In this PDF file, I will give you a brief explanation of the fMRI preprocessing steps, and then I'll show how you can implement these steps in batches with the SPM software package.

There are several different steps in fMRI data preprocessing which are:

- Slice Timing Correction
- Motion Correction
- Coregistration
- Normalization
- Smoothing
- Segmentation (sMRI only)

1. Slice Timing

To register a complete volume of the brain by functional magnetic resonance imaging (fMRI), a sequence of two-dimensional slices of the brain is imaged. Since the duration of taking each slice is different from the other slice, as a result, a time difference appears between the slices. The existence of this time difference causes an error in obtaining the BOLD signal of each voxel. As a result, before any analysis, the time difference between slices is removed using the time interpolation method. Correcting the timing of slices increases the accuracy of fMRI data analysis.

2. Motion Correction

When a person is placed inside the MRI machine, the person's head has slight movements due to breathing and involuntary factors. Even the smallest movement of the head leads to unwanted changes in the signal intensity of voxels and reduces the quality of fMRI data. The purpose of head motion correction is to equalize the position of the brain for all images taken from the same subject. This work is usually done by considering the average of all the images taken as a reference image and then applying the rotation and displacement of other images relative to the reference image.

3. Coregistration

   After performing the head motion correction step, which was performed only on the functional images, the next step is to align these images on the structural image. This allows us to apply transformations such as normalization that are applied only to the structural image directly to the functional images. In addition to functional information, the output of this step also contains spatial information.

4. Normalization

People's brains are different in shape and size. In order to be able to make a comparison between the brain images of different individuals, we must first map each person's brain to a standard brain model. This process is called normalization. We always need two images for normalization:

1. Template image: It is a standard image of the brain that is considered as a reference space and data is mapped to it. This standard image can be Talairach or MNI space or standard SPM space.
2. Source image: It is a high-resolution structural image that is used to calculate the transfer matrix of the source image on the template image. Then this matrix can be used to map functionally matched images with structure on the reference space.

5. Smoothing

The purpose of performing fMRI signal smoothing is to eliminate high-frequency physiological noise and increase the signal-to-noise ratio. Physiological noise affects the intensity of the fMRI signal and changes the level of brightness of the images obtained from the signal recorded by the MRI machine. The most common approach to remove this noise is to apply a 3D Gaussian filter to fMRI images. The amount of image smoothing is set according to the processing goal and by the width parameter in half of the maximum value of the Gaussian filter.

6. Segmentation

Segmentation is the process by which a brain is divided into different neurological sections according to a given template specification. In this section brain is divided into three main parts: gray matter, white matter, and cerebrospinal fluid.

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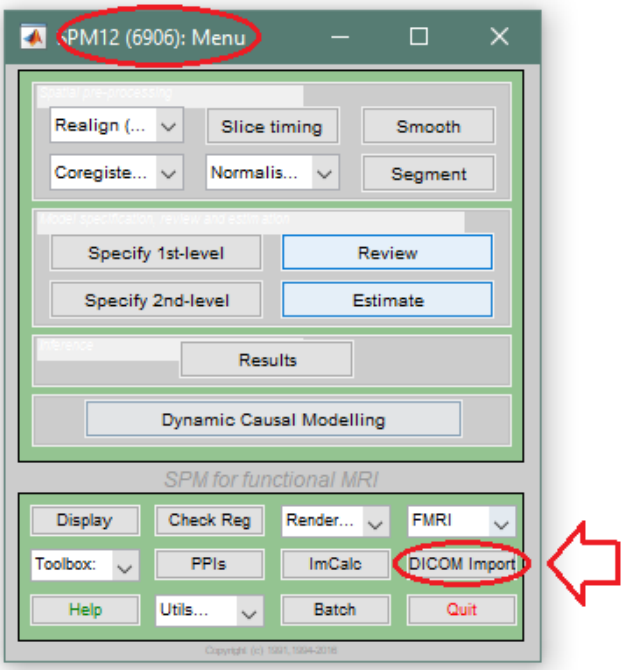
## Preprocessing Steps

Alright, let’s start from beginning :)
usually, the raw fMRI data received from the database are in DICOM format (*.dcm, *.ima for Siemens machine). For scientific analysis of fMRI data, we convert these DICOM files to NIFTY file format.

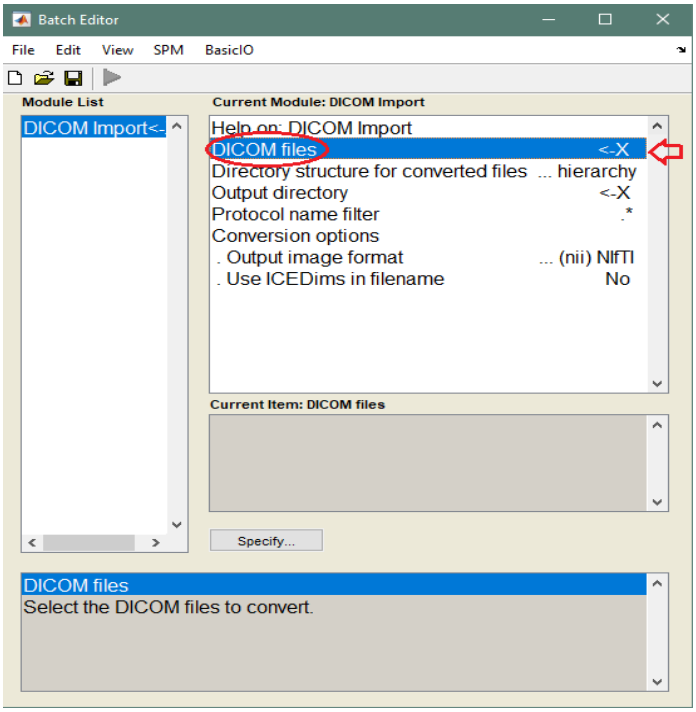
- Convert DICOM to NIFTY

  After Installing the SPM toolbox in MATLAB, open the MATLAB and then type in the Command Window Environment “spm fmri”.

