

Pre-processing of FDG-PET images

The software used in this procedure are Matlab and SPM 12 (make sure you know where the images and other batches are in the computer).

a) Importing the DICOMs

The DICOMs of the FDG-PET image will need to be grouped in order to create a unique image for the patient. Then the created image will need to be comparable to the controls and/or other patients.

1) In Matlab, type "spm pet" in the command window after the ">>", then "enter".

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Currer	it Folder	۲	Command Window
	Name 🔺		fx >> spm pet
	PT00000.dcm	^	
	PT000001.dcm		
	PT00002.dcm		
	PT000003.dcm		
	PT000004.dcm		
	PT00005.dcm		

2) SPM 12 opens: click on "DICOM import" in the Menu window.





3) In the batch that opens, indicate the DICOM files you want to group (all included in the patient folder). To do so, click on the option "DICOM files", and then "Specify"

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Batch Editor		
File Edit View SPM BasicIO		
Module List	Current Module: DICOM Import	
DICOM Import <-X	Help.or: DICCM Import DICOM Tiles Dictory structure for converted files Output directory Protocol name filter Conversion options . Output image format . Use ICEDIms in filename	No directory hierarchy <x Single file (nii) NITT No</x
DICOM files Select the DICOM files to convert.	Current Item: DICOM Filee	
		×

4) Another window opens: you will have to specify the folder that contains the DICOM files (it will have to be in "Dir") that indicates the current folder). To specify the new path, you can use different techniques, explained in the next point

	A files — 🗆	×
Dir <	C:\Users\Arianna\Desktop\FDG_PET_WORKSHOP	\rightarrow
Up	C:\Users\Arianna\Desktop\FDG_PET_WORKSHOP	\sim
Prev	C:\Users\Arianna\Desktop\FDG_PET_WORKSHOP	\sim
Drive	C:NORMA_BATCH.mat	^
COFFE hbp-d0 mricror ? Ed Selected	EE_BREAK_FDGPET-main 000052_FDG-PET-in-HC-and Red	~
		~



5) Use the following drop-down lists to move through folders:

- a. ("Up") permits to go to the parent folders
- b. *Prev* permits to see the previously opened folders (not useful if you just opened Matlab, but very useful later: you'll save time!)

Use the left panel to open folders contained by your current folder (Dir). By clicking on one of its element (e.g. Results), you will open the folder (here, Results). CLICK JUST ONCE!

The two points in this left panel (...) permit to go to the parent folder.

The right panel indicates the files contained in the current folder. If you click on it, it will be considered as the selected file.

	A files —	×
Dir	C:\Users\Arianna\Desktop\FDG_PET_WORKSHOP	
⊲up	C:\Users\Arianna\Desktop\FDG_PET_WORKSHOP	~
Prev	C:\Users\Arianna\Desktop\FDG_PET_WORKSHOP	>
Drive	C: VORMA_BATCH.mat	^
COFFE hbp-d0 mricron	STAT_BATCH.mat Template_PET_Report.docx	< >



6) When you have found the folder containing the DICOM files, click with the mouse right button on one of the DICOMs (right panel), and click on "select all".

• 💽 DICOM files	-	□ ×
Dir	C:\Users\Arianna\Desktop\FDG_PET_WORKSHOP\hbp-d000052_FDG-PET-in-HC-and-DoC\data\patients_images_dicom_fully_anonymized\FDGPET_PATIE	NT1
Up	C:\Users\Arianna\Desktop\FDG_PET_WORKSHOP\hbp-d000052_FDG-PET-in-HC-and-DoC\data\patients_images_dicom_fully_anonymized\FDGPET_PATIENT	1 ~
Prev	C:Users'Arianna\Desktop'FDG_PET_WORKSHOP'hbp-d000052_FDG-PET-in_HC-and-DoC\data\patients_images_dicom_fully_anonymized\FDGPET_PATIENT	1 ~
Drive	C: PT00000.dcm PT000002.dcm PT000002.dcm PT000003.dcm PT000005.dcm PT000005.dcm PT000006.dcm PT000006.dcm PT000006.dcm PT000008.dcm PT000008.dcm PT000008.dcm PT000008.dcm	~
Selected 0/[1] files.	(Initial selection.)	

7) The DICOMs disappear from the right panel and appear in the lower panel (Selected files). You should have around 90 files. Click on "Done". If you did a mistake and want to unselect files, click on them in the selected files panel (you can also unselect all at once by right clicking on one of them and then choosing "unselect all")





8) Back to the batch, do the same procedure for "Output directory" (in which folder you want Matlab to create the new image). Click or "Output directory" and then "Specify"

Batch Editor		- 🗆 X
File Edit View SPM BasicIO		۲
Module List	Current Module: DICOM Import	
DICOM Import <-X	Help on: DICOM Import DICOM files Directory structure for converted files Output directory Protocol name filter Conversion options . Output image format . Use ICEDims in filename	89 files No directory hierarchy <-X .* Single file (nii) NIfTI No
	Current Hami Outent directory	×
~	Specify	Ŷ
Output directory Select a directory where files are writt	en.	^

9) In the new window, indicate the target folder, by using "Prev", and then click on the single point in the right panel. The path will appear in the lower panel, and make "done" available. Click on "Done".

