a part of the brain

Regressors	Independent variable that is introduced in a statistical model to help explain signal variance.
RFX :	random effect analysis
Run:	in a BIDS data set this refers to an uninterrupted repetition of data acquisition that has the same acquisition parameters and task
Second level analysis :	in SPM this usually refers to an analysis at the group level, but for other software (e.g FSL) this could mean an analysis at the subject level.
Session:	in a BIDS data set this more or less refers to all the data that was acquired on one day (see <a href="#">here</a> for more) but for SPM this refers to the data acquired on one run
SPM:	<a href="#">Statistical Parametric Mapping</a> , the matlab-based software tool used in this workshop for functional MRI analysis
TR:	Repetition time. For functional MRI it typically means the time it takes to acquire a full image volume

## Getting and browsing the data

For this tutorial we will be using MRI data from a functional localizer for visual motion acquired at the [CPP lab](#).

This data is a [Brain imaging data structure](#) (BIDS) data set, a standardized way to organize and name your data and the metadata that relates to it: in case you want to know more, the [BIDS starter kit](#) is a good place.

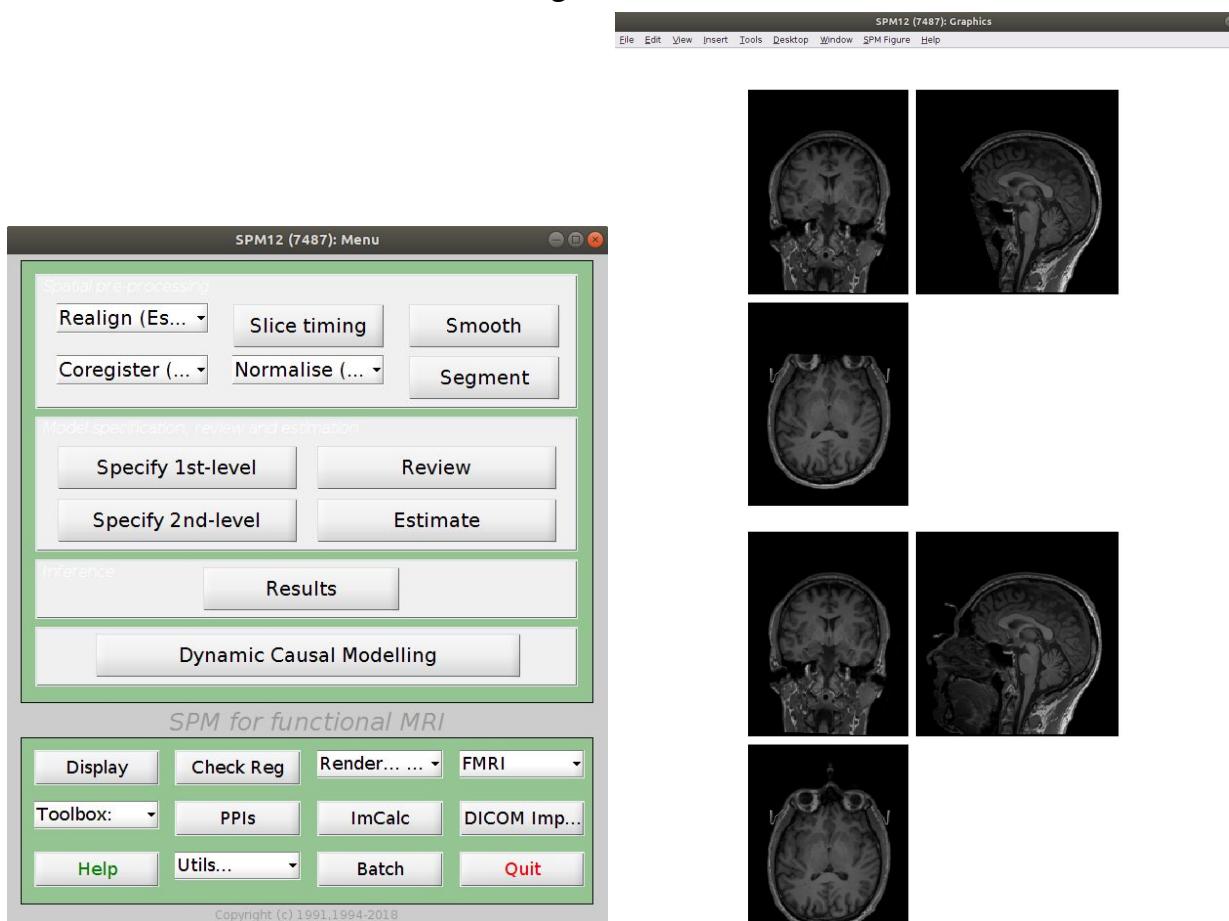
There are other BIDS data set out there (on [openneuro.org](#) for example) that you can adapt this tutorial to.

1. If you have not already done so, download the data from [zenodo](#).
  - a. The *raw\_additional.zip* is for the first part of the tutorial.
  - b. The other one is for the group level analysis of this tutorial
2. Unzip these files.
3. Check that the content of the *raw* folder is a valid BIDS data set by using the [BIDS validator](#).
4. It is good practice to leave the raw data untouched so copy the content of the *raw* folder into the *derivatives* folder where you will be working.
5. Meanwhile you can explore the content of the unzipped folder. It should match the one shown on the next page. A description of the content and where each information is located can be found in the section [What is in this data set?](#)

## Opening an anatomical image

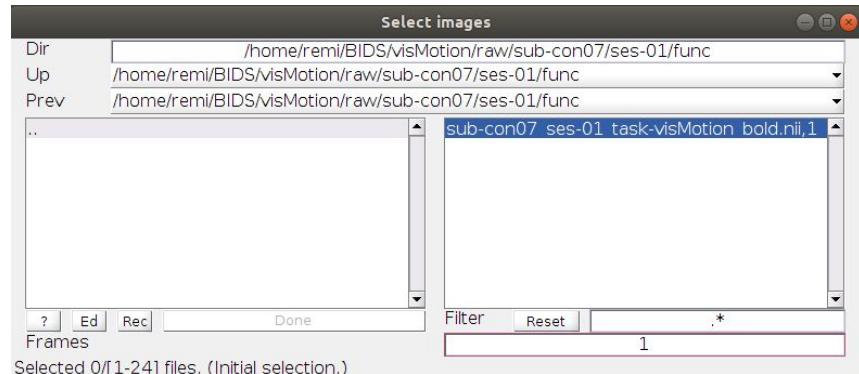
6. You can open an anatomical T1w image with [MRIcron](#) (for example *raw/sub-con07/ses-01/anat/sub-con07\_ses-01\_T1w.nii*). Opening it with [MRIcroGL](#) also allows you to render the surface of the MRI image (*Display → Render*)
7. Non defaced: you can also compare this image with the non-defaced version using SPM check-registration.

- a. Start spm by typing “*spm fmri*” in the command line
- b. Click on *Check Reg*
- c. Select
  - i. *raw/sub-con07/ses-01/anat/sub-con07\_ses-01\_T1w.nii*
  - ii. *additional/defacing/sub-con07\_ses-01\_T1w.nii*



## Opening a functional image

1. You can open a given functional volume from the 4D nifti with MRIcron. If you use SPM *Check Reg* it displays by default the first volume of any image. You can "filter"
  - a. the number of the volume you want to open in the box below the *Filter* options.
  - b. a range of volumes (e.g *1:10* for the first 10 volumes) to show several volumes and decide which ones to display (NB: using *Inf* will display all the volumes).
  - c. the name of the file that you want to see appearing by changing the *.\** by *^prefix\*file\_name\*.nii*. This is a useful trick when you have many files in one folder. For example if you want to only select the normalised, realigned images you can use *^wr\*.nii* as *w* and *r* are the SPM prefix for normalised and realigned images.



2. You can open all the images of the 4D nifti as a "movie" by right-clicking on the open image and selecting *browse...* and then selecting all the volumes of the image you want to display.<sup>1</sup>

---

<sup>1</sup> Another option is to type the following code in the command line (in this case when you are in the *func* folder for the subject 07): *spm\_check\_registration('sub-con07\_ses-01\_task-visMotion\_bold.nii')*



```
└── additional
    └── defacing
        ├── sub-con07_ses-01_T1w.nii
        ├── sub-con08_ses-01_T1w.nii
        └── sub-con15_ses-01_T1w.nii
    └── derivatives
    └── raw
        ├── CHANGES
        ├── dataset_description.json
        ├── participants.json
        ├── participants.tsv
        ├── README
        ├── sub-con07
            └── ses-01
                ├── anat
                │   ├── sub-con07_ses-01_T1w.json
                │   └── sub-con07_ses-01_T1w.nii
                └── func
                    ├── sub-con07_ses-01_task-visMotion_bold.nii
                    └── sub-con07_ses-01_task-visMotion_events.tsv
        ├── sub-con08
            └── ses-01
                ├── anat
                │   ├── sub-con08_ses-01_T1w.json
                │   └── sub-con08_ses-01_T1w.nii
                └── func
                    ├── sub-con08_ses-01_task-visMotion_bold.nii
                    └── sub-con08_ses-01_task-visMotion_events.tsv
        ├── sub-con15
            └── ses-01
                ├── anat
                │   ├── sub-con15_ses-01_T1w.json
                │   └── sub-con15_ses-01_T1w.nii
                └── func
                    ├── sub-con15_ses-01_task-visMotion_bold.nii
                    └── sub-con15_ses-01_task-visMotion_events.tsv
        └── task-visMotion_bold.json
```

Content of the file *raw\_additional.zip*

## What is in this data set?

This raw BIDS dataset is in the raw folder and contains 3 subjects:

- *sub-con07*
- *sub-con08*
- *sub-con15*

Most of the examples here are shown with the subject 07 but feel free to use any of those 3.

Each subject had one session *ses-01* with:

- an *anat* folder for the anatomical data
- a *func* folder for the functional data.

This data set is one used for a “visual motion localizer” called *visMotion*.

### How to read JSON files

All the information related to the BOLD images for this task (e.g repetition time, slice timing information, ... ) is in the file *raw/task-visMotion\_bold.json* that you can open using a text editor like atom. You can also load this information in matlab by using the *spm\_jsonread* function for example by typing this in the matlab command line:

```
bold_info = spm_jsonread('raw/task-visMotion_bold.json')
```

### How to read TSV files

The information regarding when each stimulus was presented can be found in the *\*\_events.tsv* files. Those can be opened in text editor or spreadsheet software like

excel. SPM can also load those for you by typing this in the command line for a given event file (in this case when you are in the *func* folder for the subject 07):

```
events = spm_load('sub-con07_ses-01_task-visMotion_events.tsv')
```

## Preprocessing

The raw folder should not be edited or changed. This is our raw data. Copy the raw folder into a new folder called derivatives. We will do the analysis in the derivative folder.

If you have not already done so open matlab, use the matlab file browser to go the derivative folder.

Then type *spm fmri* in the command line.

## Slice timing

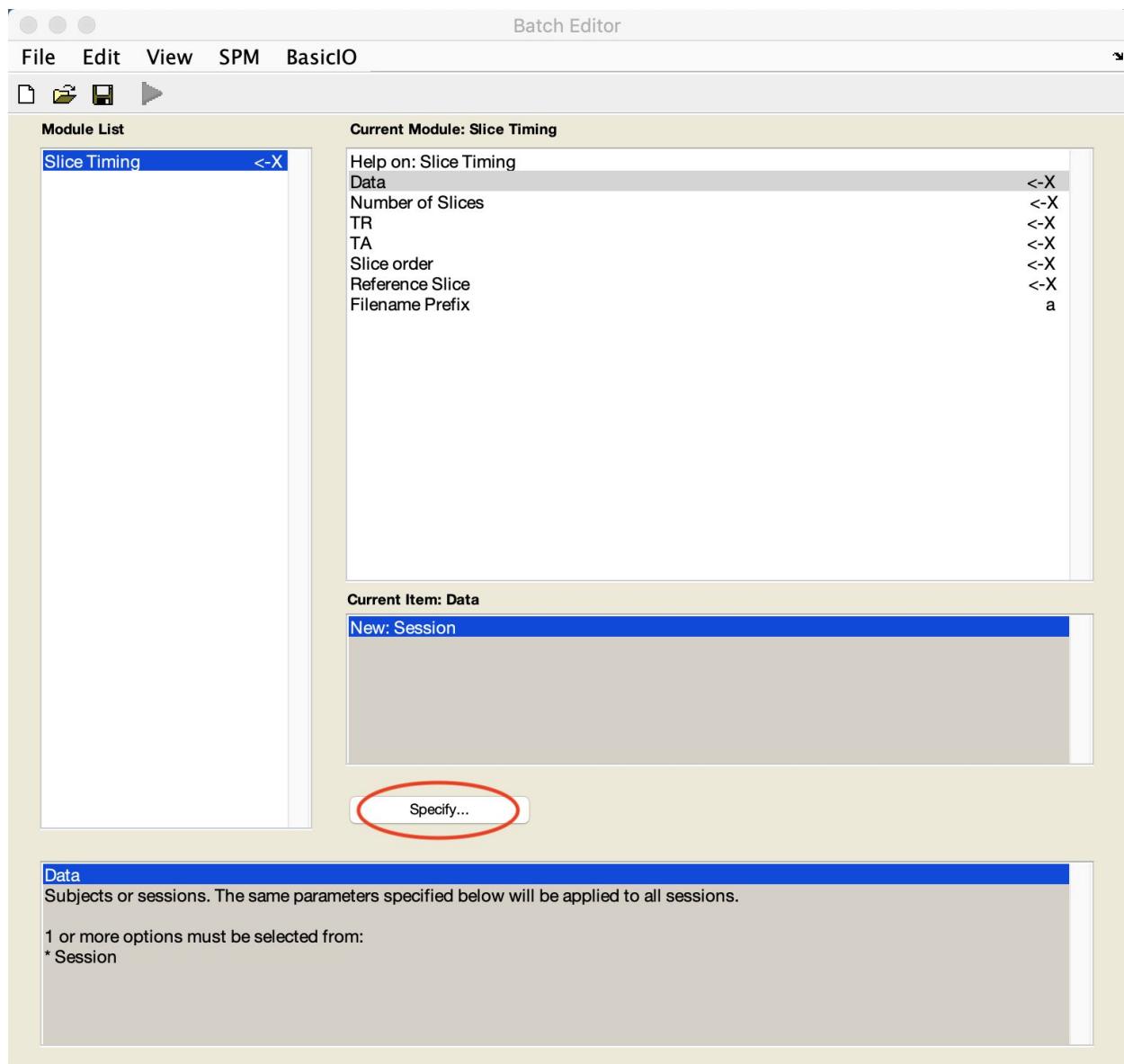
In this step we will make all the slices in a volume appear as if they were acquired at the same moment (this allows for application of single statistical estimate for the whole volume).

- 
- Input
    - 4D functional image
      - *sub-con07\_ses-01\_task-visMotion\_bold.nii*
  - Output
    - slice time corrected 4D functional image
      - *asub-con07\_ses-01\_task-visMotion\_bold.nii*
- 

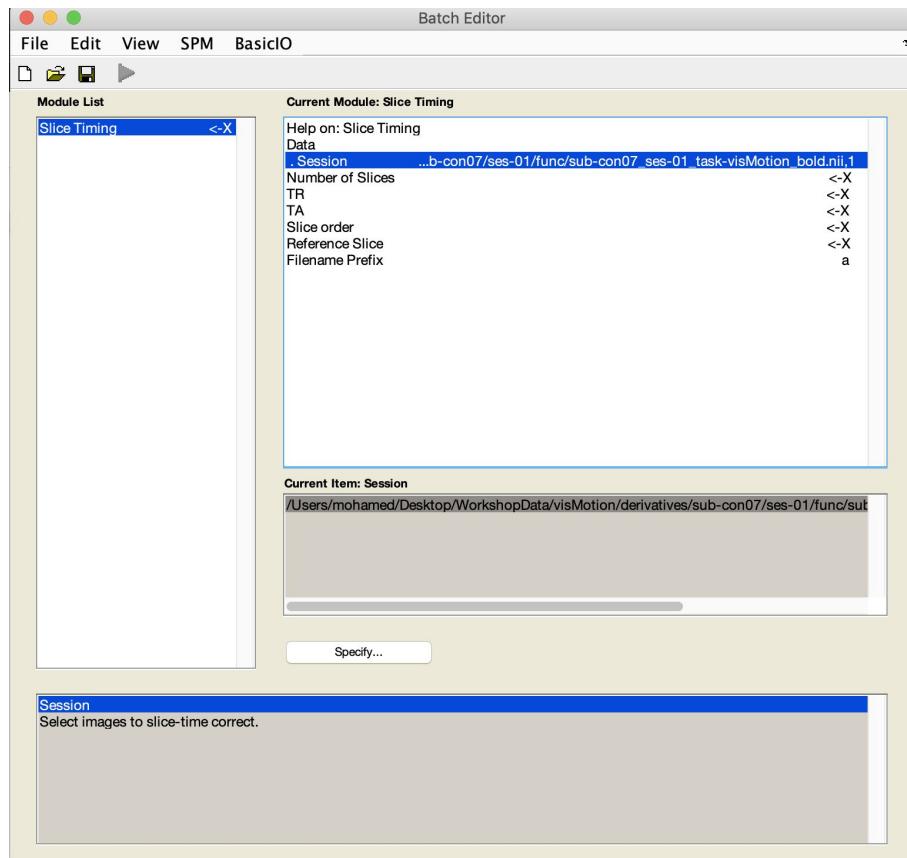
1. To start with the first step of preprocessing, in SPM GUI click on the *Slice Timing* button (see below)



2. After clicking on slice timing this window pops-up (see below). The first missing value is: *Data*.



3. In the above window, first click on *Data*, then click on *Specify* and the following window pops-up.
4. In the above window, you will notice the missing value: *Sessions*, appear below: *Data*. Click on *Sessions* and then on *Specify* at the bottom. The next window comes up.
5. Go to the directory where you have the files of the subject you have the functional data of the subject you want to start pre-processing (for example *derivatives/sub-con07/ses-01/func*) and click on 'done'
6. Select all the 252 volumes of the image *sub-con07\_ses-01\_task-visMotion\_bold.nii*. To do this filter the displayed images by replacing *1* by *Inf*(show all the volumes and not just number 1) and *.\** by *^sub.\** (shows all the image that start with *sub*)



7. The extra information you need to run this step are in the json file corresponding to this file '*task-visMotion\_bold.json*'. While SPM Slice-Timing window is open, you can open this file in a text editor and copy-paste the relevant information but it is easier to load the content of this file in matlab by typing:

```
bold_info = spm_jsonread('task-visMotion_bold.json')
```

8. And then get the relevant information by typing the following commands:

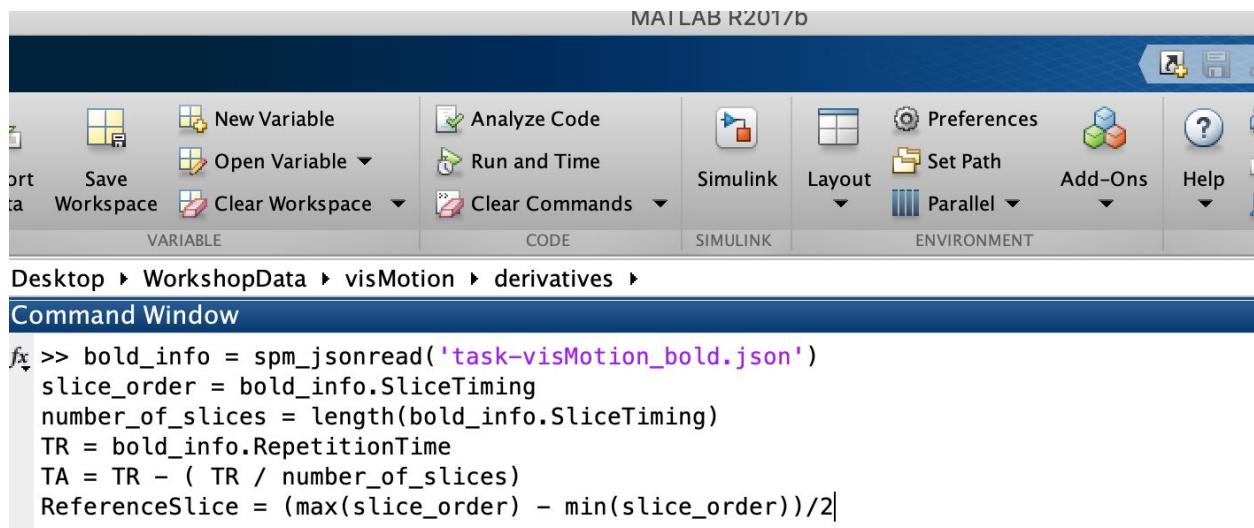
```
number_of_slices = length(bold_info.SliceTiming) # length counts how many numbers there are in a given vector
```

```
TR = bold_info.RepetitionTime
```