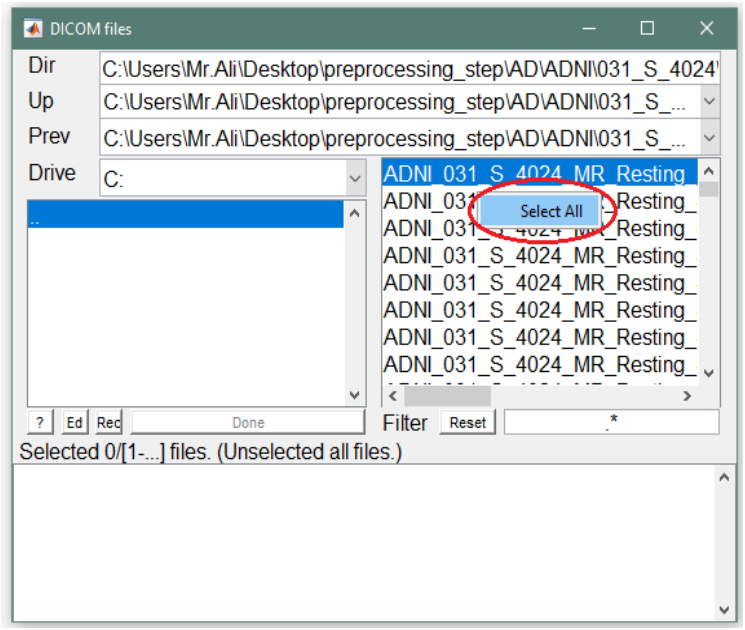
In the SPM Menu window select “DICOM Import”

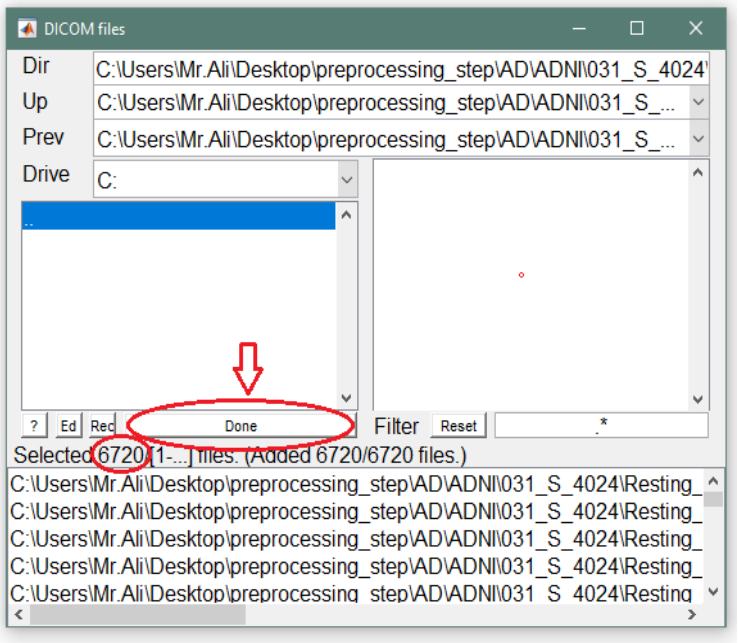


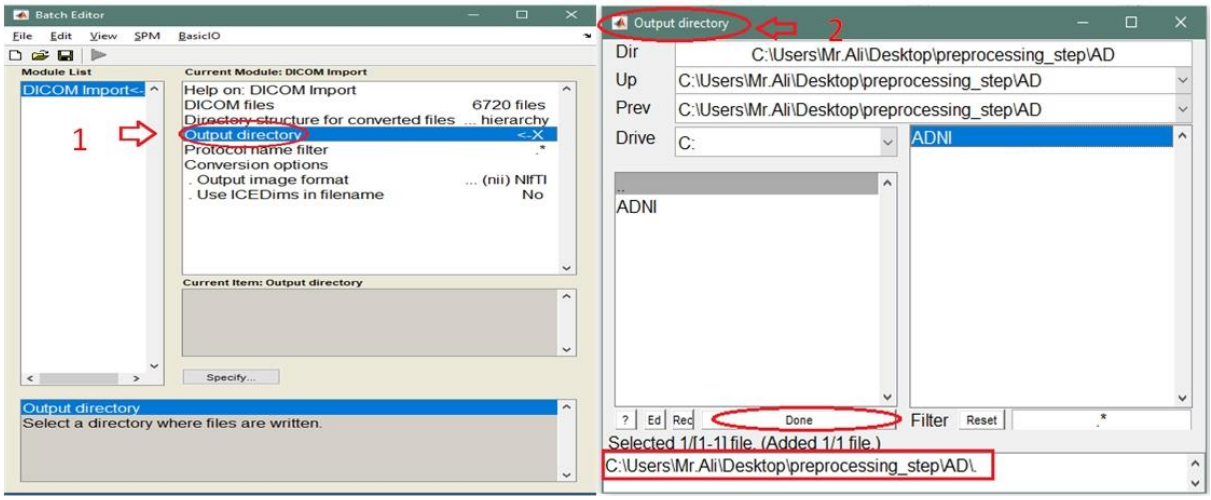

After clicking DICOM Import, the Batch Editor window will open up. In the right hand side, you can see actually DICOM files that ask you to specify DICOM files.



Go to the directory of fMRI (EPI) data files and then click the right button and select all DICOM data files then you have selected all fMRI data. Click the done button and be ready for specifying the output directory. After specifying the output directory you can click the Run button click and data files are converted to the nifty file.