Output directory		-		×
Dir	C:\Users\Arianna\Desktop\FDG_PET_WORKSHOP\hbp-d000052_FDG-PET-in-HC-and-DoC\data\patients_images_dicom_fully_anonymized\FDGPET_	PATIE	NT1	
Up	C:\Users\Arianna\Desktop\FDG_PET_WORKSHOP\bbp_d000052_EDG_PET_in HC_and_DoC\data\patients_images_dicom_fully_anonymized\FDGPET_f	PATIEN	IT1 Y	-
Prev <	Culsers/Arianna/Desktop/FDG_PET_WORKSHOP/hbp-d000052_FDG-PE7-In-hC-and-DoC/data/patients_images_dicom_fully_anonymized/FDGPET_I	PATIEN	T1 ->	>
Drive			^	•
? Ed Selected 0/[1-1] files.	Rec Done Filter Reset .*			



10) When you're back on the batch editor, click on "run" (the green "play" sign, on the left upper part of the editor).

Batch Editor				×
File Edit View SPM BasicIO				2
	Current Module: DICOM Import			
DICOM Import	Help on: DICOM Import DICOM files Directory structure for converted files Output directoryimages_dicom_fully_anonymize Protocol name filter Conversion options . Output image format . Use ICEDims in filename Current Item: Output directory C:\Users\Arianna\Desktop\FDG_PET_WORKSHOP\hbp-d000052_Ff	89 fi No directory hierar edIFDGPET_PATIEI Single file (nii) N	les chy \T1 .* JIFTI No DoC\d	
Select a directory where mes are written	ι. 			~

11) When it's done, Matlab will write "done" in the main command window.





3) <u>Reorienting the image</u>

1) When the DICOMs are imported, you need to reorient the new image (the name begins with an "s"). On the Menu window, click on "Display".



2) A window will appear to indicate which image you want to display. Using Prev choose the folder of the patient, and choose the created image (beginning with "s") by clicking on it. It appears in the lower panel, and make "done" available. Click or "Done"





- 3) A new window appears, displaying the image. To reorient the image (in order to make it comparable to the ones of the controls), indicate the change you want in radians (positive and negative numbers can be used, depending on the direction of the change you need):
 - a. Pitch is related to the upper right image
 - b. Roll is related to the upper left image
 - c. Yaw is related to the lower image





4) A correctly reoriented brain looks like put down on a table (frontal and occipital parts, not including the cerebellum) in the "pitch" part (see the red line). The "roll" and "yaw" have to be symmetric (see the green lines). When the image is correctly reoriented, you can move throughout the brain with the mouse to check that the brain is really symmetric.





5) When correctly reoriented, click on the anterior commissure with the mouse, to indicate that the origin is there (the cross should be on the anterior commissure), and click on "Set origin' (lower part of the window), and then 'Reorient' do not matter if the cross moved after your click on "set origin"



- 6) In the new window, select the current image to reorient (SPM should directly propose the correct image), and click on "done".
- 7) When done and back to the displayed image, you can click on "origin" (just below the images) to check that the reorientation and origin were correctly saved.



4) Normalisation and smoothing

1) On the Menu window, click on (batch".)



- In the batch, use "File-Load batch" or the "open folder" icon to load the "norma batch" (find the file, with the same procedure described above - you just have to click on "norma batch" – you can only select ONE file).
- 3) When opened, change the path of "source image": click of "source image" and when it is in blue, click or "specify". Delete the previously selected image by clicking on it (lower panel), and then choose the new one (same procedure than for DICOM import, but you only indicate the "s" image here). Do exactly the same for the "images to write". Make sure that "template image" is correctly pathed (change the path if needed, same procedure)





4) Check that in the smooth module (left panel), the 'images to smooth' are correctly taken from the first module (Normalised). To be sure, click or 'images to smooth' and then on dependency'. Save the batch clicking on the save icon (top left). Then click on the run button (green play icon). When done, Matlab command window indicates "done".

Module List	Current Module: Smooth
Old Normainse, Estimate & Write Smooth DEP	Help on: Smooth DEP Normalise: Estimate & Write: Normalised Imagee (Subj 1) FWHM [14 14 14] Data Type SAME Implicit masking No Filename Prefix S
	Current Item: Images to Smooth Reference from Normalise: Estimate & Write: Normalised Images (Subj 1)
* Images to Smooth Specify the images to smooth. The smooth	Specify Dependency thed images are written to the same subdirectories as the original images and are prefixed with a 's'. The prefix can be

You should now have a "sws" image in your DICOM folder: it is reoriented, normalised and smoothed.