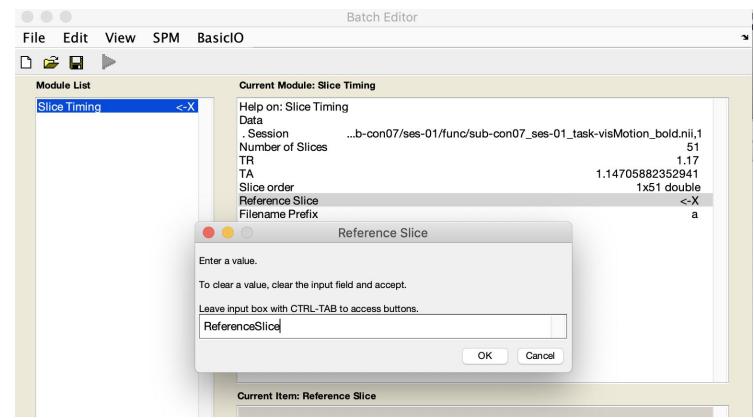
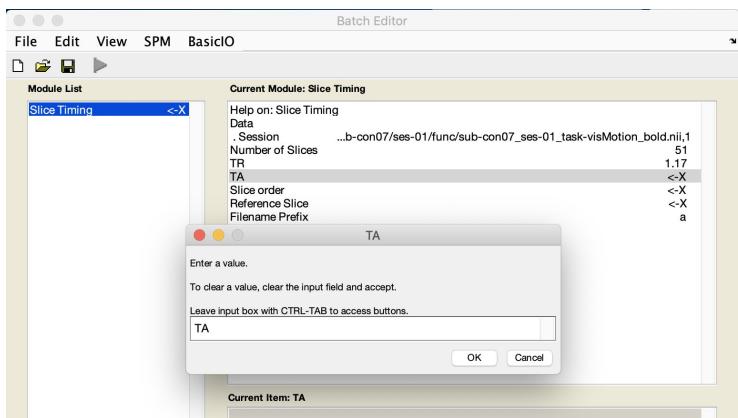
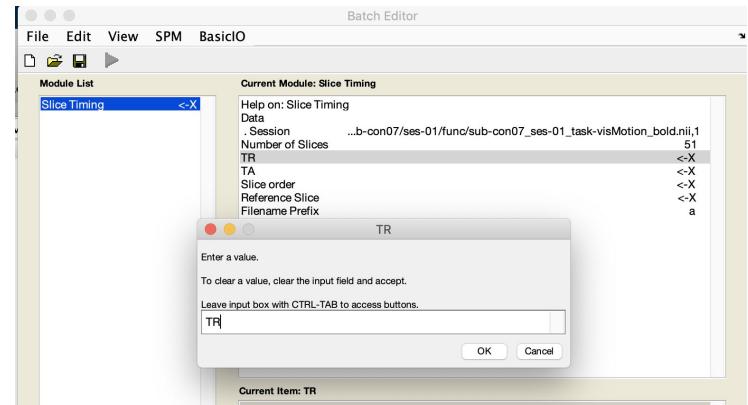
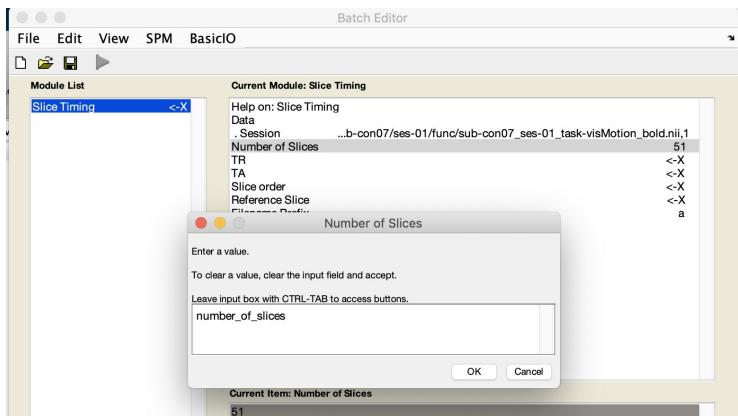
```
TA = TR - ( TR / number_of_slices) # this is acquisition time
```

```
slice_order = bold_info.SliceTiming # this is a vector of values that correspond to the time at which each slice was acquired
```

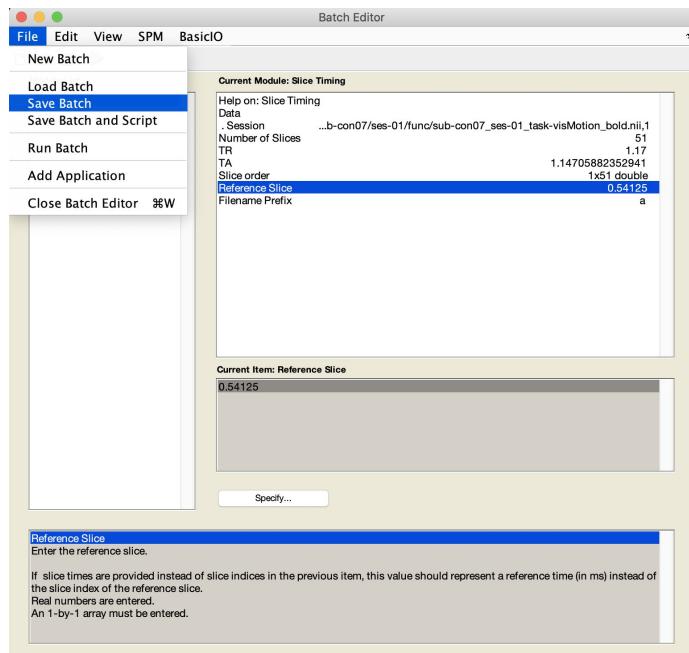
```
reference_slice = (max(slice_order) - min(slice_order))/2 # we want to use the middle point of the volume as reference
```



9. Then go back to SPM Slice-timing batch window and call these parameters.



10. Save a copy the batch by clicking on *File* → *Save Batch* and save it as *batch\_STC.mat*.



11. Run the batch by clicking the green run button



### ADVANCED TIP

The following text should appear in the matlab command line when you are doing the slice timing. One useful piece of information in this is that SPM tells you which matlab function is being used to run this module. Here it is the function: *spm\_slice\_timing*.

---

28-Nov-2019 20:19:31 - Running job #1

---

28-Nov-2019 20:19:31 - Running 'Slice Timing'

SPM12: spm\_slice\_timing (v6130) 20:19:31 - 28/11/2019

---

---

Number of slices is... : 51  
Time to Repeat (TR) is... : 1.17  
Parameters are specified as... : slice times (ms)

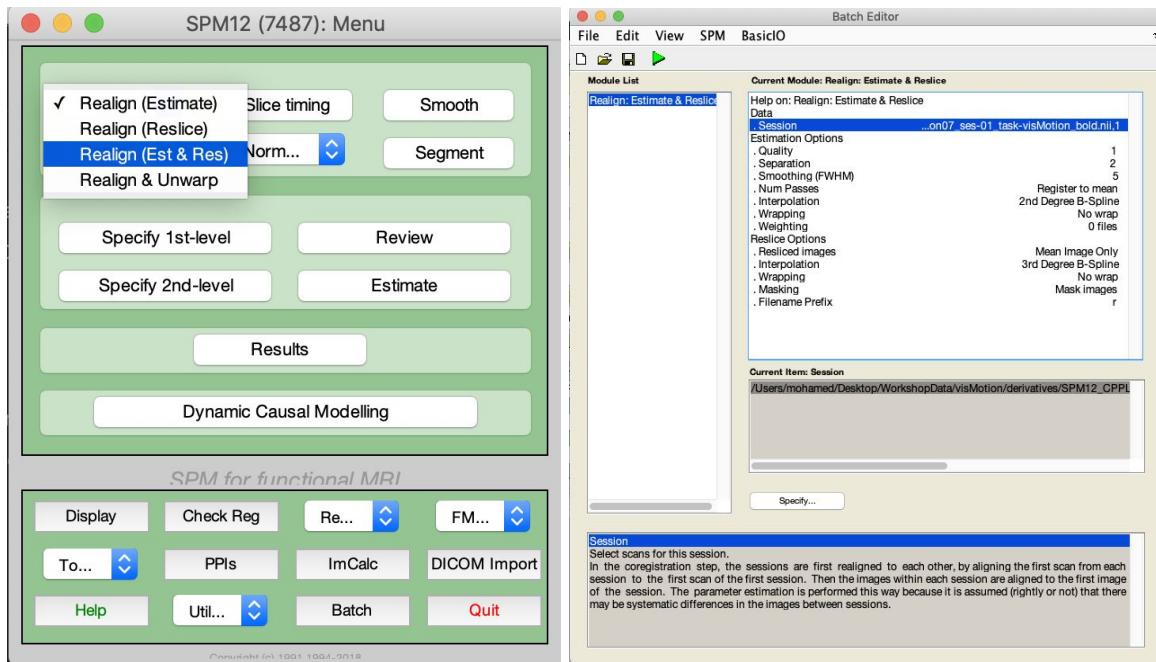
---

## Realign (Estimate and Reslice)

---

- Input
    - slice time corrected 4D functional image
      - *asub-con07\_ses-01\_task-visMotion\_bold.nii*
  - Output
    - slice time corrected AND realigned 4D functional image
      - *asub-con07\_ses-01\_task-visMotion\_bold.nii*
    - a mean image of all the realigned images
      - *meanasub-con07\_ses-01\_task-visMotion\_bold.nii*
    - a text file containing the realignment parameters for each volume of the 4D image (3 rotations and 3 translations)
      - *rp\_asub-con07\_ses-01\_task-visMotion\_bold.txt*
- 

1. In SPM GUI click on the *Realign* button and select *Estimate and Reslice* (see below).



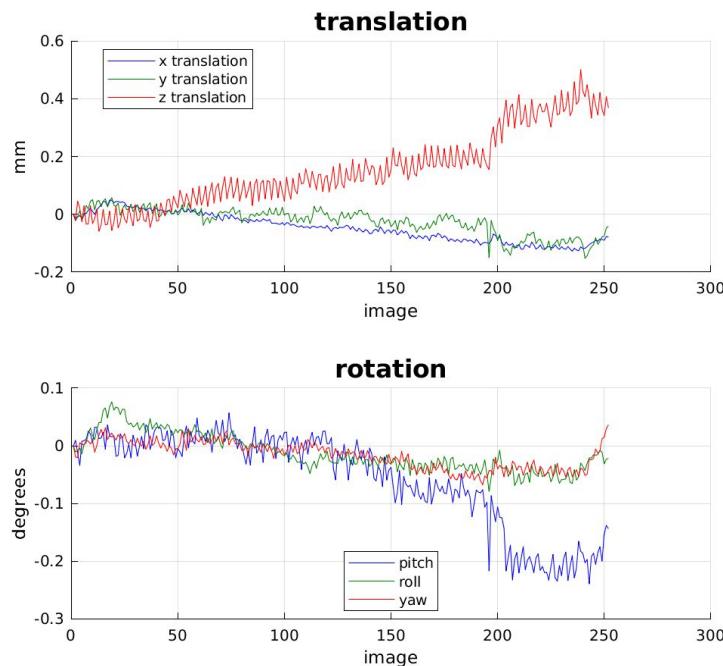
2. Click On *Data* → *Session* → *Specify*
3. Go to the directory where you have the files of the subject you have the functional data of the subject you are pre-processing (likely *derivatives/sub-con07/ses-01/func*).
4. Select all the 252 volumes of the slice-timed image: *asub-con07\_ses-01\_task-visMotion\_bold.nii*. To do this filter the displayed images by replacing *1* by *Inf* (show all the volumes and not just number 1) and *.\** by *^asub.\** (shows all the image that start with *sub*)
5. Click on *Resliced images* and choose *Mean Image Only* option. If you choose another option here, then SPM will create a resliced version of your functional images with a name starting in *rasub-* you would then need to use those in the rest of the pipeline.
6. Save a copy of the batch by clicking on *File* → *Save Batch*
7. Save it with the name *batch\_Realignment.mat*.
8. Run the batch by clicking the green run button.



Once the realignment is done, the 6 motion parameters are plotted. 3 translational motion directions and 3 rotational directions. The 6 motion parameters are also exported to a text file *rp\_asub-con07\_ses-01\_task-visMotion\_bold.txt*

## Image realignment

```
1 /home/remi/BIDS/visMotion/derivatives/sub-con07/ses-01/func/asub-con07_ses-01
2 /home/remi/BIDS/visMotion/derivatives/sub-con07/ses-01/func/asub-con07_ses-01
3 /home/remi/BIDS/visMotion/derivatives/sub-con07/ses-01/func/asub-con07_ses-01
4 /home/remi/BIDS/visMotion/derivatives/sub-con07/ses-01/func/asub-con07_ses-01
5 /home/remi/BIDS/visMotion/derivatives/sub-con07/ses-01/func/asub-con07_ses-01
6 /home/remi/BIDS/visMotion/derivatives/sub-con07/ses-01/func/asub-con07_ses-01
7 /home/remi/BIDS/visMotion/derivatives/sub-con07/ses-01/func/asub-con07_ses-01
8 /home/remi/BIDS/visMotion/derivatives/sub-con07/ses-01/func/asub-con07_ses-01
9 /home/remi/BIDS/visMotion/derivatives/sub-con07/ses-01/func/asub-con07_ses-01
10 /home/remi/BIDS/visMotion/derivatives/sub-con07/ses-01/func/asub-con07_ses-01
11 /home/remi/BIDS/visMotion/derivatives/sub-con07/ses-01/func/asub-con07_ses-01
12 /home/remi/BIDS/visMotion/derivatives/sub-con07/ses-01/func/asub-con07_ses-01
.....etc
```



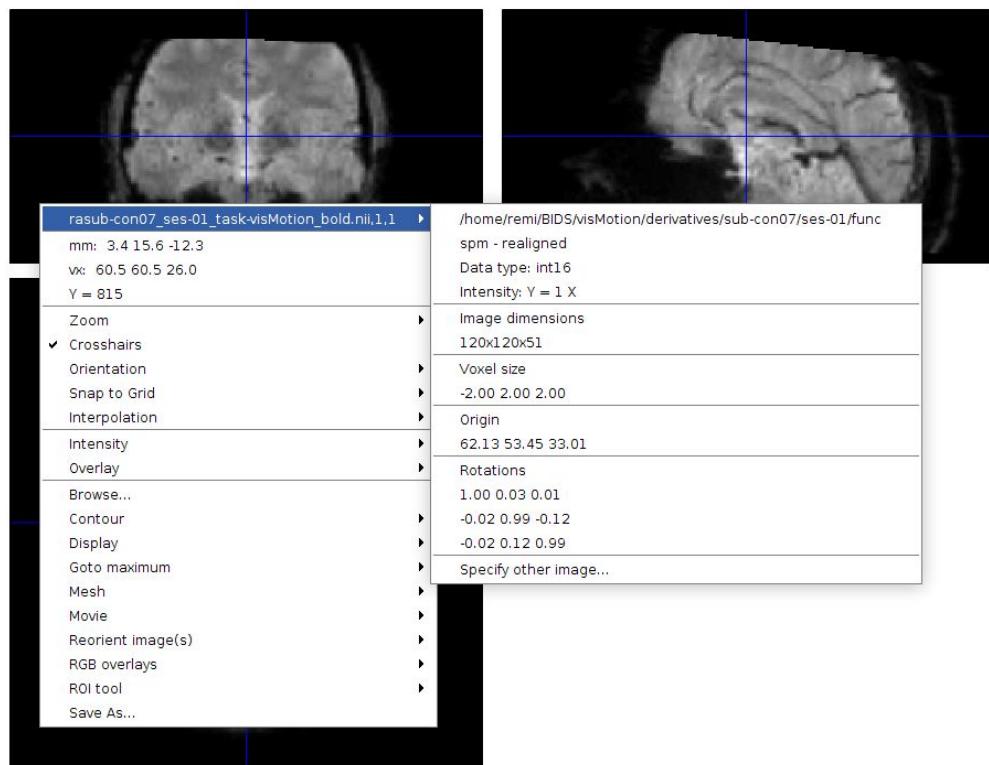
---

### ADVANCED TIP

Note that the changes to the functional images have been “saved” in transformation matrix of the image header but that no new file was created. If you want you can compare this to the transformation matrix of the same volume of the unaligned

image that is still in the raw folder.

You can see this transformation matrix using the *Check Reg* and then hovering the mouse over the name of the image (first line).



You can also check the content of the header of an MRI image by typing:

```
header = spm_vol('asub-con07_ses-01_task-visMotion_bold.nii') % loads the header  
of the 4D image
```

You can then see the content of the transformation matrix of a given volume by typing

```
header(10).mat % prints on the screen the transformation matrix of the 10th volume  
of the 4D image.
```

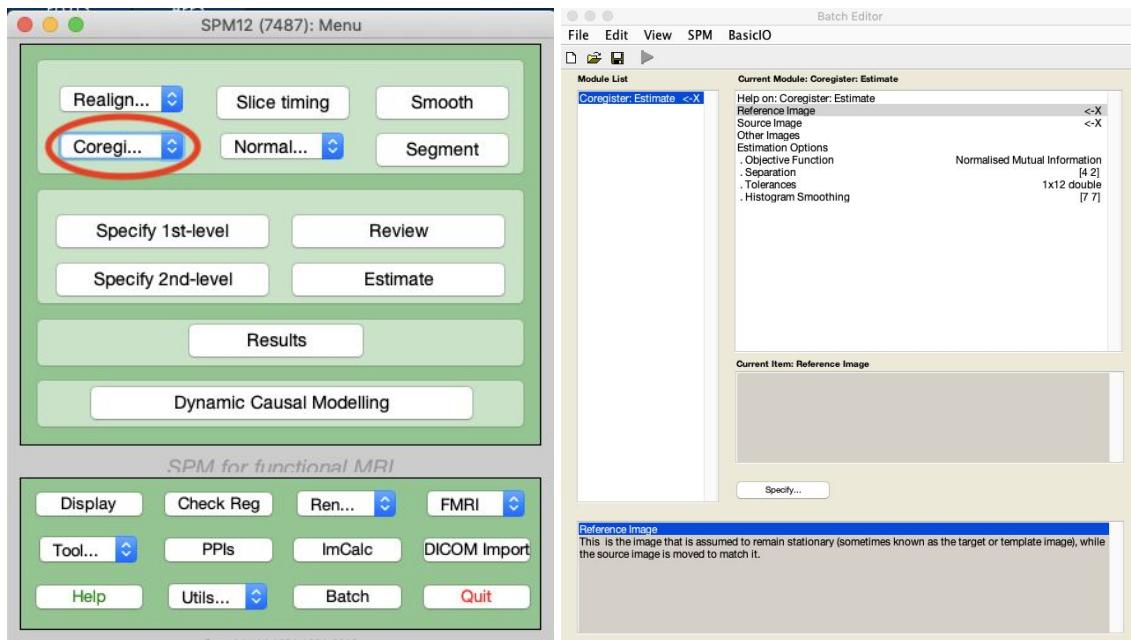


## Coregister (Estimate)

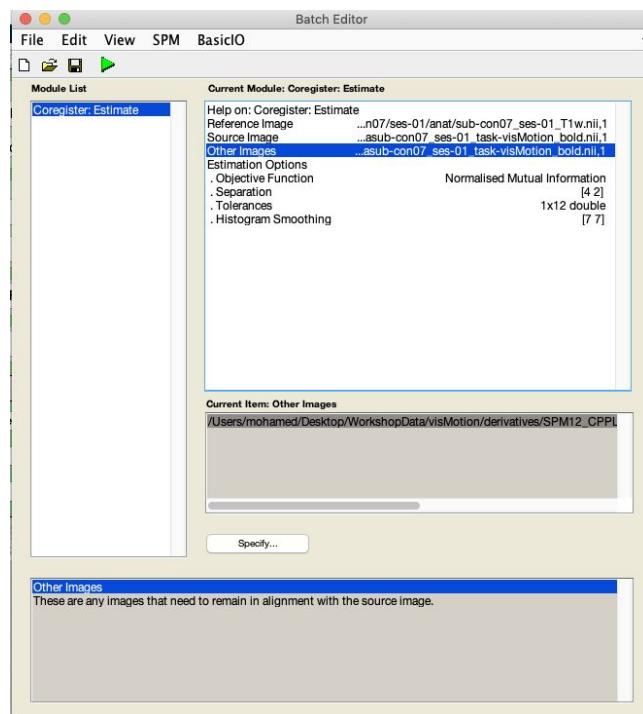
---

- Input
    - the mean image
      - *meanasub-con07\_ses-01\_task-visMotion\_bold.nii*
    - the realigned 4D functional image
      - *asub-con07\_ses-01\_task-visMotion\_bold.nii*
    - the T1w anatomical image
      - *sub-con07\_ses-01\_T1w.nii*
  - Output
    - mean and 4D functional images coregistered to the anatomical one
      - *asub-con07\_ses-01\_task-visMotion\_bold.nii*
      - *sub-con07\_ses-01\_T1w.nii*
- 

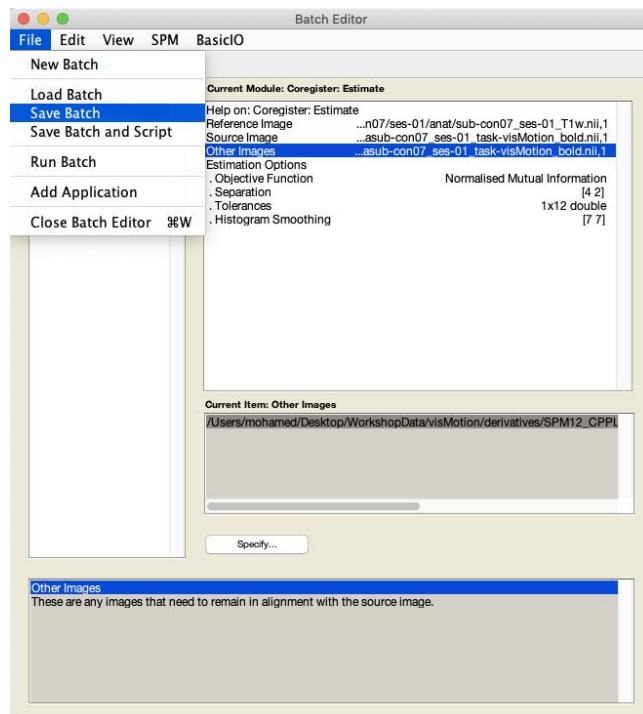
1. In SPM GUI click on the *Coregister* button and select *Estimate* (see below).