Batch Editor
File Edit View SPM BasicIO
Module List
DICOM Import<-
Current Module: DICOM Import
Help on: DICOM Import
DICOM files 6720 files
Directory structure for converted files ... hierarchy
Output directory <-X
Protocol name filter .*
Conversion options
. Output image format ... (nii) NIfTI
. Use ICEDims in filename No
1
Current Item: Output directory
Specify...
Output directory
Select a directory where files are written.
Output directory
2
Dir C:\Users\Mr.Ali\Desktop\preprocessing_step\AD
Up C:\Users\Mr.Ali\Desktop\preprocessing_step\AD
Prev C:\Users\Mr.Ali\Desktop\preprocessing_step\AD
Drive C:
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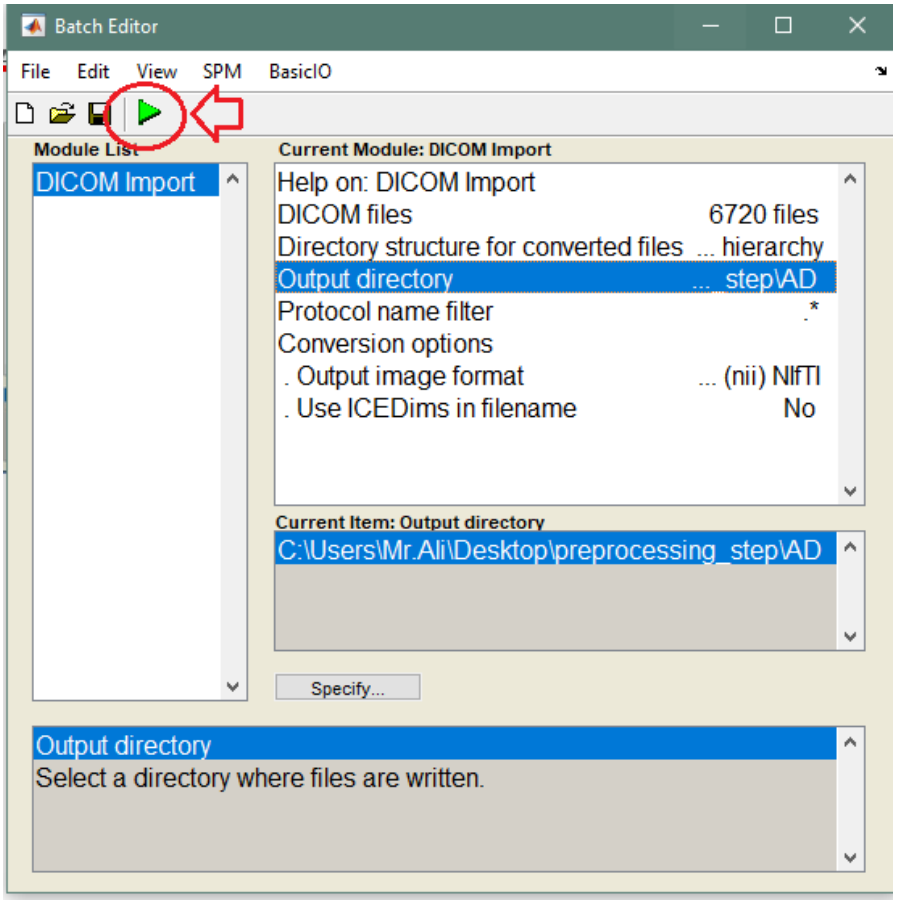
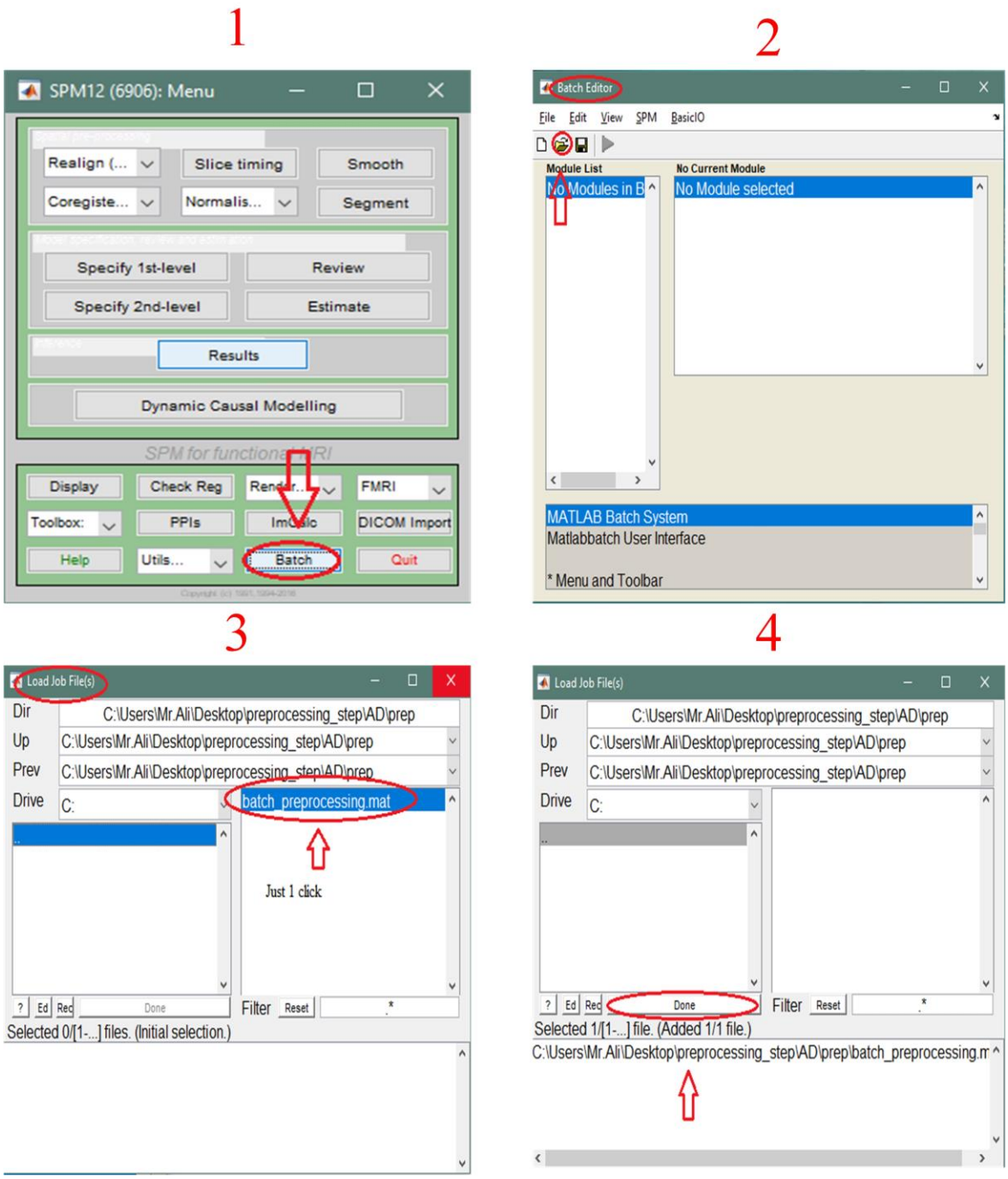
Selected 1/1-1 file. (Added 1/1 file.)
C:\Users\Mr.Ali\Desktop\preprocessing_step\AD\


Batch Editor
File Edit View SPM BasicIO
Module List
DICOM Import
Current Module: DICOM Import
Help on: DICOM Import
DICOM files 6720 files
Directory structure for converted files ... hierarchy
Output directory ... step\AD
Protocol name filter .*
Conversion options
. Output image format ... (nii) NIfTI
. Use ICEDims in filename No
Current Item: Output directory
C:\Users\Mr.Ali\Desktop\preprocessing_step\AD
Specify...
Output directory
Select a directory where files are written.

