

SPM VBM pipeline

1. Introduction

Voxel-based morphometry (VBM) is a neuroimaging analysis technique that allows investigation of focal differences in brain anatomy. In our lab, we use two software (FSL, SPM) to do the VBM. According to our experience, the SPM software has a better GM (gray matter) segmentation result than FSL. When we do the VBM, we need to create a customized template and register all T1 images to this template. For the FSL, the default option is to create a symmetric template. However, for the SPM, we can create a symmetric template or an asymmetric template. I suggest to use asymmetric template because we get weird results with symmetric template.

2. VBM Pipeline

2.1. Asymmetric template (Christian pipeline

<http://www.neuro.uni-jena.de/cat12/CAT12-Manual.pdf>)

Besides SPM, we use CAT12 toolbox, which is based on SPM12, to do some modules. In addition, we follow the CAT12 manual to do the VBM and give an explanation of these steps.

1) Segment Data

Module:

SPM→Tools→CAT12→CAT12: Segment Data

Parameters:

Help on: CAT12: Segmentation		
Volumes		<-X
Split job into separate processes		40
Options for initial SPM12 affine registration		
. Tissue Probability Map	.../spm12/tpm/TPM.nii	
. Gaussians per class	1x6 double	
. Bias regularisation	...regularisation (0.001)	
. Bias FWHM	60mm cutoff	
. Warping Regularisation	1x5 double	
. Affine Regularisation	...ate - European brains	
. Sampling distance	3	
Extended options for CAT12 segmentation		
. Affine Preprocessing (APP)		light
. Use SANLM de-noising filter	SANLM denoising	
. Strength of Noise Corrections		0.75
. Strength of Local Adaptive Segmentation		0.5
. Strength of Skull-Stripping		0.5
. Strength of Final Clean Up		0.5
. Strength of WMH Correction		0.5
. WM Hyperintensity Correction (WMHC)	...r spatial normalization	
. Spatial normalization Template	..._1_IXI555_MNI152.nii	
. Internal resampling for preprocessing		
. . Best native resolution		[1 0.1]
. Voxel size for normalized images		1.5
. Ignore errors		Yes

Writing options	
. Surface and thickness estimation	No
. Grey matter	
. . Native space	No
. . Normalized	No
. . Modulated normalized	...linear (SPM12 default)
. . DARTEL export	No
. White matter	
. . Native space	No
. . Normalized	No
. . Modulated normalized	...linear (SPM12 default)
. . DARTEL export	No
. Cerebro-Spinal Fluid (CSF)	
. . Native space	No
. . Normalized	No
. . Modulated normalized	No
. . DARTEL export	No
. White matter hyperintensities (WMH)	
. . Native space	No
. . Normalized	No
. . Modulated normalized	No
. . DARTEL export	No
. PVE label image	
. . Native space	No
. . Normalized	No
. . DARTEL export	No
. Bias, noise and intensity corrected T1 image	
. . Native space	No
. . Normalized	Yes
. . DARTEL export	No
. Jacobian determinant	
. . Normalized	No
. Deformation Fields	No

The above are the parameters for the segmentation module.

We only need to change the writing options:

Writing options:

Grey matter

Modulated normalized→No

DARTEL export→affine

White matter

Modulated normalized→No

DARTEL export→affine

Input:

SUB_ID.nii (0002.nii)

Output:

rp1*-affine.nii (rp1 grey matter) rp2*-affine.nii (rp2 white matter)

Explanation:

At first, this module does initial spm12 affine registration from native space to the spm12/tpm/TPM.nii. Then, it uses Template_1_IXI555_MNI152.nii as a template to do spatial normalization and get affine results in DARTEL space.

2) Create DARTEL template

Module:

SPM→Tools→Dartel Tools→Run DARTEL (create Templates)

Parameters:

Help on: Run Dartel (create Templates)		
Images		<-X
Settings		
. Template basename		Template
. Regularisation Form		Linear Elastic Energy
. Outer Iterations		
. . Outer Iteration		
. . . Inner Iterations		3
. . . Reg params		[4 2 1e-06]
. . . Time Steps		1
. . . Smoothing Parameter		16
. . Outer Iteration		
. . . Inner Iterations		3
. . . Reg params		[2 1 1e-06]
. . . Time Steps		1
. . . Smoothing Parameter		8
. . Outer Iteration		
. . . Inner Iterations		3
. . . Reg params		[1 0.5 1e-06]
. . . Time Steps		2
. . . Smoothing Parameter		4
. . Outer Iteration		
. . . Inner Iterations		3
. . . Reg params		[0.5 0.25 1e-06]
. . . Time Steps		4
. . . Smoothing Parameter		2
. . Outer Iteration		
. . . Inner Iterations		3
. . . Reg params		[0.25 0.125 1e-06]
. . . Time Steps		16
. . . Smoothing Parameter		1
. . Outer Iteration		
. . . Inner Iterations		3
. . . Reg params		[0.25 0.125 1e-06]
. . . Time Steps		64
. . . Smoothing Parameter		0.5
. Optimisation Settings		
. . LM Regularisation		0.01
. . Cycles		3
. . Iterations		3

Images→select two times “new: images”

Images→select the “rp1*-affine.nii” files

Images→select the “rp2*-affine.nii” files

Input:

rp1*-affine.nii (rp1 grey matter) rp2*-affine.nii (rp2 white matter)

Output:

Template_0.nii ~ Template_6.nii u_*.nii

Explanation:

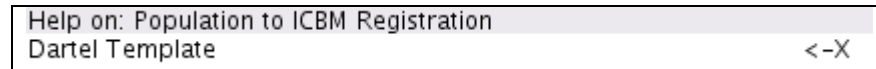
This step runs multiple iterations to create a group specific template, note that this template is slightly off from SPM TPM.nii

3) Population to ICBM

Module:

SPM→Tools→Dartel Tools→Run DARTEL (Population to ICBM Registration)

Parameters:



Dartel Template → select the final created template with the ending “_6”

Input:

Template_6.nii (The final customized dartel template)

Output:

y_*2mni.nii (Deformation field)

Explanation:

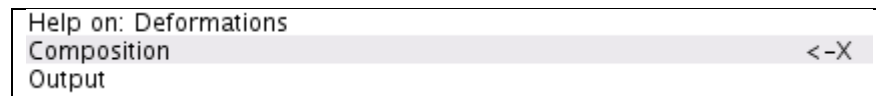
This step nonlinear maps the final Template_6.nii to XXXX and create the deformation field.

4) Apply the deformation

Module:

SPM→Util→Deformations

Parameters:



Composition→“New: Deformation Field”

Deformation Field→select the “y_*2mni.nii” file from step above.

Output→“New:Pushforward”

Apply to→select all “Template” files with the ending “_0” to “_6”.

Output destination→Output directory→select directory for saving files

Field of View→Image Defined→select final “Template” file with ending “_6”

Preserve→Preserve Concentrations (no “modulation”)

Input:

y_*2mni.nii (Deformation field), Template_0.nii ~ Template_6.nii.

Output:

wTemplate_0.nii~wTemplate_6.nii (template in MNI ICBM space)

Explanation:

This step applies the deformation field to all templates and get templates in MNI ICBM space.

5) Segment Data again

Module:

SPM→Tools→CAT12→CAT12: Segment Data

Parameters:

Help on: CAT12: Segmentation	
Volumes	<-X
Split job into separate processes	40
Options for initial SPM12 affine registration	
. Tissue Probability Map	.../spm12/tpm/TPM.nii
. Gaussians per class	1x6 double
. Bias regularisation	...regularisation (0.001)
. Bias FWHM	60mm cutoff
. Warping Regularisation	1x5 double
. Affine Regularisation	...ate - European brains
. Sampling distance	3
Extended options for CAT12 segmentation	
. Affine Preprocessing (APP)	light
. Use SANLM de-noising filter	SANLM denoising
. Strength of Noise Corrections	0.75
. Strength of Local Adaptive Segmentation	0.5
. Strength of Skull-Stripping	0.5
. Strength of Final Clean Up	0.5
. Strength of WMH Correction	0.5
. WM Hyperintensity Correction (WMHC)	...r spatial normalization
. Spatial normalization Template	..._1_IXI555_MNI152.nii
. Internal resampling for preprocessing	
. . Best native resolution	[1 0.1]
. Voxel size for normalized images	1.5
. Ignore errors	Yes
Writing options	
. Surface and thickness estimation	No
. Grey matter	
. . Native space	No
. . Normalized	No
. . Modulated normalized	...linear (SPM12 default)
. . DARTEL export	No
. White matter	
. . Native space	No
. . Normalized	No
. . Modulated normalized	...linear (SPM12 default)
. . DARTEL export	No
. Cerebro-Spinal Fluid (CSF)	
. . Native space	No
. . Normalized	No
. . Modulated normalized	No
. . DARTEL export	No
. White matter hyperintensities (WMH)	
. . Native space	No
. . Normalized	No
. . Modulated normalized	No
. . DARTEL export	No
. PVE label image	
. . Native space	No
. . Normalized	No
. . DARTEL export	No
. Bias, noise and intensity corrected T1 image	
. . Native space	No
. . Normalized	Yes
. . DARTEL export	No
. Jacobian determinant	
. . Normalized	No
. Deformation Fields	No

Volumes<-X → Select the original T1 images like in the first module “segment data”.

Extended Options for CAT12 segmentation → “Spatial normalization Template” →
Select normalized DARTEL Template “wTemplate*_1.nii”

For all other options use the same setting as in the first module, or modify.

Writing Options

Grey matter

Modulated normalized → affine + nonlinear (SPM12 default)

White matter

Modulated normalized → affine + nonlinear (SPM12 default)

Input:

SUB_ID.nii (0002.nii)

Output:

mwp1*.nii (modulated, wrapped images)

Explanation:

This step applies the customized template “wTemplate*_1.nii” to do spatial normalization and generate the modulated wrapped images. If you use affine+nonlinear to get m* files, you need to regress out the ICV effect.

If you use nonlinear to get m0* files, you don’t need to regress out ICV.

2.2. Asymmetric template (John pipeline)

<http://www.fil.ion.ucl.ac.uk/~john/misc/VBMclass10.pdf>

This pipeline only use SPM12 to do VBM and it’s an old pipeline which is not suggested. According to my experience, if we use CAT toolbox, some images may fail due to BadTissueContrast or other errors. But John pipeline is unlikely to have failed images, so if you want to preserve all images, you can use this pipeline.

2.3. Symmetric template (Kurth pipeline)

www.neuro.uni-jena.de/pdf-files/Kurth-NP15.pdf)

This pipeline will create a symmetric customized template instead of asymmetric template that we used above. However, we got weird results when we applied it to ADNI1 dataset. Therefore, I suggest to use 2.1 pipeline, you can also follow the guide in Kurth paper if you must use a symmetric template.