2. Choose the *Reference Image* (this image will not be moved and will be the reference for others): → Click on *Specify* and choose the structural image (e.g *sub-con07\_ses-01\_T1w*) in the *anat* folder of the subject you are processing (likely *derivatives/sub-con07/ses-01/anat/*)
3. Choose the *Source Image* (the images that will move to match the reference): Click on *Specify* and choose the mean functional image (for example: *func/meanasub-con07\_ses-01\_task-visMotion\_bold.nii*).
4. Click on *Other Images* → *Specify* and choose all the 252 realigned functional volumes (for example *func/asub-con07\_ses-01\_task-visMotion\_bold.nii*). To do this filter the displayed images by replacing *1* by *Inf* (show all the volumes and not just number 1) and *.\** by *^asub.\** (shows all the images that start with *asub*).



5. Click on *File* → *Save batch* and save the batch with the name *batch\_Coregister.mat*.



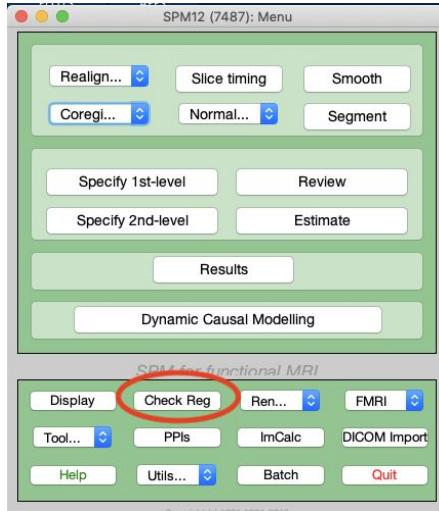
6. Run the batch by clicking the green run button



---

#### QUALITY CONTROL TIP

Use *Check Reg* that the coregistration is good enough.

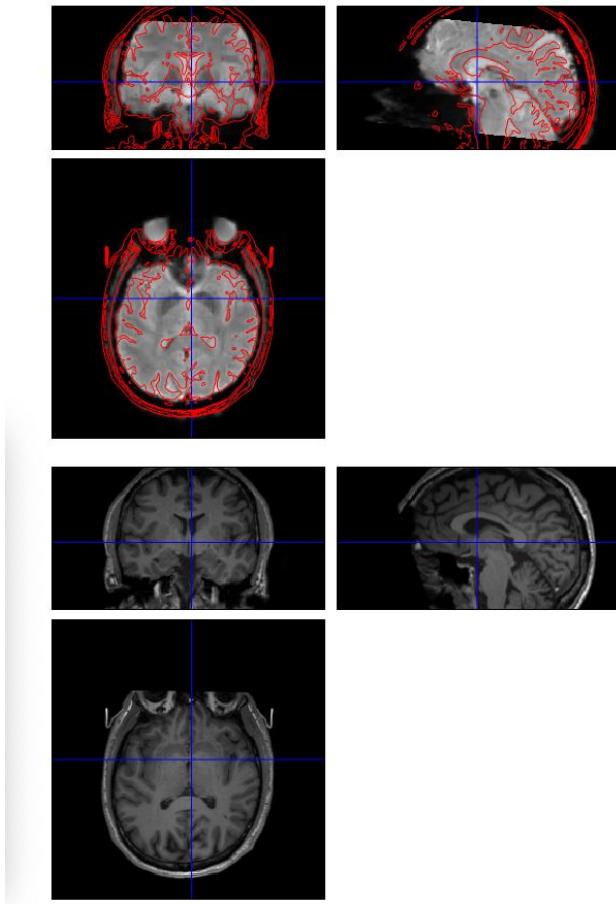


Go to the directory where you have the files of the subject you have processed (probably *derivatives/sub-con07/ses-01/*) and choose the mean functional image and the anatomical image:

- /func/meanasub-con07\_ses-01\_task-visMotion\_bold
- /anat/sub-con07\_ses-01\_T1w.nii

Right click on the structural image, then click on *Contour* → *Display onto* → *all but current* to overlay the contour of the structural image on top of the mean functional image.

You can then right click and use the *Zoom* option to find some anatomical landmark and make sure they are well aligned between images.



## Segment

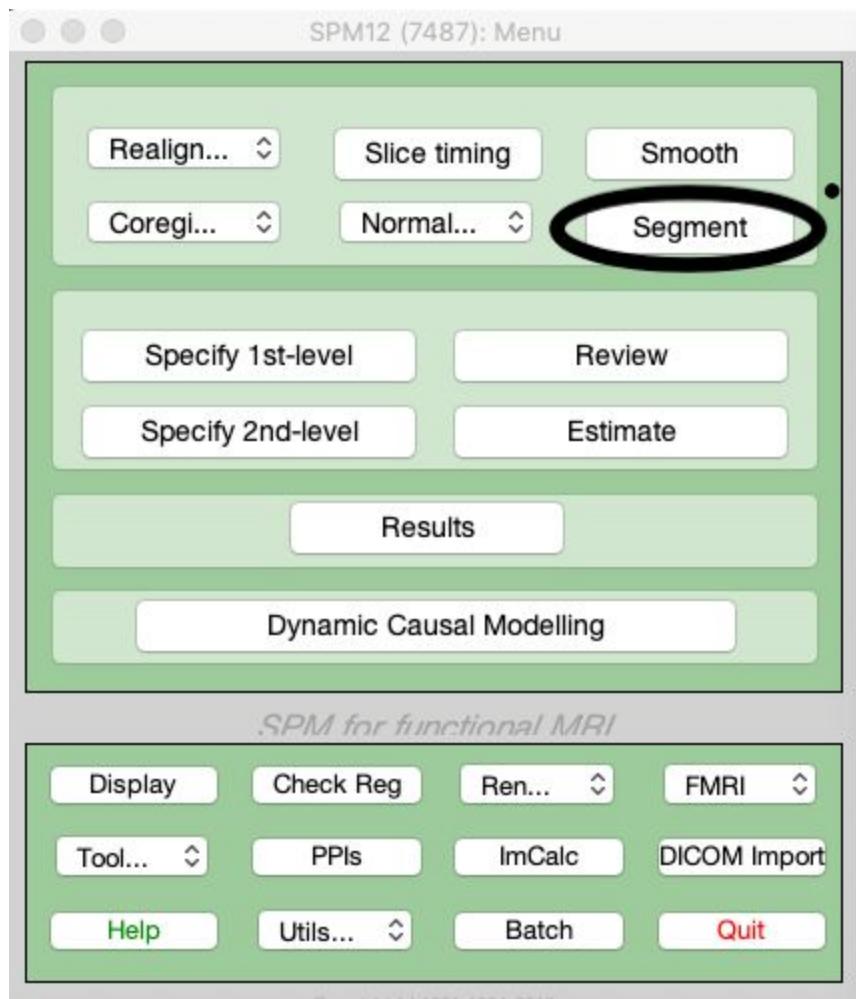
This part of the batch applies a bias correction to the anatomical T1 image and then segments into the grey matter, white matter and the cerebro-spinal fluid (CSF).

---

- Input:
  - Anatomical image
    - *sub-con07\_ses-01\_T1w.nii*
  - MNI space tissue probability maps
- Output:
  - Bias corrected anatomical image
    - *msub-con07\_ses-01\_T1w.nii*
  - Subject space tissue probability maps
    - *c1sub-con07\_ses-01\_T1w.nii*
    - *c2sub-con07\_ses-01\_T1w.nii*
    - *c3sub-con07\_ses-01\_T1w.nii*
    - *c4sub-con07\_ses-01\_T1w.nii*
    - *c5sub-con07\_ses-01\_T1w.nii*
  - Forward deformation field (from subject space to MNI space)
    - *y\_ub-con07\_ses-01\_T1w.nii*
  - Inverse deformation field (from MNI space to subject space)
    - *iy\_ub-con07\_ses-01\_T1w.nii*

---

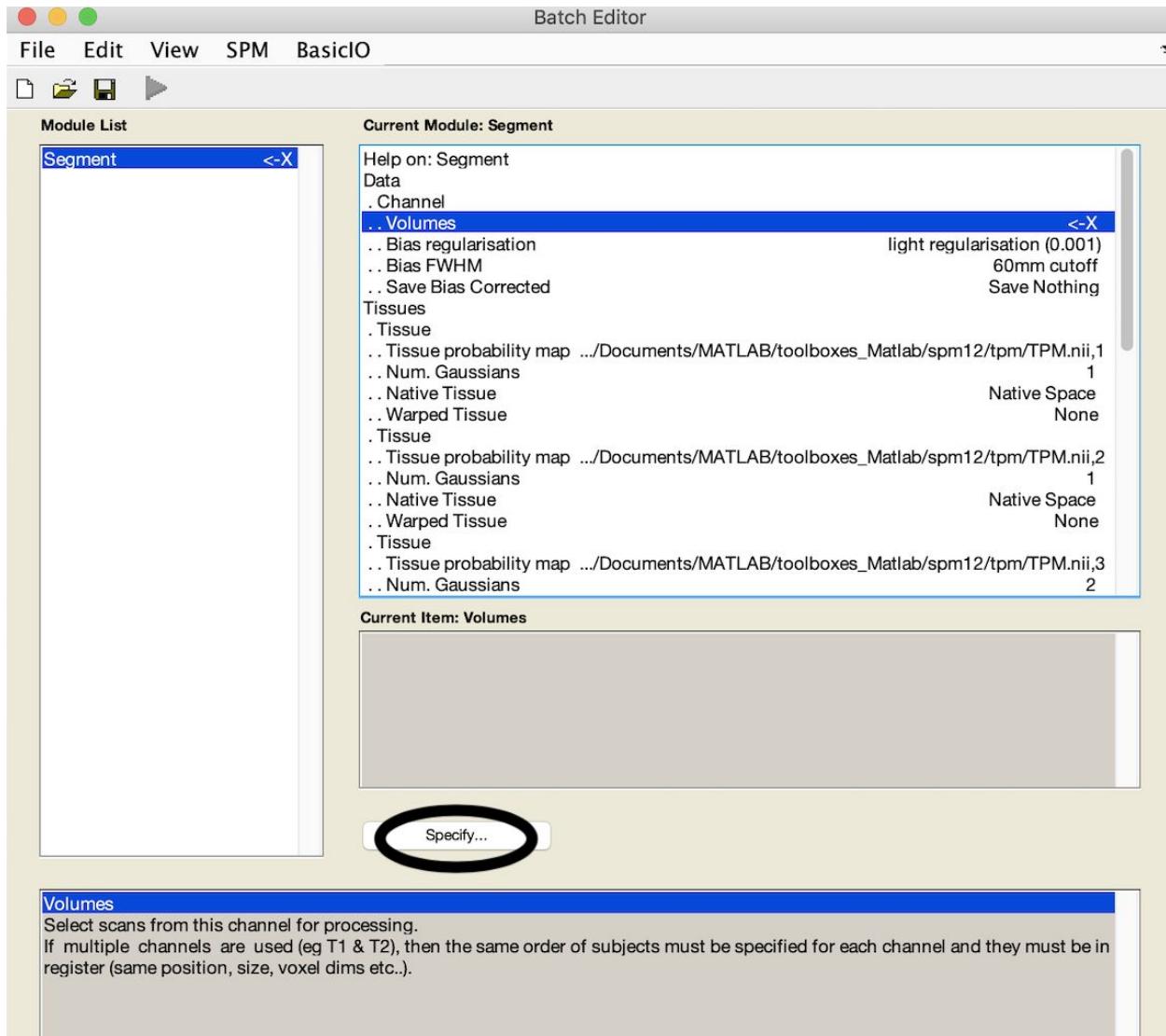
Press the *Segment* button (see below).



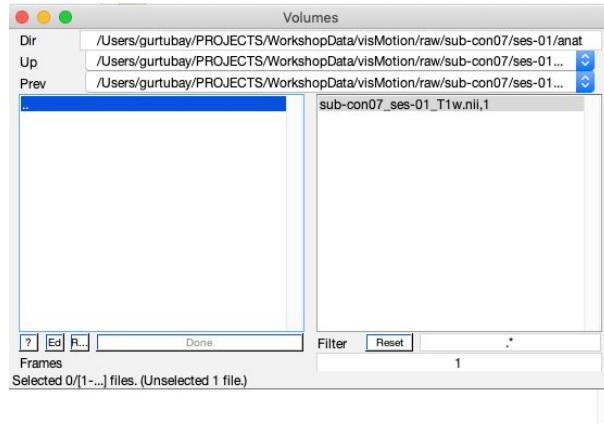
By one by one we will fill the missing values in the popped up screen (the missing values are the ones where we see an X) (see below).

1. We want to output the anatomical image corrected for the field bias so under *Data* section choose *Save Bias Corrected* and select *Save Bias Corrected*
2. We will need the deformation field to normalize the images from native space to MNI space so under *Warping & MRF* section, click on *Deformation Fields* and select *Inverse + Forward*.

3. We need to specify which image we want to segment. Click on *Volumes* and then click on *Specify* in the lower part.



4. When we click on *Specify*, the following window will pop-up:



5. Go to the directory where you have the anatomical files (probably *derivatives/sub-con07/ses-01/anat*) and choose the anatomical file (ex: *sub-con07\_ses-01\_T1w.nii*), then click *Done*.

## Normalize (Write)

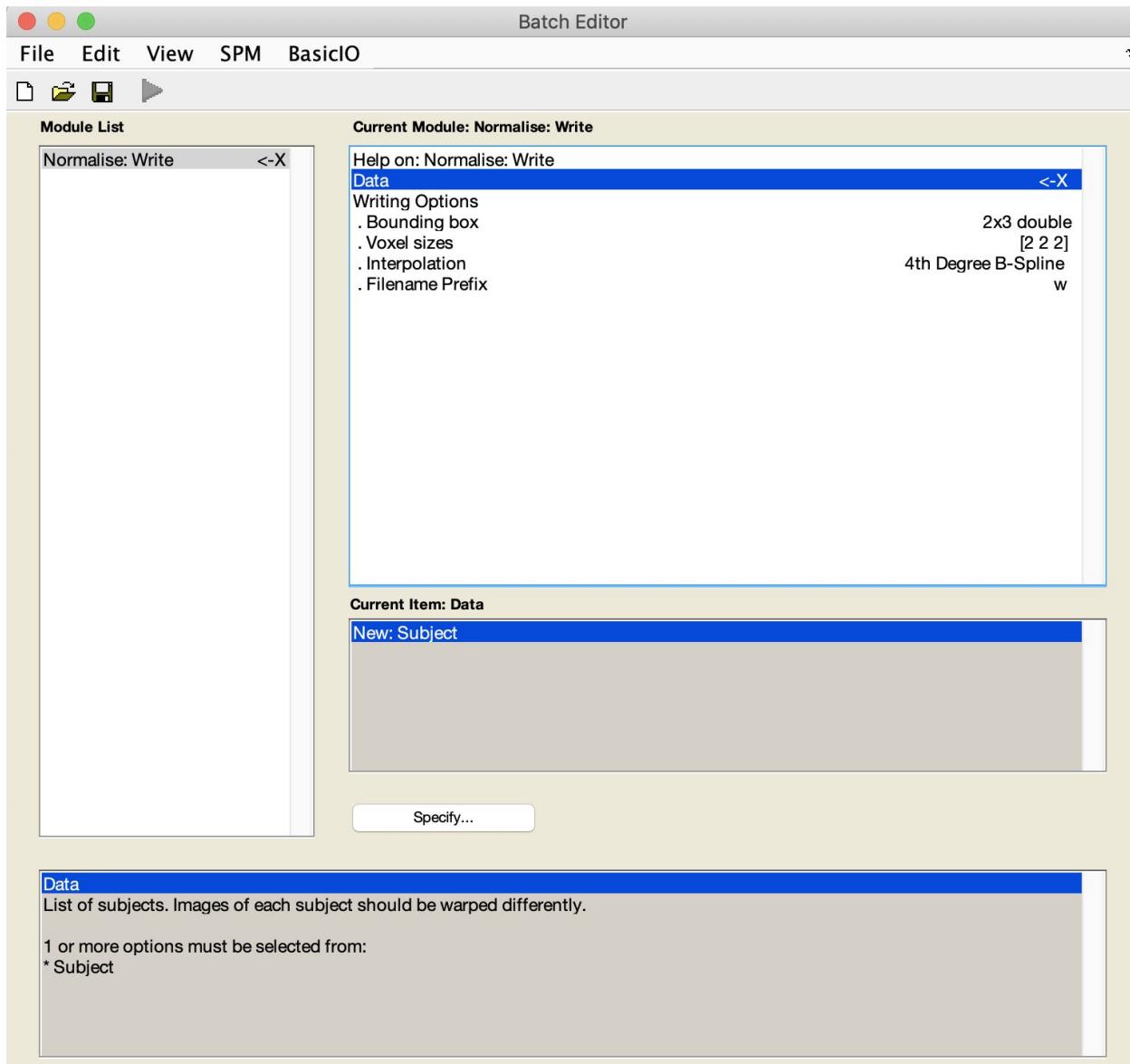
The normalisation batch includes two modules: one is for anatomical image normalisation and the second one is for functional normalisation.

### Anatomical image

This first part of this batch normalizes the anatomical image and the tissue probability maps to the standard MNI space.

- 
- Input:
    - Bias corrected anatomical image
      - *msub-con07\_ses-01\_T1w.nii*
    - Forward deformation field (from subject space to MNI space)
      - *y\_ub-con07\_ses-01\_T1w.nii*
  - Output:
    - Normalised bias corrected anatomical image
      - *wmsub-con07\_ses-01\_T1w.nii*
- 

1. In the Batch window, click on *SPM → Spatial → Normalize → Normalize: write* to add a *Normalize: write* module to the batch. Now, we will fill the missing values in the popped up screen (the missing values are the ones where we see an X).



2. We want to keep the resolution of the anatomical image close to the one used at acquisition so in *Writing Options* section click on *Voxel sizes* and *Specify* and enter **[1 1 1]**.
3. Click on *Data* and then on *New Subject*
4. Select *Deformation field* click on *Dependency*
5. Select *Segment: forward deformations* and click *OK*.