# Batch Preprocessing

In this section I've already prepared the "batch_preprocessing.mat" file for you and what you should do is now open this file and set up some configuration. Let's dive in…

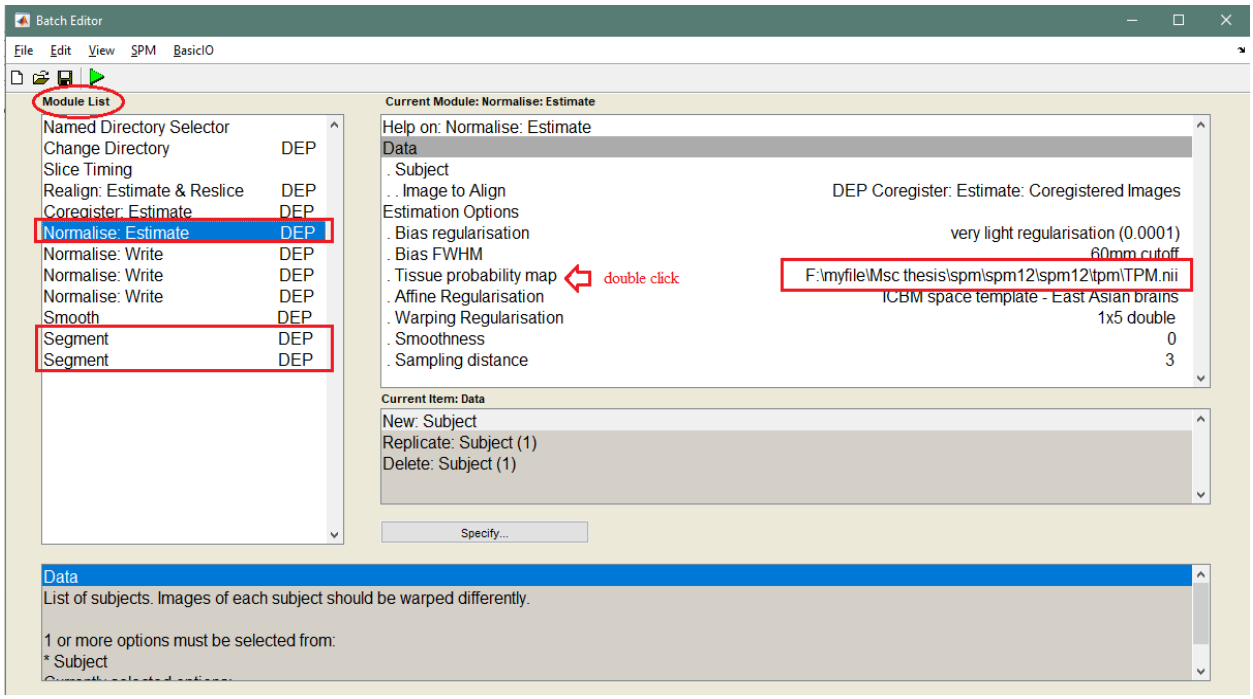
## 1. First step: open up the "batch_preprocessing" file



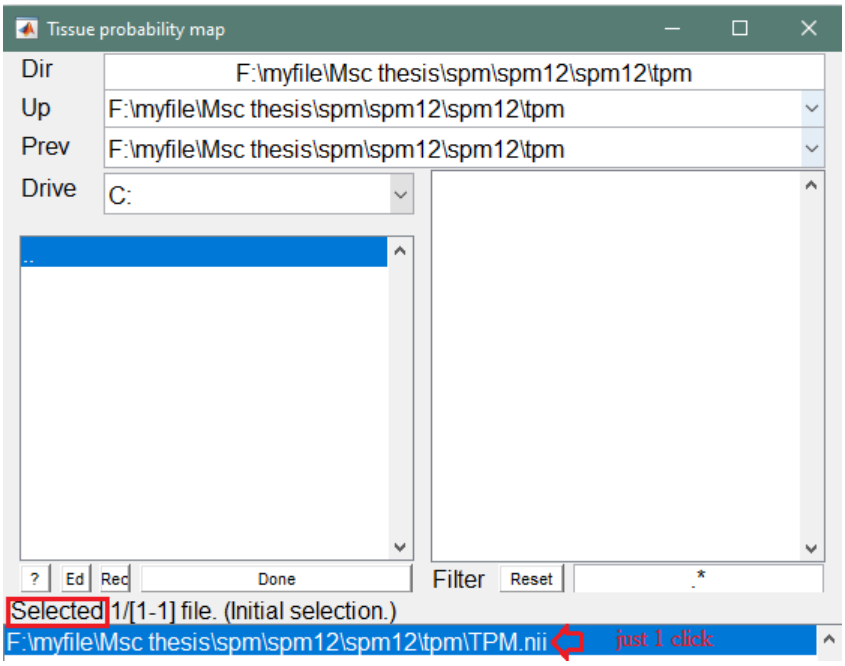
## 2. Second step: modify some settings

When you load the “batch_preprocessing” file, on the left-hand side of the batch editor windows you can see a module list that you need to modify only three modules of them (Normalise: Estimate and two segment modules). First of all, you must change the directory of the “Tissue probability map” in the module “Normalise: Estimate” because the file path is different between computers and the current directory is for my PC, not yours.
For modifying this directory just double click on the “Tissue probability map” and then unselect the current directory(by just one click on the directory in the section Selected), afterward you should set up a new directory for “Tissue probability map”, go to the SPM folder on your computer and then the tmp folder and select the “TPM.nii”.

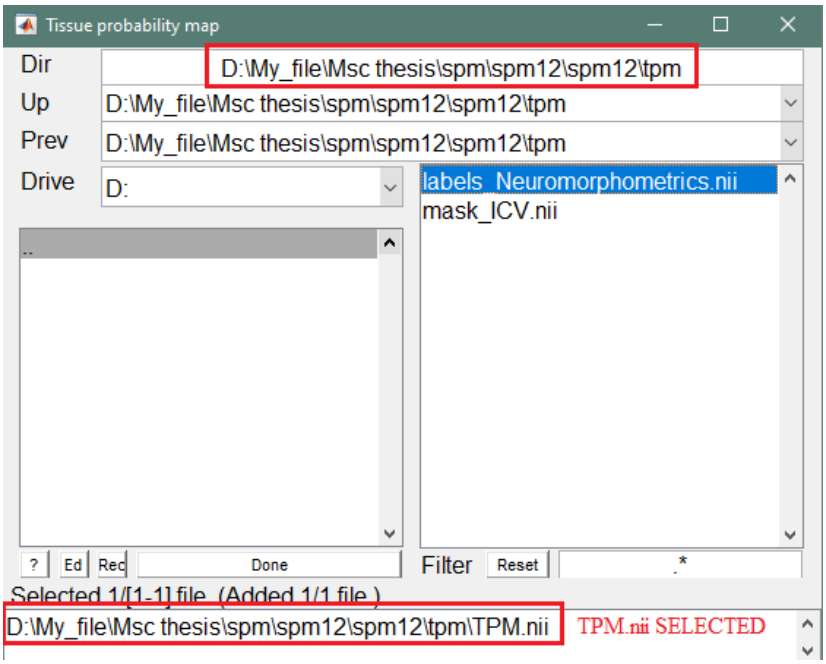
- Modify the directory of the “Tissue probability map” (Normalise: Estimate)



- Delete current the “TPM.nii” directory (just by one click).