6. Select *Images to write* and click on *Dependency*
7. Select *Segment: Bias Corrected* and click *OK*.

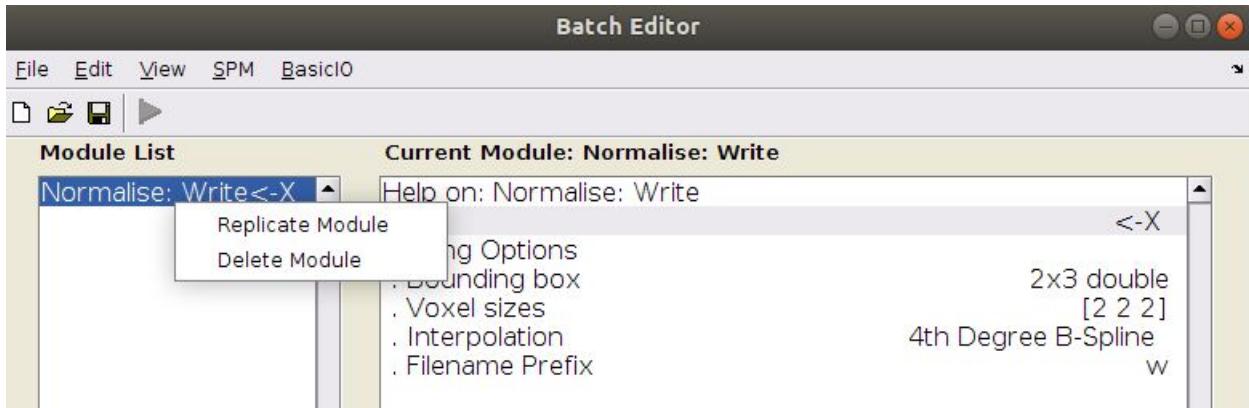
Functional, mean functional and tissue probability maps

This second part of the batch normalizes the functional data, the mean functional image and the tissue probability maps to the standard MNI space.

---

- Input:
    - Subject space tissue probability maps for grey matter, white matter and CSF
      - *c1sub-con07\_ses-01\_T1w.nii*
      - *c2sub-con07\_ses-01\_T1w.nii*
      - *c3sub-con07\_ses-01\_T1w.nii*
    - Mean functional image
      - *meanasub-con07\_ses-01\_task-visMotion\_bold.nii*
    - Realigned functional image
      - *asub-con07\_ses-01\_task-visMotion\_bold.nii*
  - Output:
    - Normalised functional and mean functional image
      - *asub-con07\_ses-01\_task-visMotion\_bold.nii*
      - *wmeanasub-con07\_ses-01\_task-visMotion\_bold.nii*
    - Normalised tissue probability maps
      - *wc1sub-con07\_ses-01\_T1w.nii*
      - *wc2sub-con07\_ses-01\_T1w.nii*
      - *wc3sub-con07\_ses-01\_T1w.nii*
- 

Create a copy of the previous *Normalize 'Write'* module you have created by right-clicking on it and selecting *Replicate module*.



This new module you will be used to set the parameters to normalize the functional images.

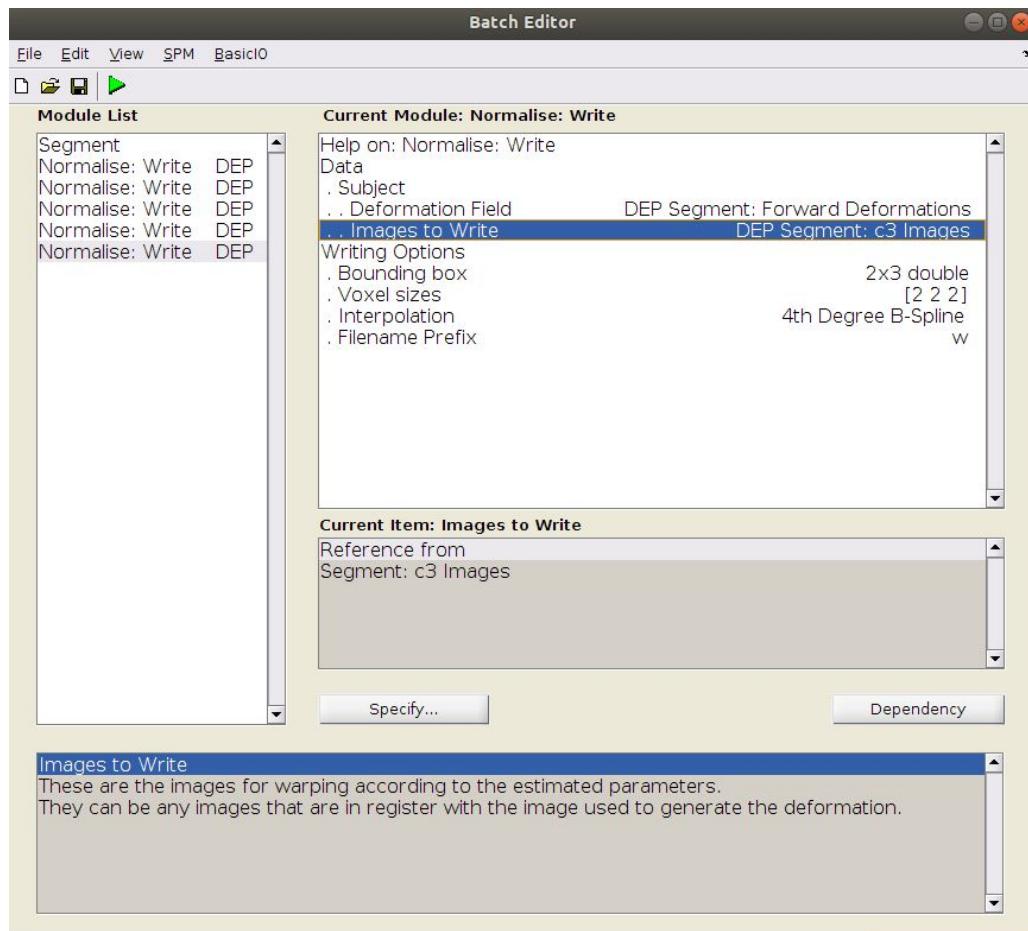
8. We want to keep the resolution of the functional image close to the one used at acquisition so click on *Voxel sizes* and *Specify* and enter *[2 2 2]*. We will also apply this resolution to the tissue probability maps in case we want to use them to create a binary mask to determine which voxels should be included in the subject level analysis<sup>2</sup>.
9. In *Data* section, select *Images to Write* and click on *Specify*
10. First, go to the directory where you have the functional images (probably: *derivatives/sub-con07/ses-01/func*) and choose 2 images:
  - a. the mean functional image (ex: *meanasub-con07\_ses-01\_task-visMotion\_bold.nii*)
  - b. The 252 realigned functional volumes (ex: *asub-con07\_ses-01\_task-visMotion\_bold.nii*). To do this filter the displayed images by replacing *1* by *Inf* (show all the volumes and not just number 1) and *.\** by *^asub.\** (shows all the image that start with *asub* - if you chose to reslice the images during realignment then you would have to select the files that start with *ra*).
11. You can then replicate this module 3 times and change the *Images to Write* in each of them and use the *Dependency* to select

---

<sup>2</sup> They can also be used to perform a skull stripping.

- a. Segment: c1 image
- b. Segment: c2 image
- c. Segment: c3 image

12. Your batch should look like this:



13. Save the batch with the name: "batch\_segment\_normalize.mat" by clicking on *File → save batch*

14. Run the segment and normalization batch by clicking the green run button



---

#### NOTE

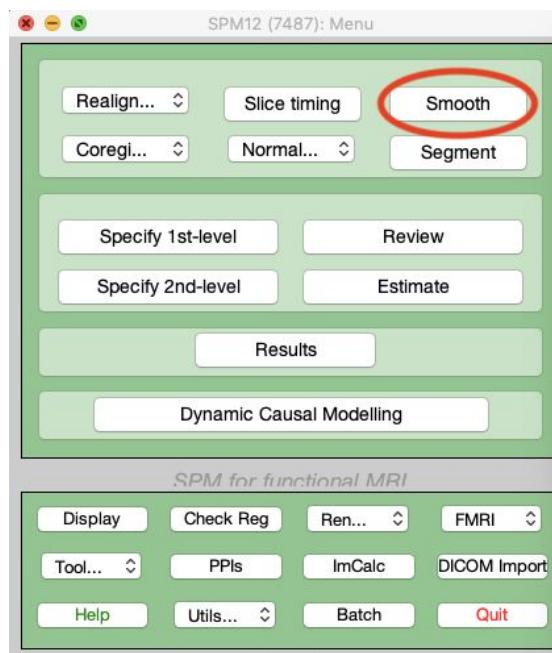
- The MNI templates that SPM uses are in the the SPM folder *spm12/canonical*
-

## Smoothing

Spatial smoothing consists of applying a small blurring kernel across your image, to average part of the intensities from neighboring voxels together. The effect is to "blur" the image, the main aim is to increase your signal-to-noise ratio.

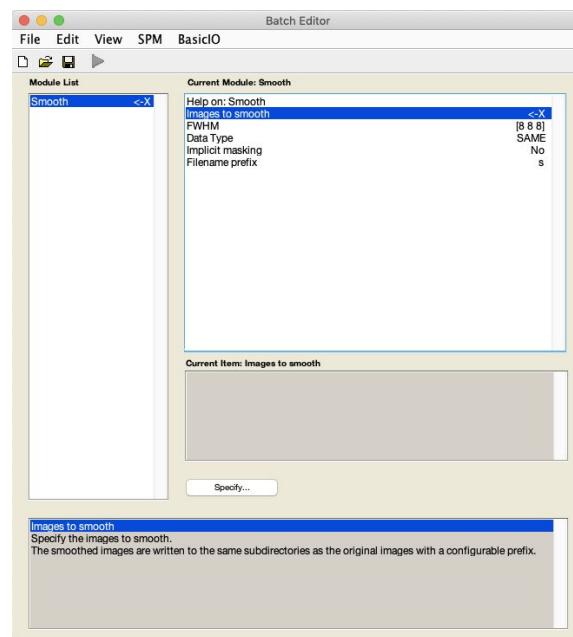
- 
- Input
    - Normalized functional images:
      - *wasub-con07\_ses-01\_task-visMotion\_bold.nii*
  - Output
    - Smoothed normalized functional images:
      - *s6wasub-con07\_ses-01\_task-visMotion\_bold.nii*
- 

1. In the SPM window, click on *Smooth*

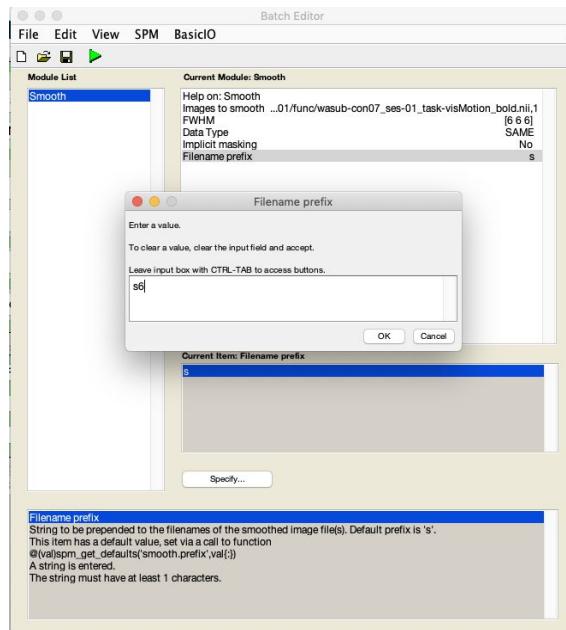


2. Click on *Images to smooth* and *Specify*

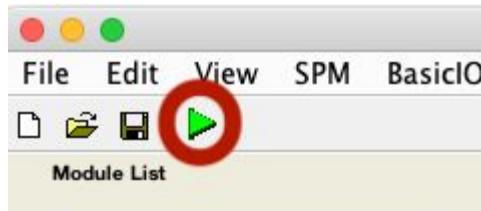
3. Go to the directory where you have the functional images (probably: *derivatives/sub-con07/ses-01/func*) and choose all the 252 normalized functional volumes (ex: *wasub-con07\_ses-01\_task-visMotion\_bold.nii*). To do this filter the displayed images by replacing *1* by *Inf* (show all the volumes and not just number 1) and *.\** by *^wasub.\** (shows all the image that start with *wasub*)
4. Choose the Full Width Half Maximum (FWHM) smoothing Kernel that you want to apply. We will apply a smoothing kernel of 6 mm. Click on *FWHM* and type: **[6 6 6]**



5. Click on *Filename prefix* and click *Specify*. Rename the prefix to *s6*. This way we will know the smoothing kernel in mm applied from the name/header of the file.



6. Save a copy the batch with the name "*batch\_smooth.mat*" by clicking on *File → Save batch*.
7. Run the batch by clicking "run" (the green arrow)



## Statistical analysis - Subject level (First-level)

In this step, we are going to specify and estimate the subject level model.

## Model specification

---

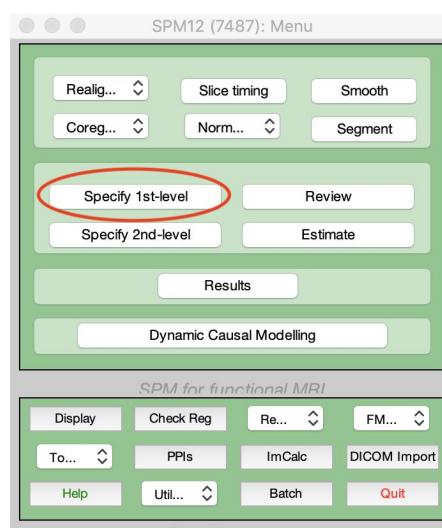
- Input:
    - Smoothed normalized functional images (*s6w\*.nii*)
    - Experimental design (conditions, onsets, durations)
    - Regressors of no interest (motion parameters)
  - Output
    - SPM.mat
- 

1. Create the output folder to save the fixed effects (ffx) statistical results :  
*derivatives/sub-con07/stats/ffx\_visMotion/ffx\_6*

You can do this from matlab directly by using the "make directory" command. For example if you are in the folder derivatives/sub-con07 you can type:

*mkdir stats/ffx\_visMotion/ffx\_6*

2. In SPM, and click on: *Specify 1st level*



3. To specify the path of where to save the ffx results, click *Directory* and choose:

`/derivatives/sub-con07/stats/ffx_visMotion/ffx_6`

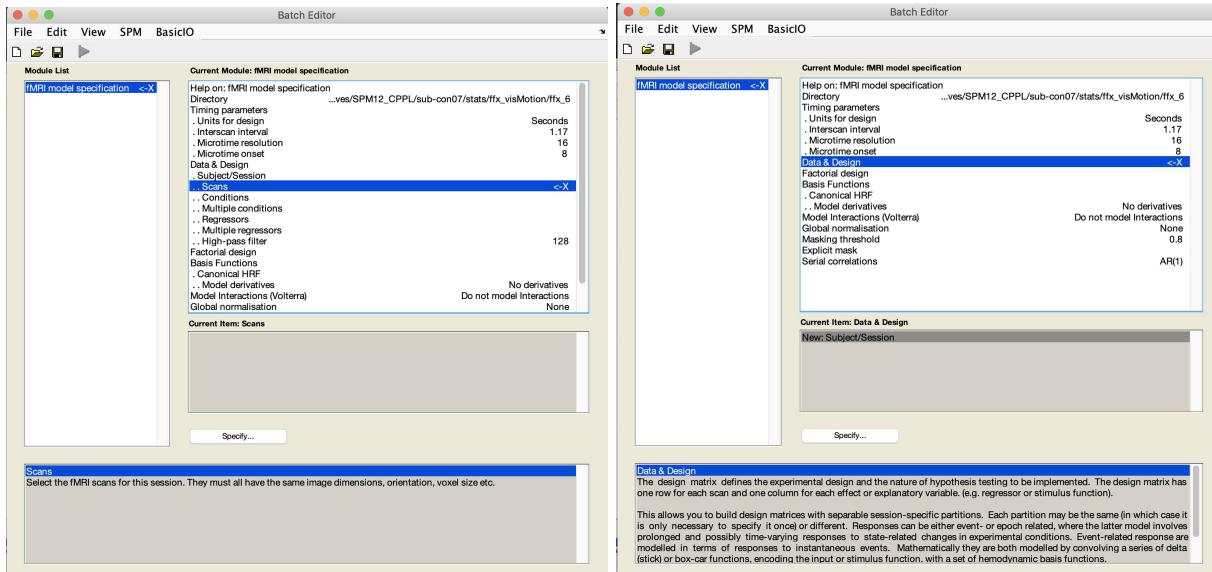
4. In *Timing parameters* section, *Unit of design* has to be set to *Seconds*
5. *Interscan interval* is the repetition time: see the section [Slice timing](#) to know where to find this information.

To more accurately model the predicted hemodynamic response function (HRF). SPM convolves the onset regressor with the HRF basis set at a higher temporal resolution than the one used at acquisition, so we need to provide SPM with more information on how to do this.

6. *Microtime resolution* has to be set to match the number of slices present in each volume: see the section [Slice timing](#) to know where to find this information. It should be 51.
7. *Microtime onset* has to be set to match the value of the reference slice used in the [Slice timing](#) section. We have used the middle slice so 26.

We will use SPM FAST method of modelling autocorrelation rather than the default autoregressive model (AR1).

8. At the bottom of the list, set *Serial correlations* to *FAST*.
9. For *Data & Design*, click on *New subject/Session*
10. *Scans*: Click on *Scans* and add all the volumes the 252 preprocessed smoothed normalized functional volumes (e.g `s6wasub-con07_ses-01_task-visMotion_bold.nii`). To do this filter the displayed images by replacing `1` by `Inf`(show all the volumes and not just number 1) and `.*` by `^s6wasub.*`(shows all the image that start with `swasub`).
- 11.