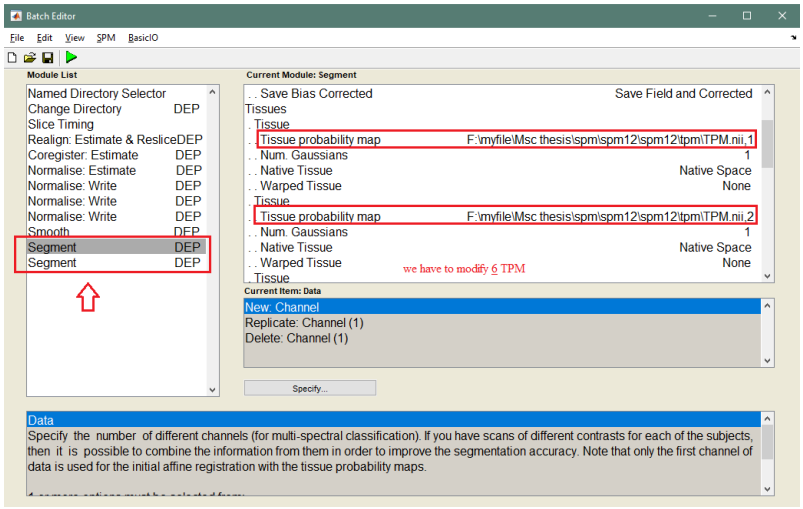

- Select the “TPM.nii” from SPM toolbox directory.



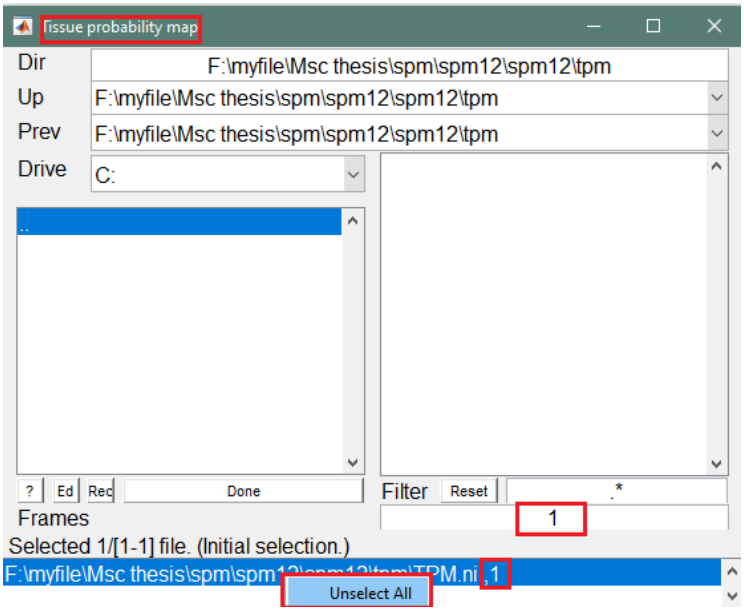
- Modify file path for TPM in the section “Segment”

  In this section we need to modify 6 “Tissue probability map”

  - TPM.nii,1
  - TPM.nii,2
  - TPM.nii,3
  - TPM.nii,4
  - TPM.nii,5
  - TPM.nii,6

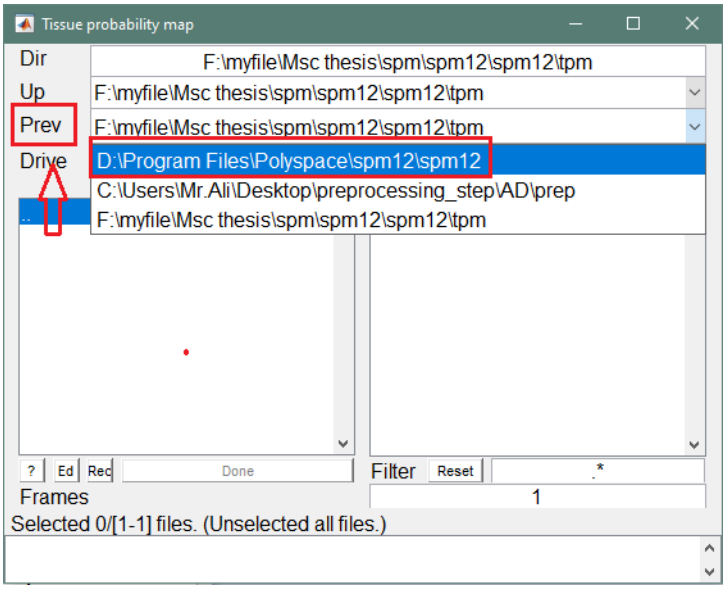



- Unselect TPM.nii,1



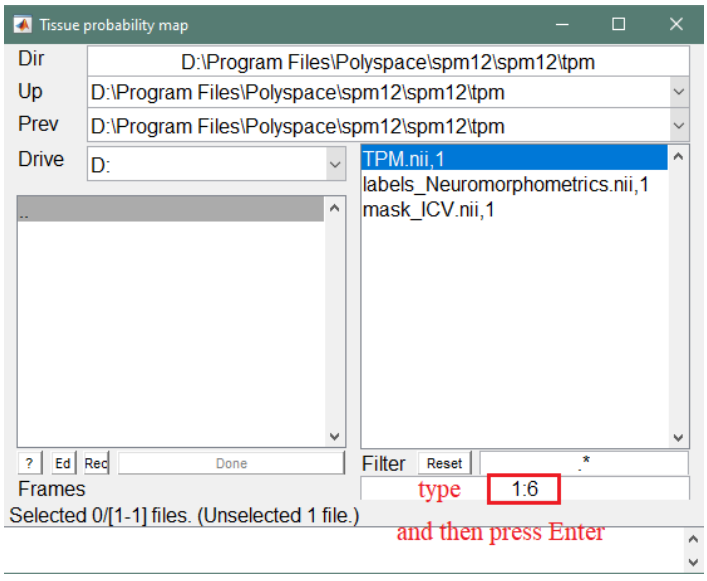
- Select directory of the “TPM.nii,1, TPM.nii,2, TPM.nii,3, TPM.nii,4, TPM.nii,5, TPM.nii,6”