Now we need to define our experimental conditions (Motion and Static blocks). The information about the conditions are available in the events.tsv file (e.g *sub-con07\_ses-01\_task-visMotion\_events.tsv*). You can open the tsv file in excel<sup>3</sup> spreadsheets:

---

<sup>3</sup> You can also load the information in MATLAB directly by using the command:  
`events = spm_load('sub-con07_ses-01_task-visMotion_events.tsv')`

	A	B	C
1	onset	duration	trial_type
2	2.050940565	15.21279939	VisMot
3	25.27959897	15.19883858	VisStat
4	48.49504276	15.19944798	VisMot
5	71.71075579	15.199255	VisMot
6	94.92658637	15.19871453	VisMot
7	118.1419602	15.19957335	VisStat
8	141.3583341	15.19897906	VisMot
9	164.5737866	15.19921266	VisStat
10	187.7895525	15.79844149	VisMot
11	211.6054762	15.19909512	VisStat
12	234.8210741	15.19922253	VisMot
13	258.0364725	15.79867674	VisStat

Another possibility is to load into matlab the onset times and durations for each condition you can use the following code:

```
events = spm_load('sub-con07_ses-01_task-visMotion_events.tsv') % loads the tsv file
in matlab
```

```
vis_motion_index = strcmp(events.trial_type, 'VisMot') % identify which lines of the
tables contains "VisMot"
```

```
vis_static_index = strcmp(events.trial_type, 'VisStat') % identify which lines of the
tables contains "VisStat"
```

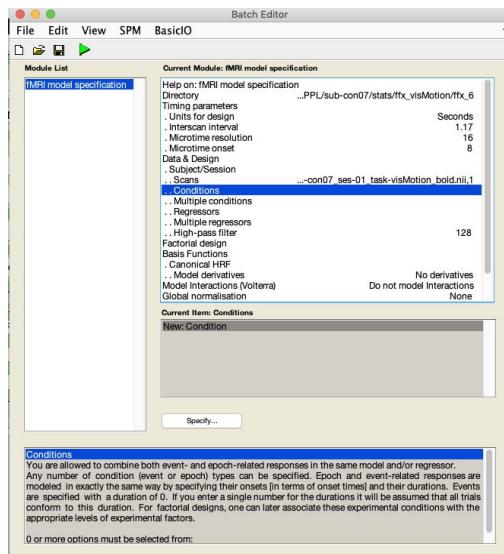
```
events.onset(vis_motion_index) % onsets for VisMot
```

```
events.onset(vis_static_index) % onsets for VisStat
```

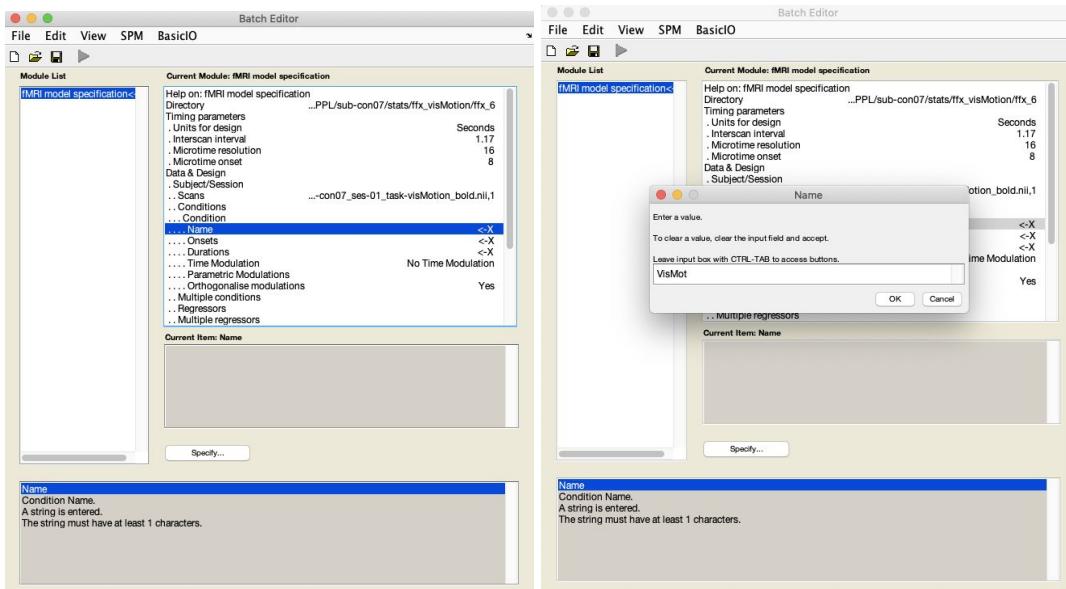
```
events.duration(vis_motion_index) % durations for VisMot
```

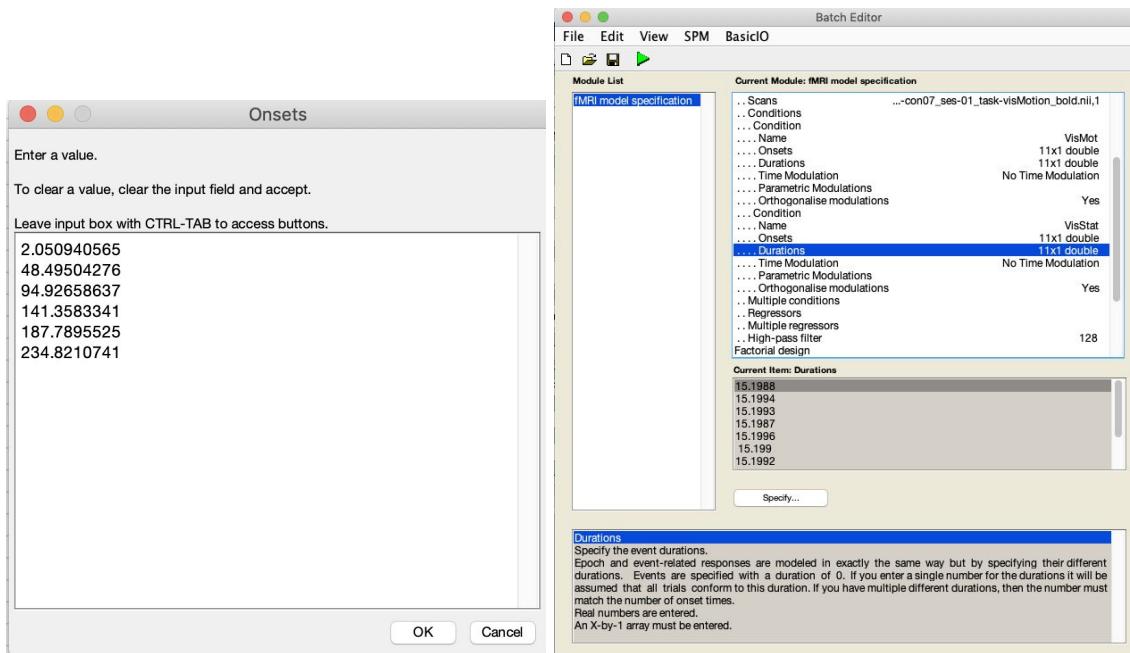
```
events.duration(vis_static_index) % durations for VisStat
```

12. Press on *Condition* and then *New condition*



13. Add the name of the condition *VisMotion*, and add on the onsets and durations of *visMotion*

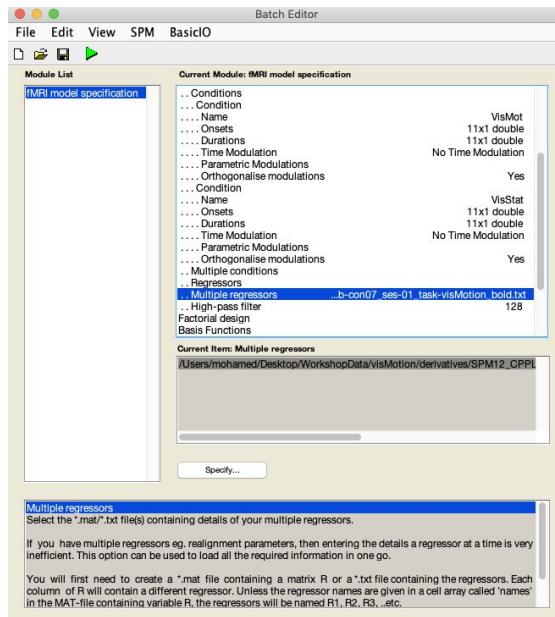




14. Repeat the same process for the “VisStat” condition.

We now finished defining the regressors/conditions of interest (Motion and static). But there are other regressors-of-no-interest that we need to control for head motion. Therefore we need to add the motion parameters as regressors-of-no-interest. Now we will add the 6 motion parameters as 6 regressors of no interest.

15. Click on *Multiple regressors* and click *Specify*. Load the head motion parameters text file (*rp\_\*.txt*) that contains the 6 motion regressors (e.g. *rp\_asub-con07\_ses-01\_task-visMotion\_bold.txt*).



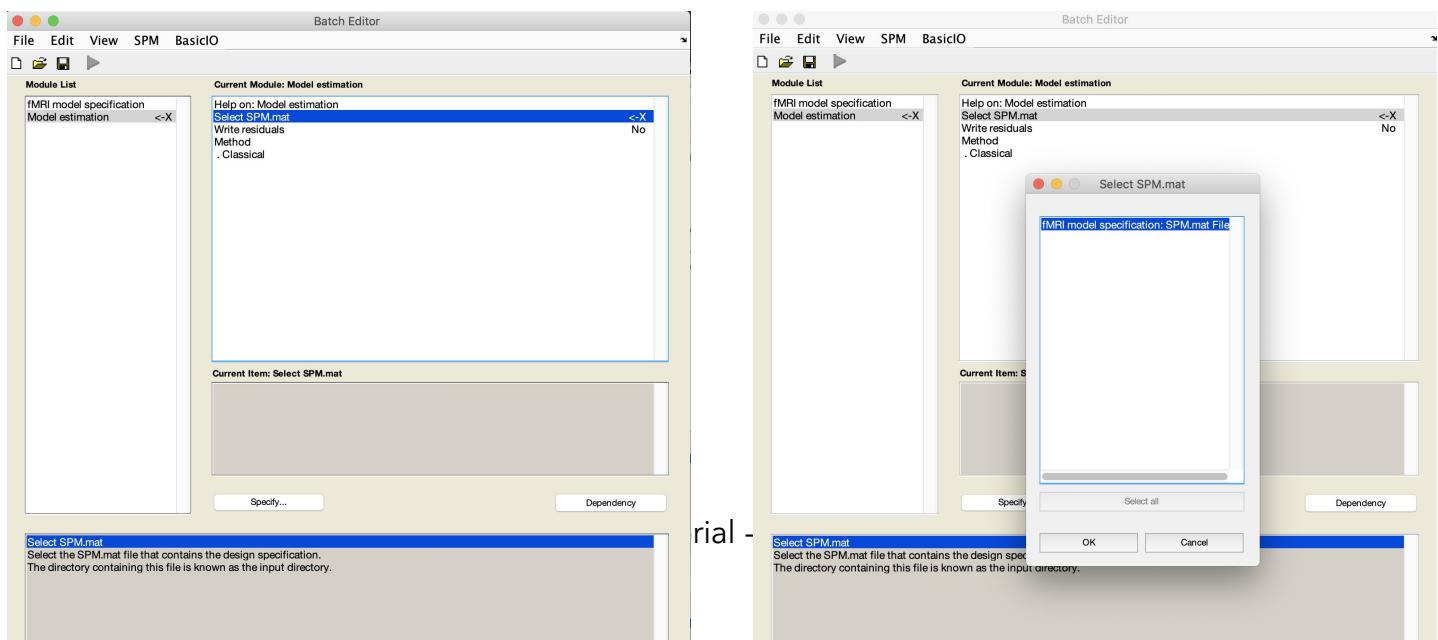
## Model estimation

We defined the model in the previous step, now we need to run it.

---

- Input:
  - *SPM.mat* from the model specification
- Output:
  - beta maps
    - *beta\_\*.nii*
  - Inclusion mask
    - *mask.nii*
  - Residual variance estimate and residuals
    - *ResMS.nii*
    - *Res\_\*.nii*
  - Estimated RESELS per voxel
    - *RPV.nii*

- 
1. In the batch window, click on SPM - STATS - MODEL ESTIMATION
  2. Select *SPM → Dependency*
  3. Select *fMRI model specification: SPM mat file*

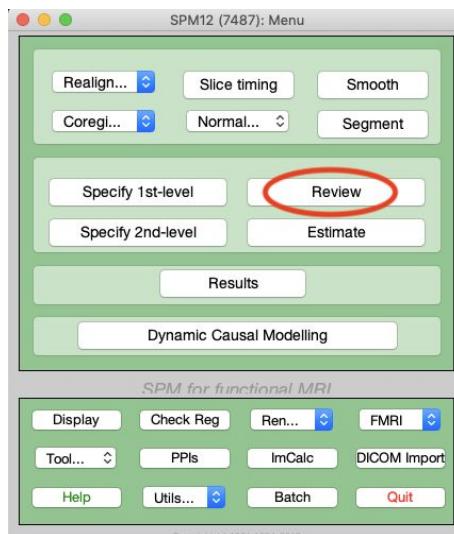


4. For *Write residuals* select *yes*
5. Click on *File* → *Save batch* and save the batch as *FFX\_modelEstimation.mat*.
6. Press Run batch (the green arrow)

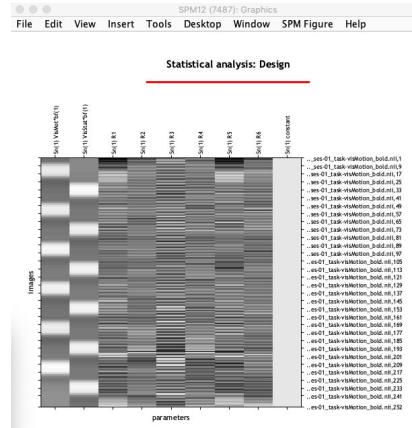


## Review your model

1. On the SPM window → click *Review*

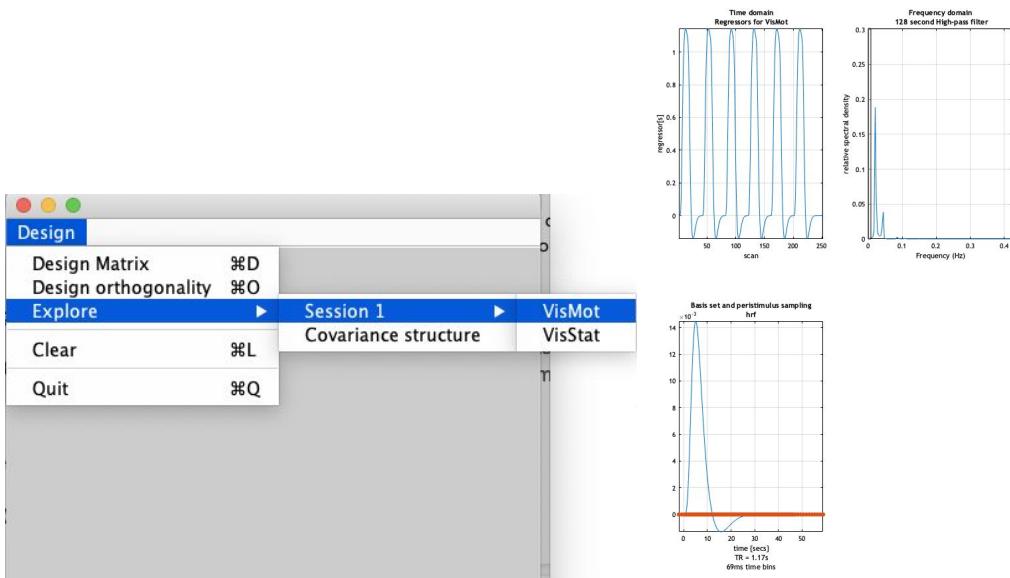


2. Choose the *SPM.mat* from the subject analysis directory (for example *derivatives/sub-con07/stats/ffx\_visMotion/ffx\_6/SPM.mat*)



You can review your model (design matrix). The first regressor is the motion condition. The second regressor is the static condition. The following 6 regressors are the 6 head motion parameters.

You can visualize the orthogonality of the different regressors of your model and you can explore each condition in more detail by clicking on the *Design* → *Explore* → *Session1* → *VisMotion*.



This will allow you to explore your design in the time domain and the frequency domain.

---

### QUALITY CONTROL TIP

The model estimation creates a *mask.nii* image in the output folder. This image is a binary mask that shows all the voxels that were included in the GLM by SPM. It is important to check none of the brain regions you are interested in were excluded by SPM.

Open this image by using the SPM *Check Reg* tool. All voxels that were included have a value of 1 and are shown in white while the voxels that were excluded have a value of 0 and are shown in black.

---

### QUESTION

- How many beta images should you expect to have after estimation?
  - How many residual images should you expect to have after estimation?
- 

### NOTE

- You can review your design before its estimation which can be a useful thing to do to make sure that everything is OK before you launch the computation.
- The design matrix might look different before and after estimation. This is because after estimation SPM displays the design matrix that takes into account the non-sphericity of the data (for example the fact that 2 consecutive time points in the fMRI time series are not independently sampled data point and their error terms might be correlated).
- You can also use the module *SPM → stats → fMRI model specification (design only)* to design your model even before you acquire your data.

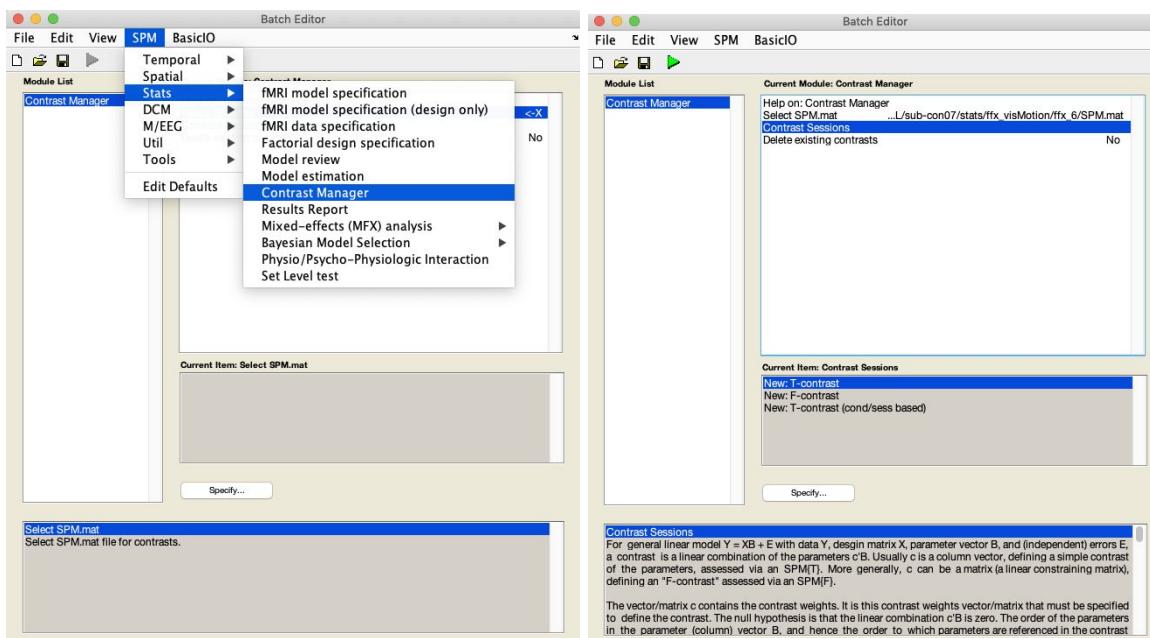
- The *SPM.mat* file contains all the information about your statistical model. It is quite a complex matlab structure but this [blog post](#) can help you navigate it.
-

## Contrast manager

In this step we are going to create contrast images which are the linear combination of some of the beta images outputted by the model estimation.

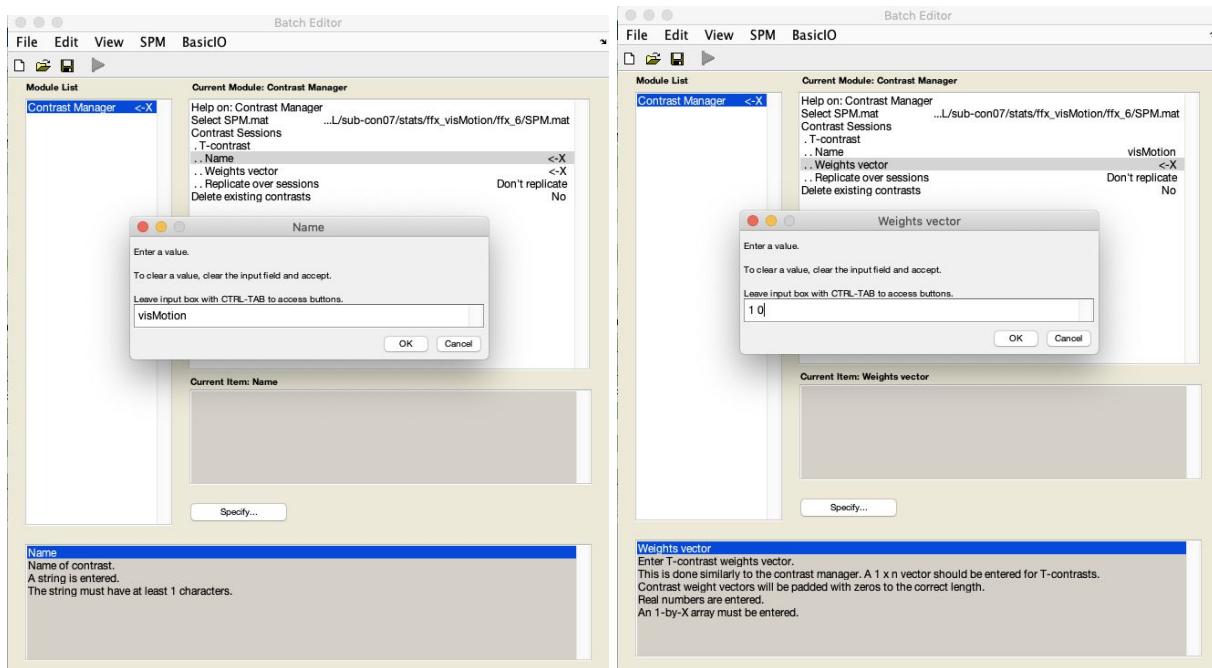
- Input:
  - beta images for different conditions
- Output:
  - spm t-maps
    - *spmT\_\*.nii*
  - spm con images
    - *con\_\*.nii*

1. Press on *SPM* → *Stats* → *Contrast Manager*
2. Select the *SPM.mat* file inside the ffx folder



3. Now we define the contrasts. Click on: *New T contrast*

4. Enter the name : *visMotion*



5. Click on *Weight vector* and *Specify* : [1]. SPM will add any missing 0 at the end of the vector of values you enter (i.e. zero padding).
6. Repeat the same procedure for the other contrasts by using the values of this table:

	Name	Weight vector	con image name
1rst contrast	visMotion	[ 1 ]	con_0001.nii

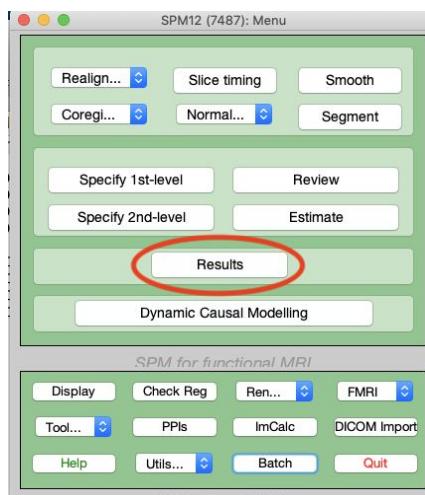
2nd contrast	visStat	[ 0 1 ]	con_0002.nii
3rd contrast	visMotion_gt_visStat	[ 1 -1 ]	con_0003.nii
4th contrast	visStat_gt_visMotion	[-1 1 ]	con_0004.nii

7. Press Run (Green arrow)

To explore those results you can simply follow the general procedure described in [Explore the results](#).

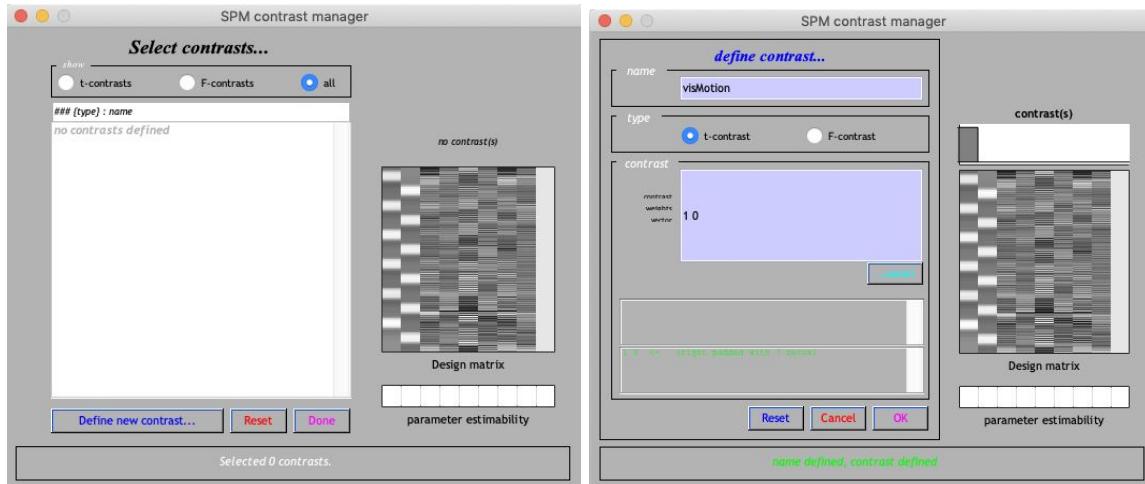
Another way to compute the contrasts:

1. On the SPM window, click on *Results*



2. Choose the *SPM.mat* in the stats folder (e.g. *derivatives/sub-con07/stats/ffx\_visMotion/ffx\_6/SPM.mat*)
3. The contrast manager window is opened → click *Define new contrast*
4. Enter the name of the contrast *visMotion*

5. Enter the vector weight: [1 0]



6. Repeat the same procedure for the other 3 contrasts. Then click *OK*.

---

#### NOTE

- If you use this second method of generating the contrasts, SPM will only generate the con and spmT images corresponding to this contrast if you view the results (see section [Explore the results](#)).
  - If you want to test the effect of motion , you need to do an F test by entering column of the reduced model you want to test: specify [1 2 9] in the field *columns for reduced design* of the SPM .
-

## QUESTION

- Use the *Check Reg* button to open both the images *beta\_0001.nii* and *con\_0001.nii*. Do you see any difference between them? If so, why? If not, why not?
  - Use the *Check Reg* button to open the images *beta\_0009.nii*, *beta\_0001.nii* and one volume from the smoothed 4D image you used as input for this model. Is *beta\_0009.nii* more similar to the other beta image or to the smoothed input image? Can you guess why?
-

## Statistical analysis - Group level (Second-level)

## Getting and browsing the group data

Unzip the file *derivatives\_group.zip*. The content of this file should match the one summarized in the following page.

This zip file contains the results of the subject level estimation of each subject in the respective *stats* folder and the normalized anatomical image of each subject in their respective *anat* folder.

To make this zip file lighter the following files have been replaced by empty dummy files. So don't try to open them because it will not work.

- *anat/sub-con\*\_ses-01\_T1w.nii*
- *anat/sub-con01\_ses-01\_T1w.json*
- *func/sub-con17\_ses-01\_task-visMotion\_.\**

```
SPM12_CPLP
├── sub-con01
│   ├── ses-01
│   │   └── anat
│   │       ├── sub-con01_ses-01_T1w.json
│   │       ├── sub-con01_ses-01_T1w.nii
│   │       └── wmsub-con01_ses-01_T1w.nii
│   └── func
└── stats
    └── ffx_visMotion
        └── ffx_6
            ├── beta_0001.nii
            ├── ...
            ├── beta_0009.nii
            ├── con_0001.nii
            ├── ...
            ├── con_0005.nii
            ├── mask.nii
            ├── RPV.nii
            ├── SPM.mat
            ├── spmT_0001.nii
            ├── ...
            └── spmT_0005.nii
└── sub-con17
    ├── ses-01
    │   └── anat
    │       ├── sub-con17_ses-01_T1w.json
    │       ├── sub-con17_ses-01_T1w.nii
    │       └── wmsub-con17_ses-01_T1w.nii
    └── func
    └── stats
        └── ffx_visMotion
            └── ffx_6
                ├── beta_0001.nii
                ├── ...
                ├── beta_0009.nii
                ├── con_0001.nii
                ├── ...
                ├── con_0005.nii
                ├── mask.nii
                ├── RPV.nii
                ├── SPM.mat
                ├── spmT_0001.nii
                ├── ...
```

└── spmT\_0005.nii

Content of the file *derivatives\_group.zip*

The subject 2 to 16 are not shown here for brevity.

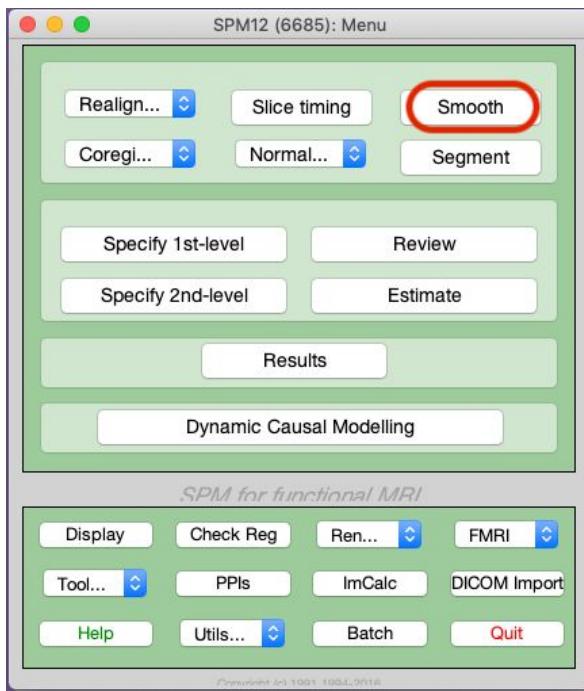
## Smooth con images

Spatial smoothing consists of applying a small blurring kernel across your image, to average part of the intensities from neighboring voxels together. The effect is to "blur" the image, the main aim is to increase your signal-to-noise ratio.

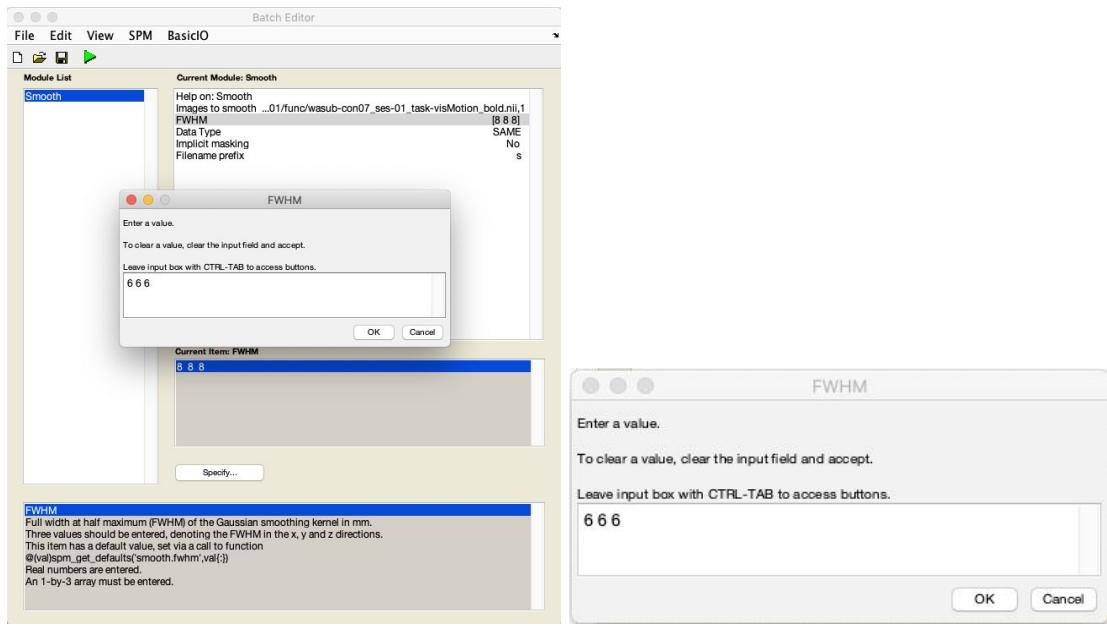
- 
- Input:
    - con images generated at the first level for each subject
      - *sub-con\*/stats/ffx\_visMotion/ffx\_6/con\_000\*.nii*
  - Output:
    - Smoothed con image files with the prefix s6
      - *sub-con\*/stats/ffx\_visMotion/ffx\_6/s6con\_000\*.nii*
- 

The smoothing procedure has to be repeated for each subject.

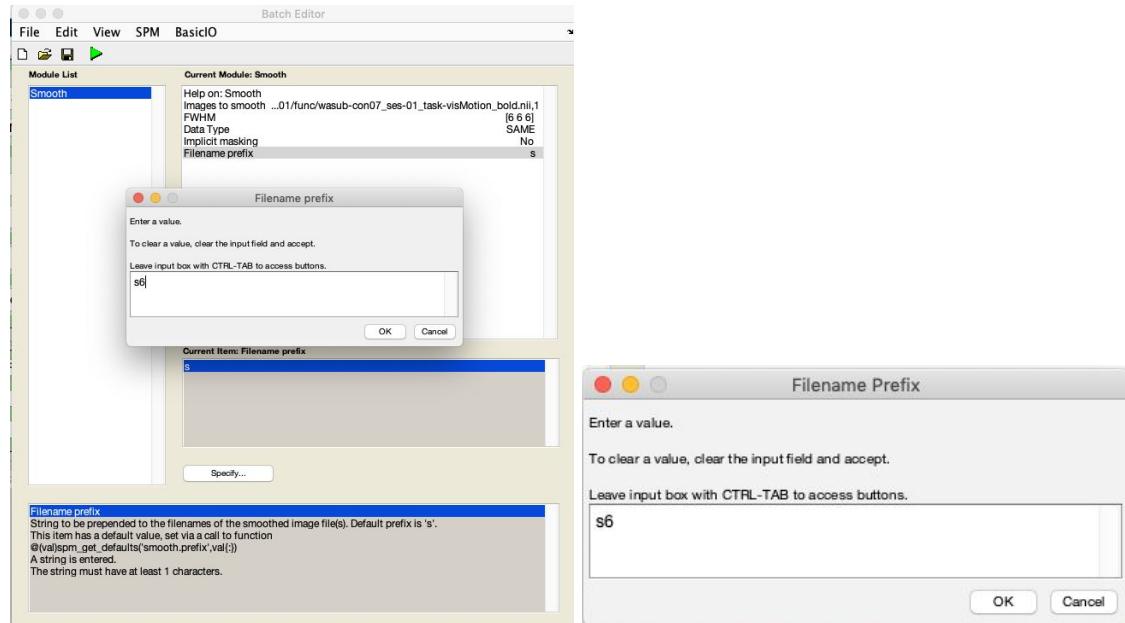
1. In the SPM window, click on *Smooth*



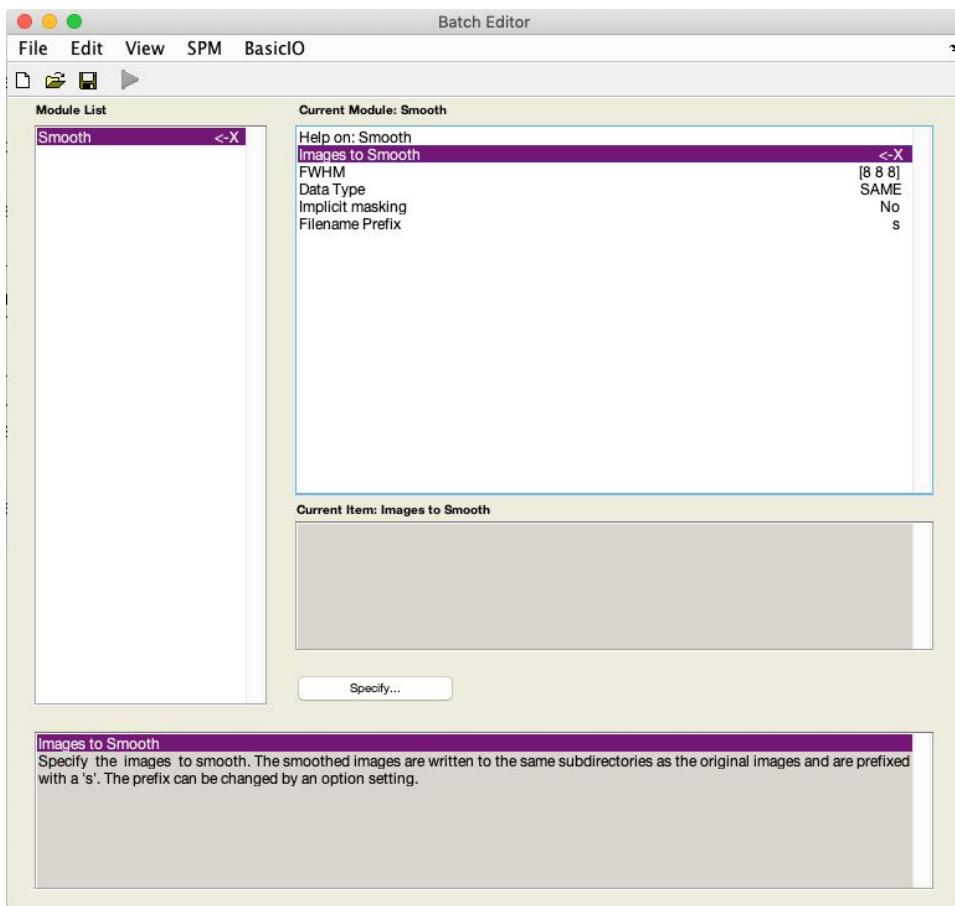
2. Choose the Full Width Half Maximum (FWHM) of gaussian smoothing kernel that you want to apply. We will apply a smoothing kernel of 6 mm. Click on *FWHM*, delete the [8 8 8](that SPM put by default) and type: [6 6 6]



- Click on *Filename prefix* and click *Specify*. Rename the prefix to *s6*. This way we will know the smoothing kernel mm applied from the name of the file.



- Click on *Images to smooth*, then in *Filter* box replace *\*.\** by *^con\*.\** to only display the image whose name start by *con*. Then go to the *stats* directory of subject 01 (*derivatives/sub-con01/stats/ffx\_visMotion/ffx\_6/*) and right click on the *con* images and choose *select all* to add all the con images of that subject to the batch.



- Repeat the number 4 for each subject so you can add all the con images of all subjects.
- Save a copy the batch with the name “batch\_smooth.mat” by clicking on *File → Save batch*.
- Run the batch by clicking “run” (the green arrow)



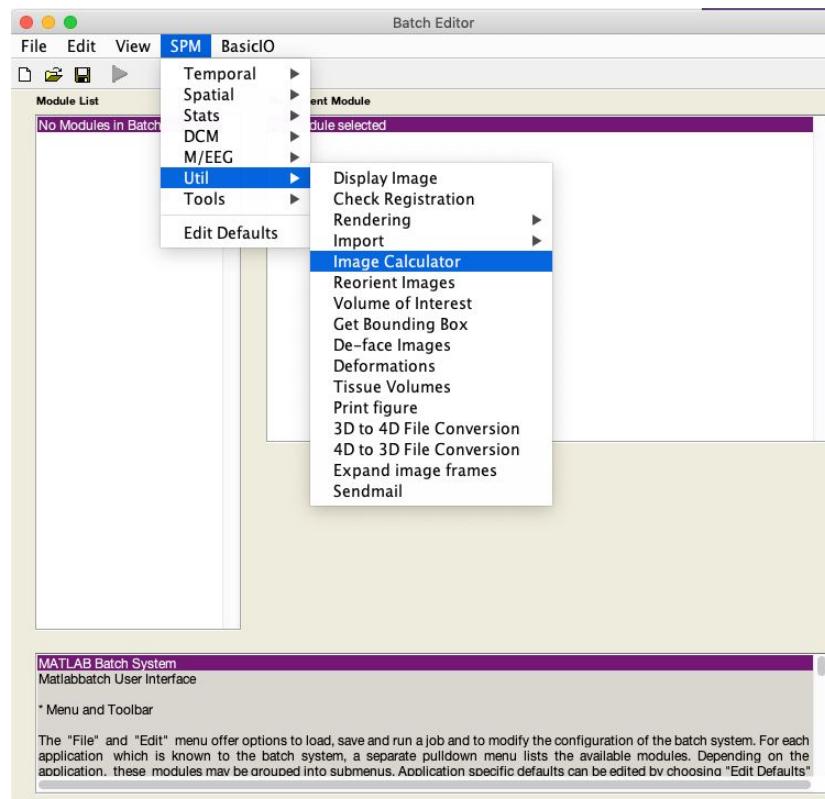
## Image calculator

Creating a mean anatomical image

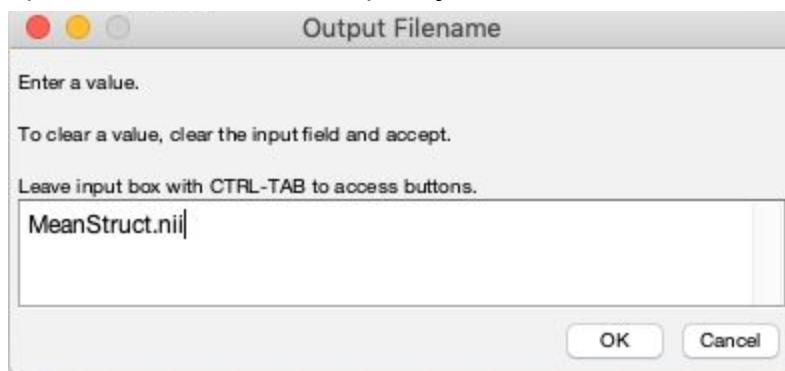
This step is to create a mean structural image across all the subjects.

- 
- Input:
    - the structural image of each subject
      - *wmsub-con\*\_ses-01\_T1w.nii*
  - Output:
    - *MeanStruct.nii*
- 

1. Create the directory:  
derivatives/RFX\_visMotion/RFX\_FunctSmooth6\_ConSmooth\_6
2. In the Batch Editor click on *SPM → Util → Image Calculator*.