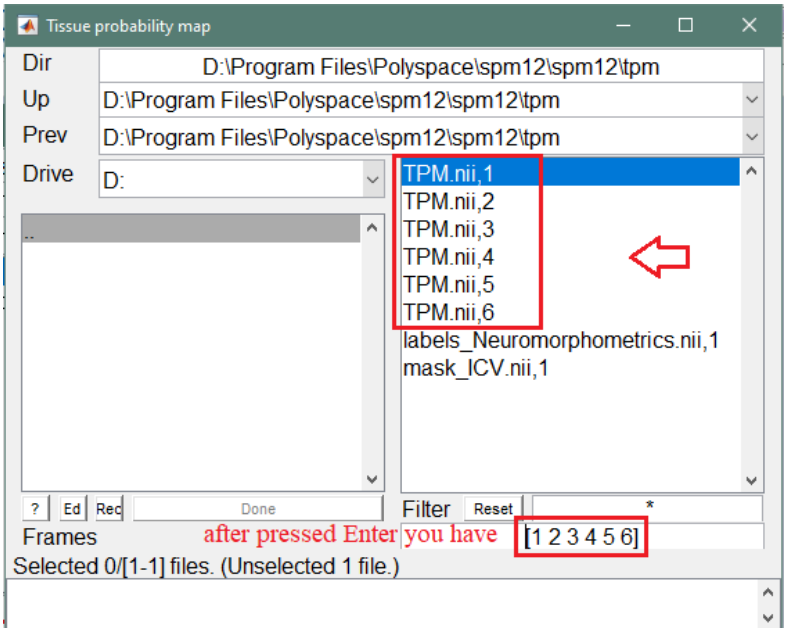
  For convenience select the “Prev” section and navigate to the “tpm” path on your computer.



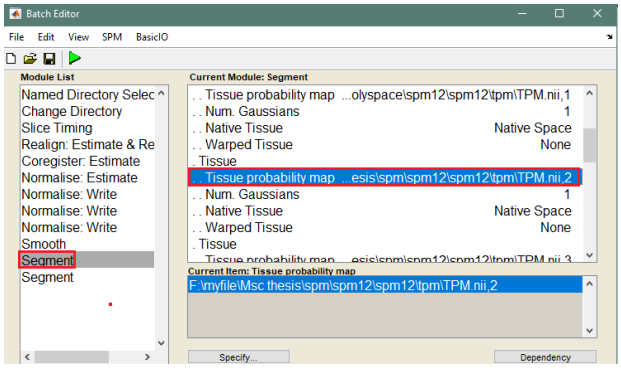

**Note**: In this section we should expand the “TPM.nii” to six TPM.nii part (TPM.nii,1 is gray matter map, TPM.nii,1 is white matter map and so on)

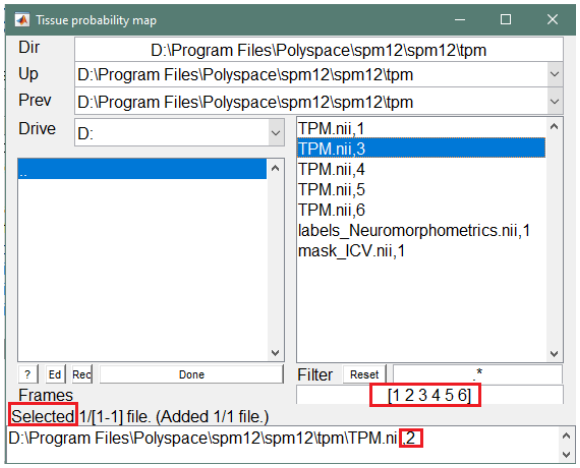
For do this pay attention to the figures below.



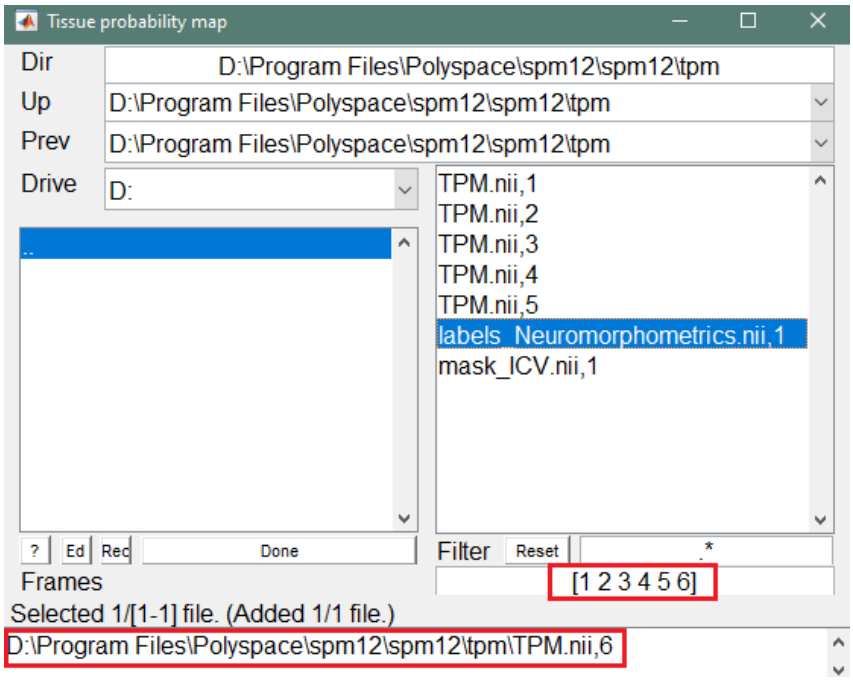



For the first "Tissue probability map" select TPM.nii,1 and for the second "Tissue probability map" select TPM.nii,2 and so on.