3. Select *Output Filename*, click on *Specify*, write *MeanStruct.nii* and click *OK*.



4. Select *Output Directory*, click on *Specify*, select the folder: *RFX\_visMotion/RFX\_FunctSmooth6\_ConSmooth\_6* and click on the button *Done*.
5. Click on *Expression*, insert the expression below (i.e the formula for the mean of all the images) and click on *OK*.

$$(i1+i2+i3+i4+i5+i6+i7+i8+i9+i10+i11+i12+i13+i14+i15+i16+i17)/17$$

6. Select *Input Images* and press on *Specify*. Then go to the *anat* directory of each subject and select the normalized anatomical image for each of them (*wmsub-con\*\_ses-01\_T1w.nii*).

### Creating a mean mask image

This step of the batch is to create a mean mask image across all the subjects. We will use this group mask to specify in which voxel the group level analysis must be run.

- 
- Input:
    - the mask image of each subject
      - *stats/mask.nii*
  - Output:
    - *MeanMask.nii*
- 

1. Duplicate the previous module
2. In this new module, change the *Expression* to now be the one below. This will create a mask to include the voxels that have data in at least 75% of the subjects.

$$(i1+i2+i3+i4+i5+i6+i7+i8+i9+i10+i11+i12+i13+i14+i15+i16+i17)>0.75*17$$

3. Select *Output Filename*, click on *Specify*, write *MeanMask.nii* and click *OK*.
4. Select *Input Images* and press on *Specify*. Remove the normalized anatomical images and then go to the *stats* directory of each subject and select the mask image for each of them (*mask.nii*).
5. Save a copy the batch with the name “*batch\_img\_calc.mat*” by clicking on *File* → *Save batch*.
6. Click on the Run symbol.



## Factorial design

This section is to specify the design of your group level analysis. In this case it is the simplest type we can have: a design with one factor and one level per factor (also known as a one sample t-test<sup>4</sup>).

We will show how to do it for one of the contrast defined at the subject level: the VisMotion > VisStat contrast that corresponds to the con\_0003.nii for each subject.

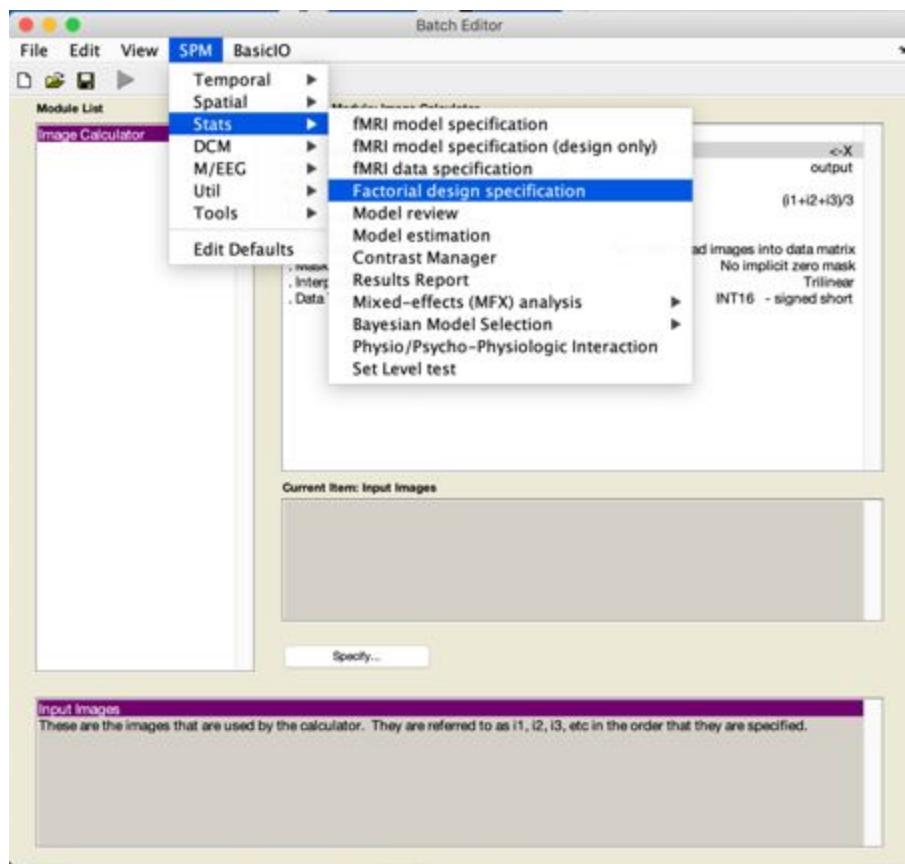
Feel free to do that with any other contrasts.

- 
- Input:
    - Smoothed con images with the prefix s6
      - *s6con\_0003.nii*
  - Output:
    - SPM.mat file that contains the design specification
- 

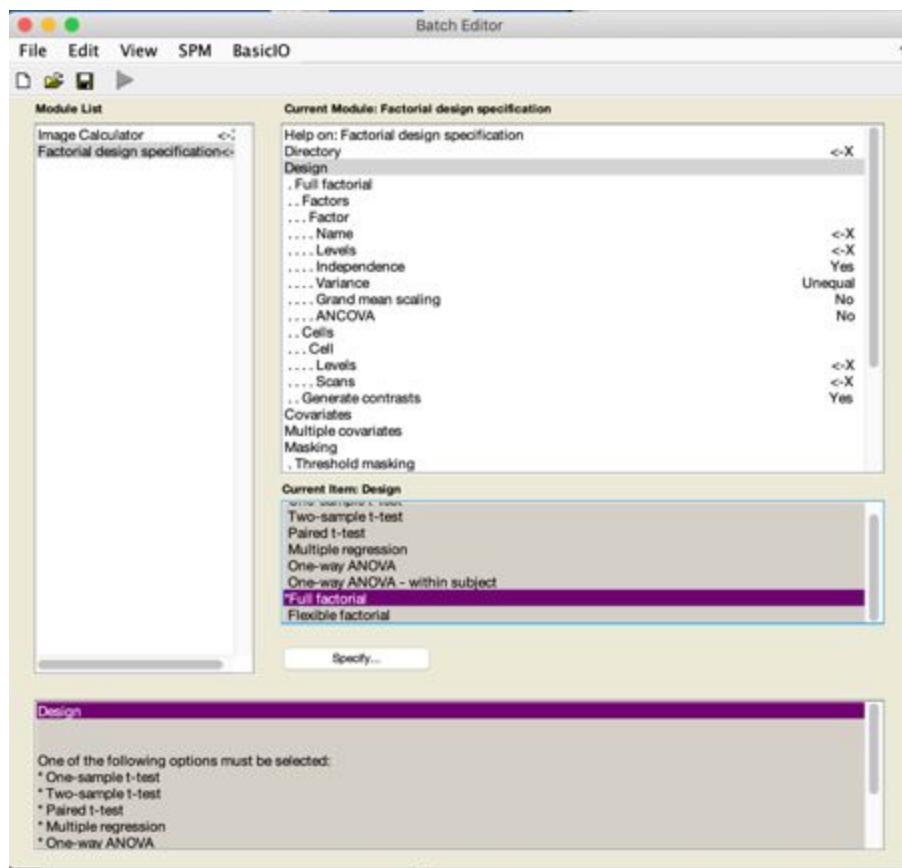
1. Create the directory:  
derivatives/RFX\_visMotion/RFX\_FunctSmooth6\_ConSmooth\_6/VisMot\_get\_VisStat
2. In the Batch Editor click on *SPM → Stats → Factorial design specification*

---

<sup>4</sup> SPM can also directly do a one and 2 samples t-test, so feel free to try it directly if you want.



3. Select the item *Directory* and select the directory `derivatives/RFX_visMotion/RFX_FunctSmooth6_ConSmooth_6/VisMot_get_VisStat` and then click on *Done*.
4. Click on the item *Design* and select *Full Factorial*



5. Under the item *Factor* you have to change the variable *Name* and *Levels*:

Help on: Factorial design specification	<-X
Directory	<-X
Design	<-X
... Full factorial	
... Factors	
... Factor	
... Name	<b>GROUP</b>
... Levels	<b>1</b>
... Independence	Yes
... Variance	Unequal
... Grand mean scaling	No
... ANCOVA	No
... Cells	
... Cell	
... Levels	<-X
... Scans	<-X
... Generate contrasts	Yes
Covariates	
Multiple covariates	
Masking	
... Threshold masking	

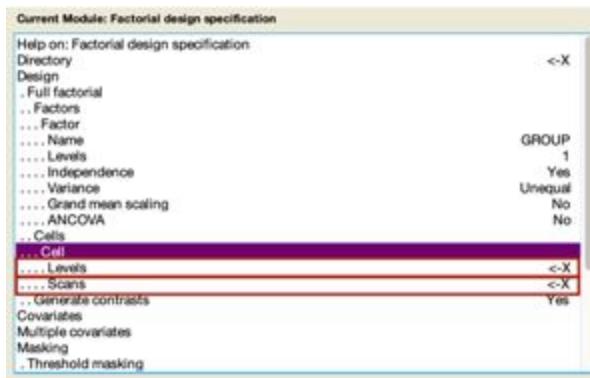
6. Select *Name*, click on *Specify* and type: *GROUP*



7. Select *Levels*, click on *Specify* and type: 1



8. Under the item *Cell* you have to change the variables *Levels* and *Scans*:



9. Select *Levels*, click on *Specify* and type: 1

10. Select *Scans*, click on *Specify* and select in the *stats* folder of each subject, the file: *s6con\_0003.nii* and click on *Done*.

11. Select the item *Explicit Mask* and click on *Specify*. Select the *MeanMask.nii* image inside the folder: *RFX\_FunctSmooth6\_ConSmooth\_6*.

**Current Module: Factorial design specification**

Help on: Factorial design specification	<-X
Directory	<-X
Design	
. Full factorial	
.. Factors	
.. Factor	
.... Name	
.... Levels	
.... Independence	
.... Variance	
.... Grand mean scaling	
.... ANCOVA	
.. Cells	
.. Cell	
.... Levels	
.... Scans	
.. Generate contrasts	
Covariates	
Multiple covariates	
Masking	
. Threshold masking	
.. None	
. Implicit Mask	
. Explicit Mask	Yes
Global calculation	
. Omit	
Global normalisation	
. Overall grand mean scaling	

**Current Item: Explicit Mask**

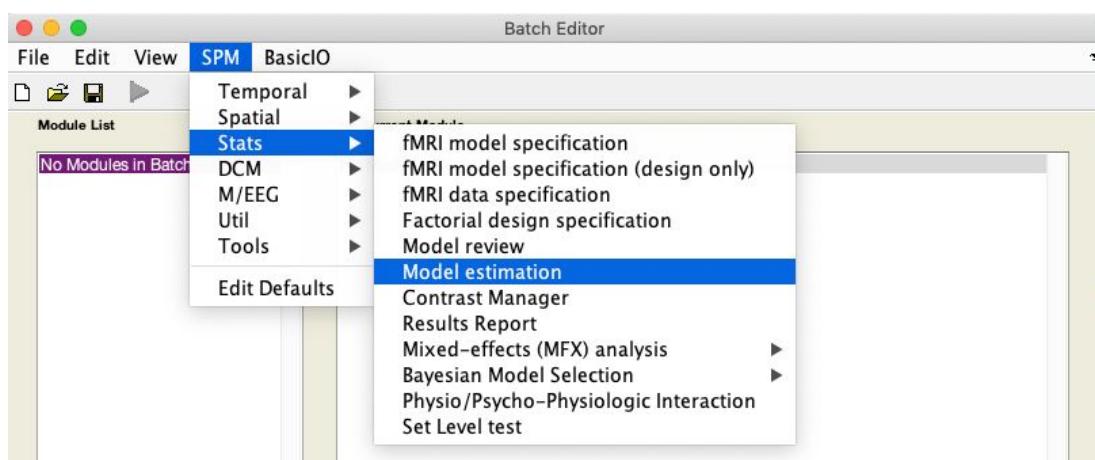
## Model estimation

---

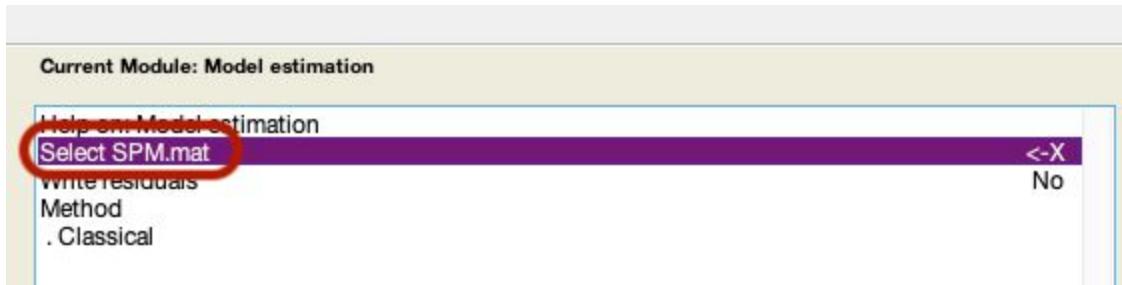
- Input:
  - *SPM.mat* from the model specification
- Output:
  - beta maps
    - *beta\_\*.nii*
  - Inclusion mask
    - *mask.nii*
  - Residual variance estimate and residuals
    - *ResMS.nii*
    - *Res\_\*.nii*
  - Estimated RESELS per voxel
    - *RPV.nii*

---

1. In the Batch Editor click on *SPM* → *Stats* → *Model Estimation*



2. Select the item *Select SPM.mat* and click on *Dependency*.



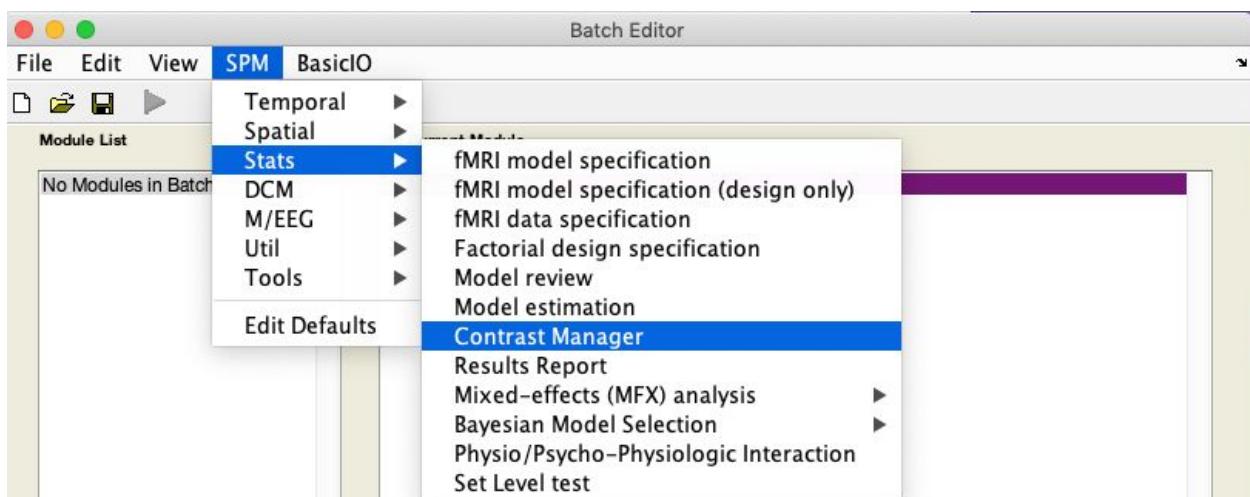
3. Select *Factorial design specification: SPM.mat* file and click on *OK*.

## Contrast manager

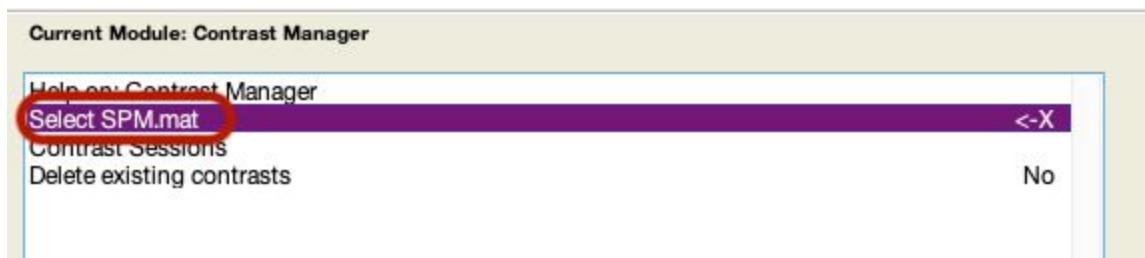
In this section you specify the statistical contrast you want to investigate. In this example, since there is only one group and one condition, the only contrast will be a t-test against zero. In case you have more than one group, you would be able to look at the contrast between conditions and/or between groups.

- 
- Input:
    - beta images for different conditions
  - Output:
    - spm t-maps
      - spmT\_\*.nii
    - spm con images
      - con\_\*.nii
- 

1. In the Batch Editor click on *SPM → Stats → Contrast Manager*



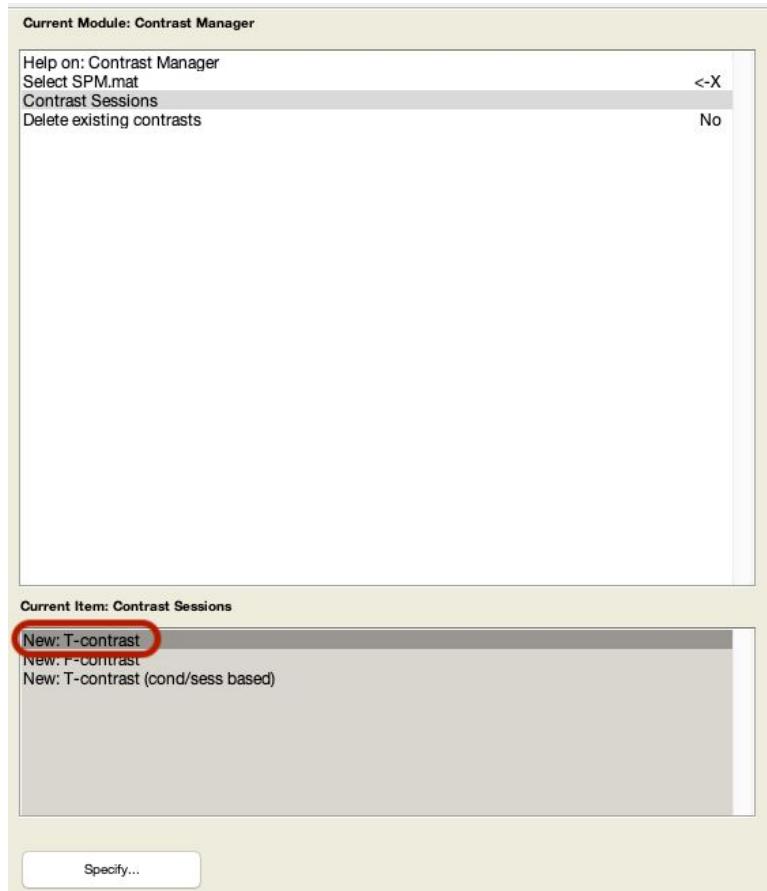
2. Select the item *Select SPM.mat* and click *Dependency*



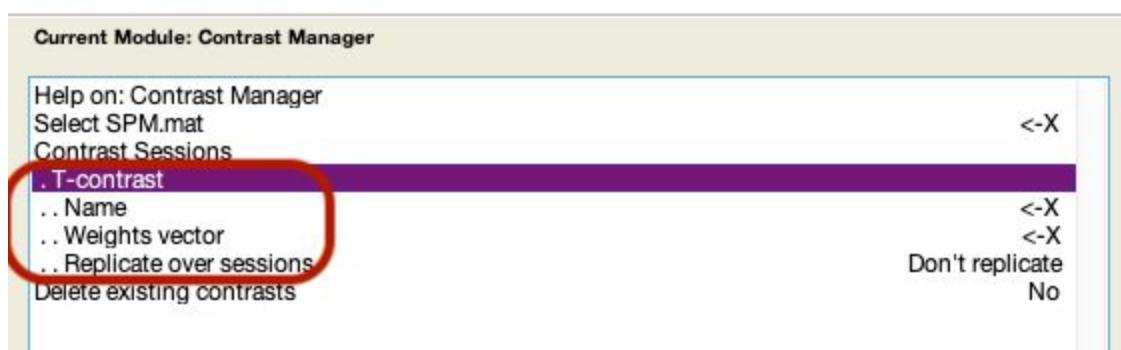
3. Select *Model estimation: SPM.mat* and click on *OK*.
4. Select the item *Contrast Sessions*



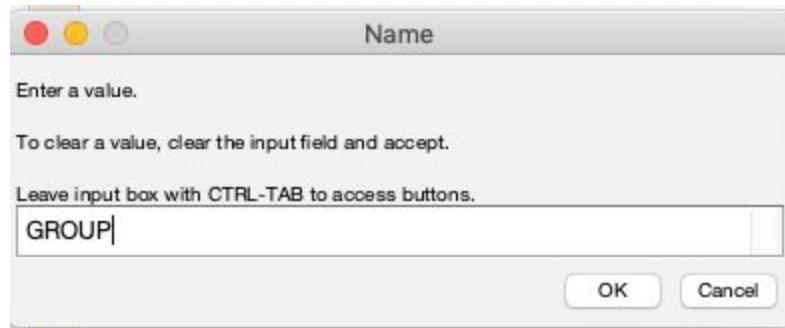
5. Some options will appear in the window below, click on *New: T-Contrast*.



6. As soon as you click some new items will appear in the list above under the item *Contrast Sessions*:



7. Select the item *Name*, click on *Specify*, assign the name *GROUP* and click *OK*:



8. Select the item *Weights vector*, click on *Specify*, assign the value *1* and click *OK*:



9. Click on the *Run* symbol on the top left corner of the Batch Editor to make the factorial design, the model estimation and the contrast manager modules to be run:



## Explore the results

### Display statistical results

10. In the SPM main window, click on Results
11. Select the SPM.mat file in the folder derivatives/RFX\_visMotion/RFX\_FunctSmooth6\_ConSmooth\_6/VisMot\_get\_VisStat and click *Done*.
12. Select the t-contrast *GROUP* and click *Done*
13. For *apply masking* select *none*
14. For *P value adjustment to control* select *FWE*. This will apply a family wise error correction to your results using random field theory.
15. Then you need to enter the voxel level threshold<sup>5</sup> when asked for *p-value (FWE)*, enter *0.05*
16. You then need to enter the cluster threshold: the minimum cluster size in voxels you are interested in. Leave it at 0 for now.

You should get the following *SPM figure window*, with a glass brain at the top left, the design matrix on the right and the contrast you are viewing above it.

---

<sup>5</sup> Also sometimes called *peak level threshold* or *cluster forming threshold*.

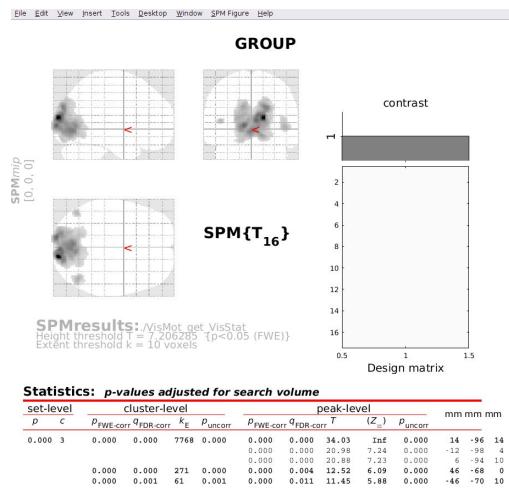
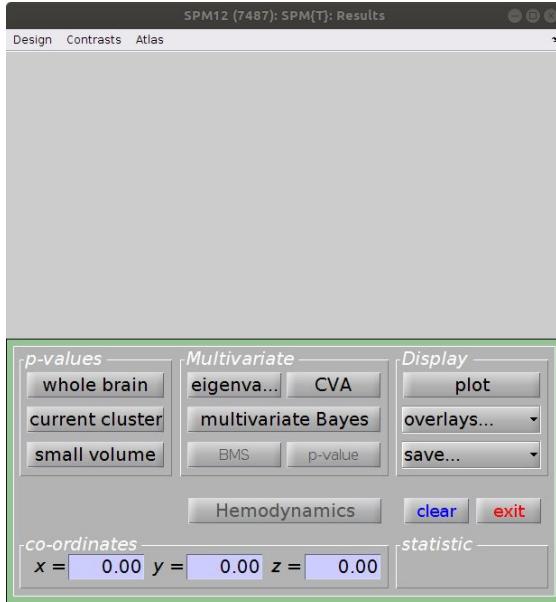


table shows 3 local maxima more than 8.0mm apart  
 Height threshold T = 7.21, p = 0.000 (FWE)  
 Extent threshold k = 10, p = 0.110 (0.006)  
 Expected voxels per cluster, <k> = 4.053  
 Expected number of clusters, <c> = 0.01  
 FWEp: 7.206, FDRp: 10.014, FWEC: 7, FDRc: 61  
 Degrees of freedom = 15.2  
 Volume = 15.2 15.0 14.8 mm mm mm; 7.6 7.5 7.4 (voxels)  
 Volume: 1513296 = 189162 voxels = 416.5 resels  
 Voxel size: 2.0 2.0 2.0 mm mm mm; (resel = 421.53 voxels)

To more comfortably explore the statistical results, let's display them in a separate window.



In the *SPM figure window*, go in the *SPM Figure* menu and then click on *Results table*, then in the *SPM results window* click on *whole brain* button to display the statistical results in the new window you have just opened.

### Display results on the average brain

We then want to view our results on the average brain image we created. In the *SPM results window*, click on *overlays...* and select *sections*. You should then select the *MeanStruct.nii* you have created.

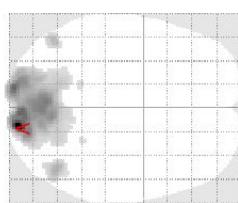
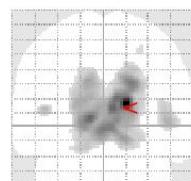
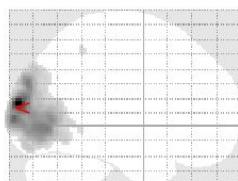
You can then navigate the results spatially either by clicking on the brain image and its overlay or by dragging the red arrow on the brain glass.

You can also use the *slices* or *montage* of the *overlays...* menu to get different visualizations.

File Edit View Insert Tools Desktop Window SPM Figure Help

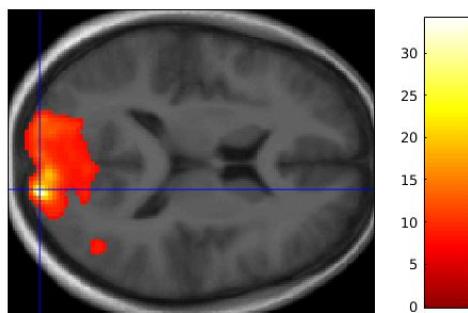
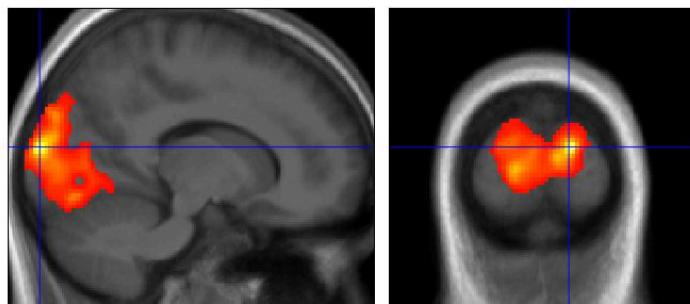
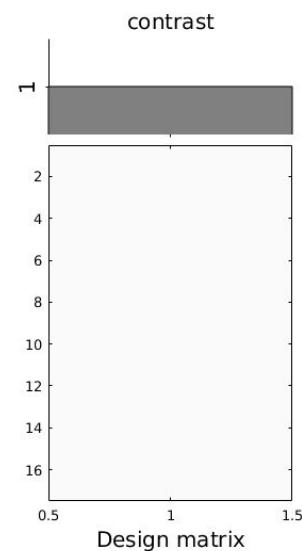
## GROUP

SPMmip  
[14, -96, 14]



SPM{T<sub>16</sub>}

SPMresults: ./VisMot gt VisStat  
Height threshold T = 7.206285 {p<0.05 (FWE)}  
Extent threshold k = 0 voxels



## Understanding the statistical results

The statistical table shows you the different significant clusters in your results with different information about each of them:

- p value
- k: number of voxels in that cluster
- FDR-corr: p value corrected for multiple comparisons using false discovery rate
- FWE-corr: p value corrected for multiple comparison using family wise error (using random field theory)

For each cluster SPM then gives you information about several (3 by default) peaks in each cluster.

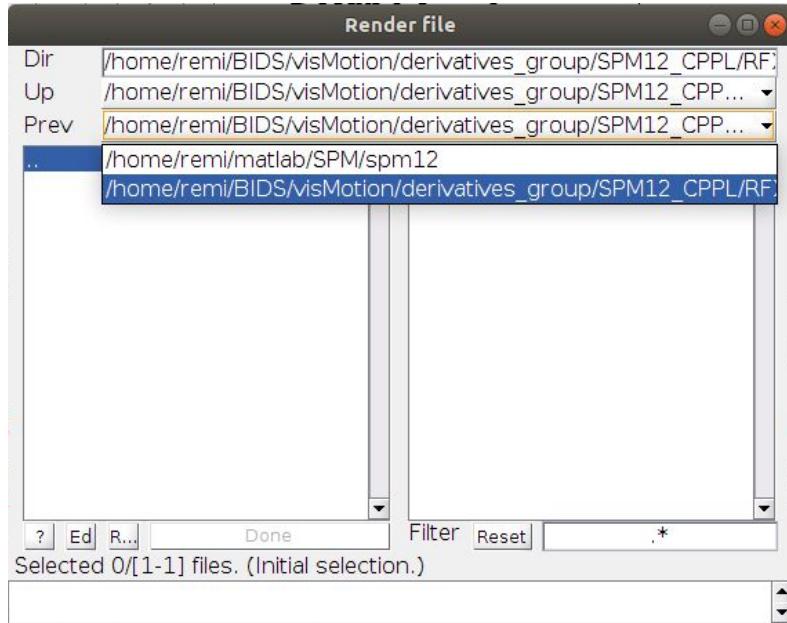
- Coordinates: x, y, z coordinates in MNI space of that voxel
- p value at that peak
- Z value at that peak
- t value at that peak
- FDR-corr: p value corrected for multiple comparisons using false discovery rate
- FWE-corr: p value corrected for multiple comparison using family wise error (using random field theory)

In the *SPM results window*, you can use the *Contrasts* menu to quickly:

- change statistical threshold
- change or create new contrasts

## Render results on a surface

SPM allows you to render results on the surface. In the *SPM results window*, click on *overlays...* and select *render*. Then go to the *canonical* folder the spm12 directory (there is a quick way to go to it by clicking in the *Prev* field in the file selection window).



Select one of the cortex giftii images (cortex\*.gii) to view the activation on the surface. You can also inflate the brain by right clicking on it.

---

#### NOTE

If you want better quality rendering and more display options, we recommend you use [bspmview](#) which also has a fairly intuitive interface.

---

Use batch to output results

In the *SPM results window*, you can also use the *save...* button to output a 3D image of your results:

- as *Thresholded SPM* for a thresholded statistical map of the results at the threshold you are currently using,
- as *Binary maps* (of all the cluster or of a single cluster) if you want to use this as a mask for an orthogonal analysis.

You can also use the batch module *SPM → Stats → Results report* to output all of those results. You will need to specify the:

1. The SPM.mat of the estimated model
  2. The contrast number (this number will correspond to the number in the name of the con image).
  3. The type of thresholding (peak and cluster level threshold, type of multiple comparison correction)
  4. Then in the *Export results*, you can select
    - a. *Figure* with different format (tiff, jpeg, png...)
    - b. *CSV* to output the results table as comma separated values that can easily be opened in excel.
    - c. *Clusters* as binary images or thresholded SPM
    - d. *NIDM* (neuroimaging data model) is very useful format that makes it super easy to upload all the results of your analysis onto neurovault.
- 

## NOTE

- You can obviously look at the results of each subject by using the same procedure as the one described above.
-

## How to script

### Creating your first script

It is usually easier to start creating batches via the graphic interface.

Many resources are available on-line to help you getting started writing your own batch with SPM, see for example [here](#).

SPM also has a *batches* folder (*spm12/batches*) that contains examples that can be interesting.

1. Open one of the batch you have created today by clicking *File → Load Batch* in the SPM batch window.
2. This time save it using *File → Save batch and script*. This will create 2 matlab .m files that you can start using to build your own scripts.
3. Open the one that ends with *\_job.m* in the matlab file editor. You should now see how the batch you have just saved is coded by matlab.
4. Add the following line at the end of this code:

```
spm_jobman('run', matlabbatch);
```

5. Click the Run button in the matlab editor and your batch should be running.

## Using the CPP pipeline

Make sure you have downloaded the latest version of the CPP lab pipeline (from [zenodo](#) or get the latest version from [github](#).

The script `batch_download_run.m` in the `demo` folder has an example of how this pipeline can be used to download data from the internet and analyze in one fell swoop.

To make sure that your previous work is not overwritten<sup>6</sup>, you can rename or create a back-up of your `derivatives` folder (maybe into something original like `derivatives_back_up`).

This codebase is designed to minimize the number of files you have to edit to adapt it to a new BIDS dataset.

The next page contains a brief overview of the content of the pipeline.

---

<sup>6</sup> The pipeline should create new files into a `SPM12_CPP` subfolder into the `derivatives` folder so in theory your previous work is fine but YNK (you never know :-)).

```
. └── batch.m
    └── demo
        ├── batch_download_run.m
        └── model-MoAE_smdl.json
    └── getopt.m
    └── getopt_template
    └── model
        └── model-visMotionLoc_smdl.json
    └── README.md
    └── spm_my_defaults.m
    └── subfun
        ├── BIDS_copyRawFolder.m
        ├── BIDS_FFX.m
        ├── BIDS_Results.m
        ├── BIDS_RFX.m
        ├── BIDS_Smoothing.m
        ├── BIDS_SpatialPrepro.m
        ├── BIDS_STC.m
        ├── checkDependencies.m
        ├── convertTsv2mat.m
        ├── getBoldFilename.m
        ├── getData.m
        ├── getFFXdir.m
        ├── getInfo.m
        ├── getPrefix.m
        ├── getSliceOrder.m
        ├── inputFileValidation.m
        ├── make4Dmaps.m
        └── NiftiTools
            └── pmCon.m
    └── test
```

## Preprocessing and subject level analysis

You should only have to change the `getOption.m` file and the `batch.m` file.

6. Open `getOption.m` in the matlab editor
7. Specify which group you want to analyze by changing the field `opt.groups`. In our dataset we only have the 'con' group. So you can have one of the following:

```
opt.groups = {'con'}; % run the pipeline on all the subjects whose identity start by con  
opt.groups = '{}'; % run the pipeline on all the groups present in this data set
```

8. Specify which subjects you want to analyze by changing the field `opt.subjects`. So you can have one of the following:

```
opt.subjects = {[7]}; % run only subject 7  
opt.subjects = {[7 8 15]}; % run only subject 7, 8, 15  
opt.subjects = {[ ]}; % run all subjects
```

9. Specify which task you want to analyze in the data set by changing the field `opt.taskName`. Our data set only has the task `visMotion`, so set the task like this:

```
opt.taskName = 'visMotion';
```

10. Specify where the data is located on your computer. It could look something like this:

```
opt.dataDir = '/home/remi/BIDS/visMotion/raw/'; % For Linux  
opt.dataDir = 'C:\Users\remi\Desktop\frmi_workshop\raw'; % For Windows  
opt.dataDir = '/Users/remi/Desktop/frmi_workshop/raw'; % For MAC
```

11. Specify where the model json file is located on your computer by changing the field `opt.model.univariate.file`. This file specifies which contrast should be

computed at the subject and group level. For this data set, the model file is directly included in the pipeline folder so you should simply have to specify:

```
opt.model.univariate.file = fullfile(pwd, 'model-visMotionLoc_smdl.json');
```

12. Now open batch.m in the matlab editor
13. The end of this file should look like this

```
% copy raw folder into derivatives folder
BIDS_copyRawFolder(opt, 1)

% preprocessing
BIDS_STC(opt);      % run the slice timing correction
BIDS_SpatialPrepro(opt); % run the realign, coregistration, segmentation,
normalization
BIDS_Smoothing(6, opt); % smooth with a gaussian kernel of 6 mm FWHM

% subject level Univariate
BIDS_FFX(1, 6, opt);           % specify and estimate the subject level model using
the data smoothed with a gaussian kernel of 6 mm FWHM
BIDS_FFX(2, 6, opt);           % specify and estimate the subject level model using
the data smoothed with a gaussian kernel of 6 mm FWHM

% The following lines are commented out (i.e they start with a "%") because we do
not want to run the group level analysis (RFX) yet.

% group level univariate
% BIDS_RFX(1, 6, 6)
% BIDS_RFX(2, 6, 6)

% BIDS_Results(6, 6, opt, 0)

% subject level multivariate
% isMVPA=1;
```

```
% BIDS_FFX(1, 6, opt, isMVPA);
% BIDS_FFX(2, 6, opt, isMVPA);
% make4Dmaps(6,opt)
```

14. Click the Run button in the matlab editor and this should start the pipeline running to do the preprocessing and the first level analysis.

## Group level analysis and exporting results

1. Open *getOption.m* in the matlab editor
2. Specify which subjects you want to analyze by changing the field *opt.subjects*. Here we want to run the group analysis by including all the subjects so you can have the following line (but feel free to pick a subset of subjects to see how it affects the final results):

```
opt.subjects = {[ ]}; % run all subjects
```

3. Specify where the data is located on your computer. It could look something like this:

```
opt.dataDir = '/home/remi/BIDS/visMotion/derivatives/'; % For Linux
opt.dataDir = 'C:\Users\remi\Desktop\frmi_workshop\derivatives'; % For Windows
opt.dataDir = '/Users/remi/Desktop/frmi_workshop/derivatives'; % For MAC
```

4. Now open *batch.m* in the matlab editor
5. We only want to run the the group level analysis and see the results so only the lines for RFX and Results should be uncommented. So the end of the *batch.m* should look like this:

```
% copy raw folder into derivatives folder
```

```
% BIDS_copyRawFolder(opt, 1)
```

```
% preprocessing  
% BIDS_STC(opt);  
% BIDS_SpatialPrepro(opt);  
% BIDS_Smoothing(6, opt);
```

```
% subject level Univariate  
% BIDS_FFX(1, 6, opt);  
% BIDS_FFX(2, 6, opt);
```

```
% group level univariate  
BIDS_RFX(1, 6, 6)  
BIDS_RFX(2, 6, 6)
```

```
BIDS_Results(6, 6, opt, 0)
```

```
% subject level multivariate  
% isMVPA=1;  
% BIDS_FFX(1, 6, opt, isMVPA);  
% BIDS_FFX(2, 6, opt, isMVPA);  
% make4Dmaps(6,opt)
```

6. Click the Run button in the matlab editor and this should start the pipeline running to do the preprocessing and the first level analysis.



# Where to find help

## Books

- Handbook of Functional MRI Data Analysis by Russell A. Poldrack, Jeanette A. Mumford and Thomas E. Nichols

What this book lacks in mathematical depth, it makes up for in breadth and conceptual clarity. It also has an unofficial companion youtube channel where Jeanette A. Mumford has a fantastic series of videos on neuroimaging analysis. The channel also has facebook group (as well as a tumblr and twitter account) if you have questions.

- Statistical Analysis of fMRI Data by F. Gregory Ashby

This one covers fewer topics, the essential actually (preprocessing, GLM, multiple comparison problem, group analysis) but goes into more details, with some maths and examples or matlab code.

## List of resources

Here is [messy list of resources](#) I (Rémi) have compiled, it needs sorting but you can find many useful links there.

## On the web

If you have question linked to a specific software, check the documentation/FAQ/manual/wiki/tutorial for that software first. Then you can turn to

the mailing list related to that software: but always start by looking through the archives of those mailing lists first before sending a question that has already been answered.

But if you have more general questions you can also try :

- the neurostars forum
- social medias: there are some specialised Facebook groups or good hashtags on twitter that will succeed when your google fu fails you.

## For SPM

There are plenty of resources for SPM but make sure you check the official ones first.

- The manual
- The mailing list
- The course/tutorial
- The wikibook

And there are some very good unofficial ones:

- [http://ernohermans.com/wp-content/uploads/2016/09/spm12\\_startersguide.pdf](http://ernohermans.com/wp-content/uploads/2016/09/spm12_startersguide.pdf)
- <https://www.youtube.com/playlist?list=PLxItDNjOWyDVMOrTs-ZRwtQSE76ULm5>
- <https://www.youtube.com/user/Shala5ha5ka>