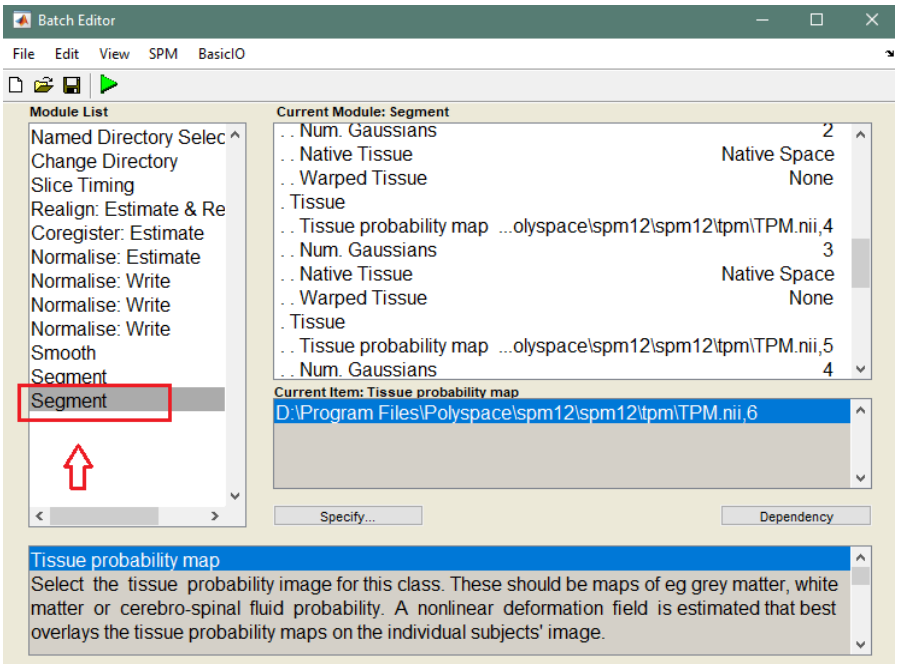


For the sixth “Tissue probability map” TPM.nii,6 is selected



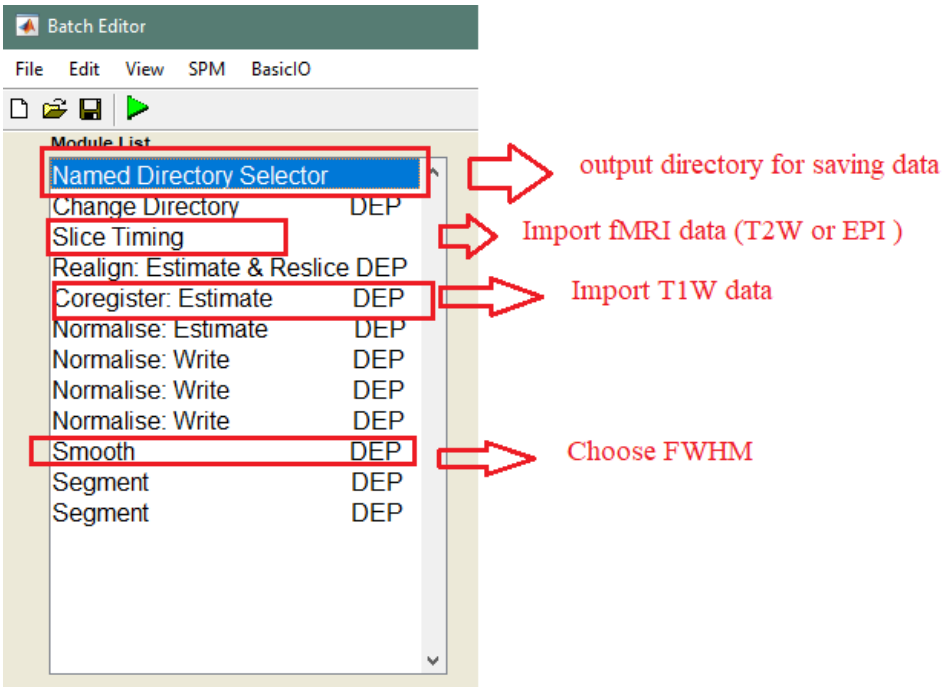

- Do the same thing for the second “Segment” part:



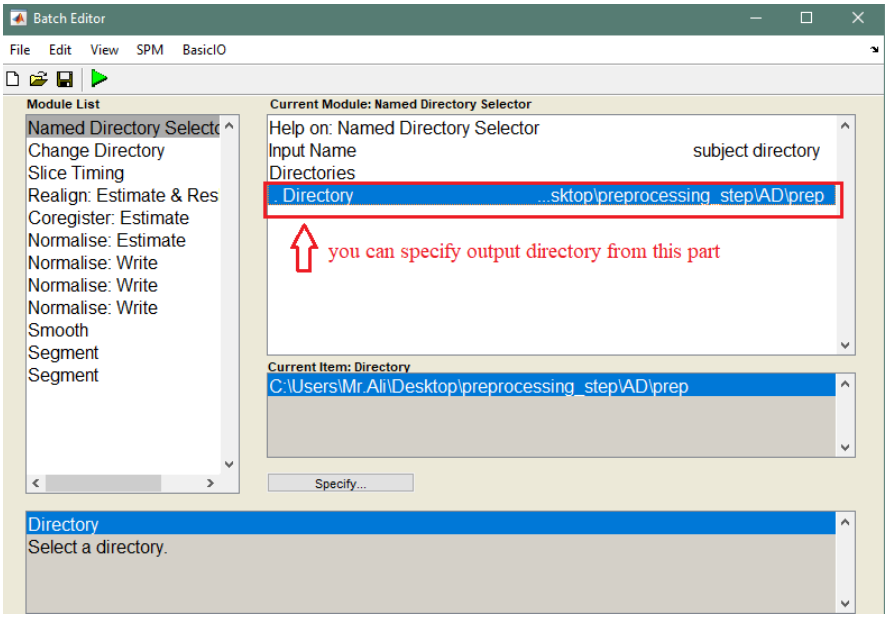

**Note:** After modifying these sections please save the “batch_preprocessing” file.

## 3. Import Date to the “batch_prerocessing” File

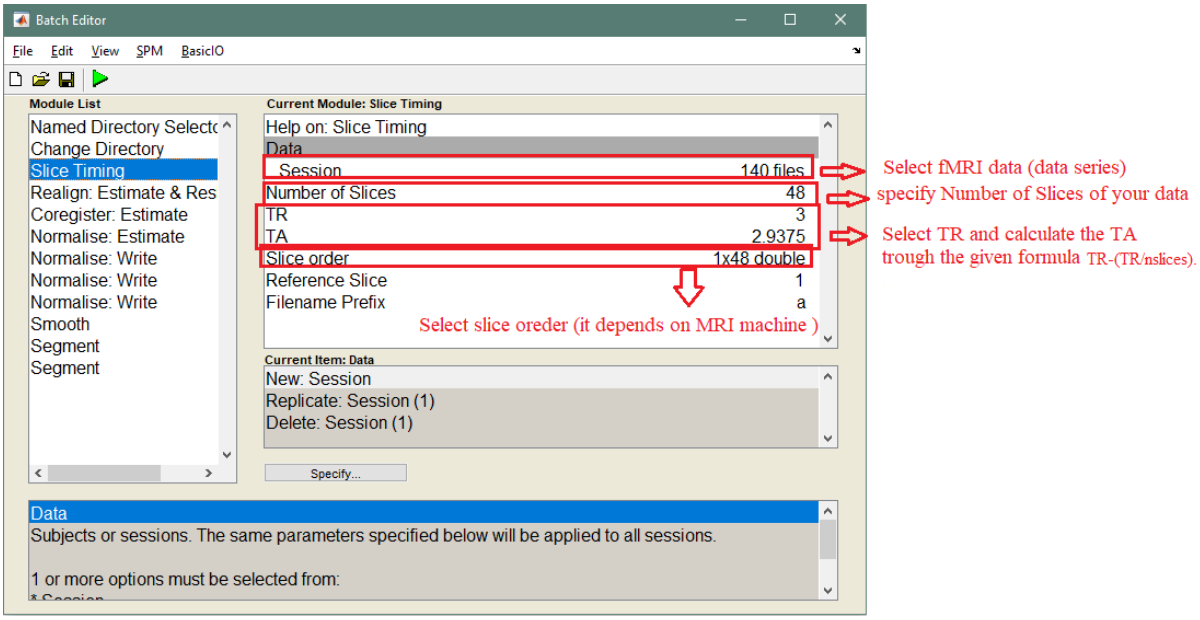
In this section you should import your fMRI data



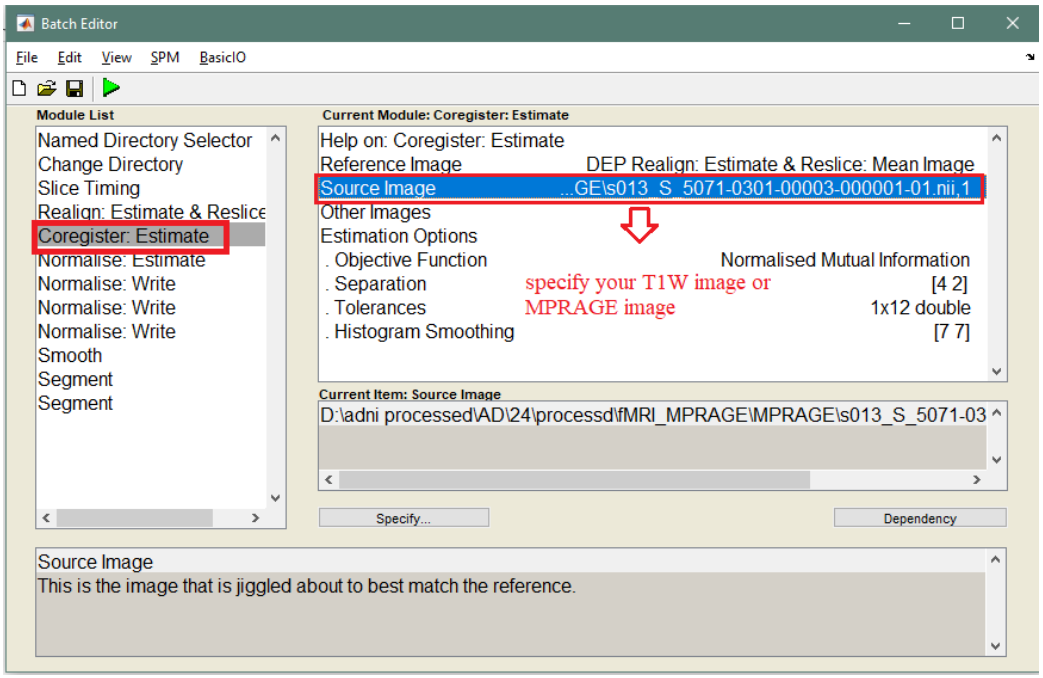

- Modify Named Directory Selector



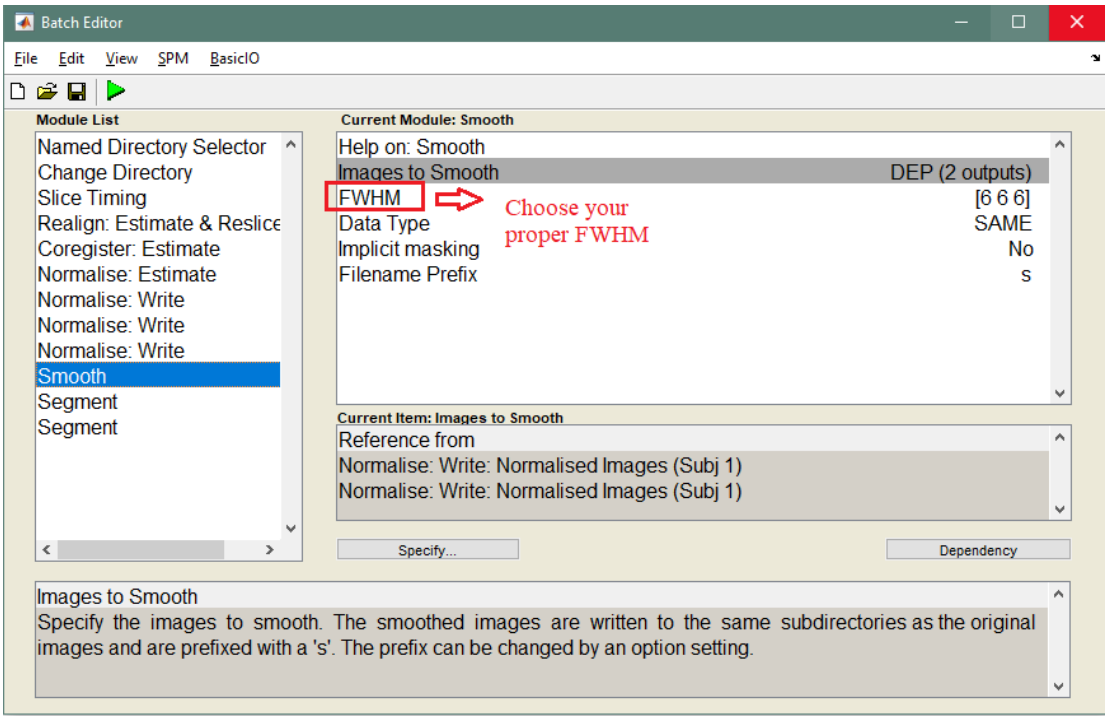
- Modify Slice Timing




- Modify Coregister: Estimate (select MPRAGE image or T1W)



- Modify Smooth section




Finally press the Run button :)