# Adding a subject to the template data set

This is a step-by-step procedure for adding a subject to the template data set. The creation of the template is an automatic procedure which, for each subject, takes as input the DICOM PATHs and returns the data completely processed (i.e., straightened, registed to the template space and vertebrae aligned). However, it is inevitable to add for each subject small adjustements (see below).

## I- At the end what should have I done?

### 1- Files that need to be created

At the end, here are the files that you shall have created for one subject :

-‘crop.txt’ : a .txt file that will inform the pipeline where to crop the data

-‘centerline\_propseg\_RPI.nii.gz’ : a label nifti image (binary) to help propseg generating the segmentation of the spinalcord

-‘labels\_vertebral.nii.gz’ : a label nifti image that will inform the pipeline where are located 2 specific points of the brainstem and the vertebral corps (from C2-C3 to T12-L1) of your subject

N.B.: Those files need to be generated for both contrast T1 and T2 (so 6 files in total).

### 2- Files that need to be modified

At the end, here are the files that you shall have modified when adding a subject to the dataset:

-dev/template\_preprocessing/pipeline\_template.py : the pipeline used to create the template

-> you need to add your subject to the list SUBJECT\_LIST\_TOTAL

-dev/template\_preprocessing/preprocess\_data\_template.py : a file made to create from scratch all the files that you will have bravely generated yourself for your subject (see above Files that need to be created)

**II- What to do?**

Every subject of the template needs to present a T1 and a T2. Subjects that contain only a T1 or only a T2 can not be accepted in the template dataset. If your subject presents both you may add it and you’ll need to do the following process for each contrast.

Process to follow for each contrast

1. First you need to convert the dicoms into a nifti image (function: dcm2nii, output: data.nii.gz)
2. Change the image’s orientation to RPI (function: sct\_orientation –i data.nii.gz –s RPI, output: data\_RPI.nii.gz)
3. From this RPI image you need to create the file labels\_vertebral.nii.gz. It localises

two particular points of the brainstem and the vertebral levels of the subject in the image.

3-1 Open data\_RPI.nii.gz in fslview and create a mask from this image by tapping (cmd+C)

3-2 Put a label of value 1 at this strategic point of the brainstem

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| hd1_local:Users:tamag:Dropbox:Screenshots:Screenshot 2015-07-23 12.36.34.png |
| hd1_local:Users:tamag:Dropbox:Screenshots:Screenshot 2015-07-23 12.37.13.png |

3-3 Put a label of value 2 at this strategic point (PMJ) of the brainstem

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| hd1_local:Users:tamag:Dropbox:Screenshots:Screenshot 2015-07-23 12.38.09.png |
| hd1_local:Users:tamag:Dropbox:Screenshots:Screenshot 2015-07-23 12.39.56.png |

3-4 Put labels of value 3 to 20 on vertebral levels going from C2-C3 to T12-L1  
C2-C3: value 3, C3\_C4: value 4, …, C7-T1: value 8, T1-T2: value 9, …, T12-L1: value 20. Labels should be placed on the left side of the vertebral disks (see screenshots below)

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| hd1_local:Users:tamag:code:spinalcordtoolbox:dev:template_preprocessing:Snap3_labels_vertebral.png |
| hd1_local:Users:tamag:code:spinalcordtoolbox:dev:template_preprocessing:Snap4_labels_vertebral.png |
|  |

1. You need to crop the image a little above the brainstem and a little under L2-L3 if the size of the data allows it (if it doesn’t, make sure the image goes at least after T12-L1 (sct\_crop\_image –I data\_RPI.nii.gz –dim 2 … , output: data\_RPI\_crop.nii.gz). You need to report where you are cropping the image in the file crop.txt.   
     
   Format: zmin\_anatomic,zmax\_anatomic (e.g.: 15,623 if you are cropping between slices 15 and 623). If there is a need to crop along y axis (as for some data from marseille that present artefacts) please specify as follow: zmin\_anatomic,zmax\_anatomic,ymin\_anatomic, ymax\_anatomic (e.g.: 15,623,30,200 if you are adding a crop along y axis between slices 30 and 200).  
   At this point, the file crop.txt must be of one of this two forms:

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| hd1_local:Users:tamag:Dropbox:Screenshots:Screenshot 2015-07-23 14.33.36.png | hd1_local:Users:tamag:Dropbox:Screenshots:Screenshot 2015-07-23 14.33.21.png |

1. From the cropped image data\_RPI\_crop.nii.gz, you need to create a label file centerline\_propseg\_RPI.nii.gz that will be used to initiate the segmentation of propseg. Open data\_RPI\_crop.nii.gz with flsview and create a mask (cmd+C). Put labels of value 1 at the center of the cord all along the spinalcord. One every 30 slices is generally a good set for propseg. Note that you need to put a label at the first slice (z=0) and at the last slice (z=nz) as this file will be used for the straightening of the image.
2. Generate the segmentation using propseg and make sure it is a good one. As propseg often diverges at edges we will also crop the segmentation. Crop the segmentation and report the crop in the file ‘crop.txt’.  
   Format: zmin\_anatomic,zmax\_anatomic,zmin\_seg,zmax\_seg or zmin\_anatomic,zmax\_anatomic,ymin\_anatomic,ymax\_anatomic,zmin\_seg,zmax\_seg if you cropped along y at step 4.  
   N.B.: If you only want to crop the segmentation at the bottom, you can write ‘max’ instead of zmax\_seg (e.g.: 15,max if you are cropping at slice 15).  
   At this point, the file crop.txt must be of one of this two forms:

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| --- | --- |
| hd1_local:Users:tamag:Dropbox:Screenshots:Screenshot 2015-07-23 14.49.55.png | hd1_local:Users:tamag:Dropbox:Screenshots:Screenshot 2015-07-23 14.50.18.png |

1. You have now generated all the necessary files for the pipeline to work. Test the pipeline’s ‘do\_preprocessing’ step for this subject only and make sure the results are good. Important tests are: 1) checking the resulting image (data\_RPI\_crop\_normalized\_straight\_crop.nii.gz) and 2) checking that no vertebral label has disappeared in the process (i.e. that labels\_vertebral\_dilated\_reg\_2point\_crop.nii.gz still contains 20 labels).
2. Now that you have finished to generate all the necessary files for one contrast, don’t forget to repeat the process for the second contrast.
3. Now that everything works fine for this subject, you can add it to the data set.   
   To do that, add it to the list SUBJECT\_LIST\_TOTAL of pipeline\_template.py.   
   Complete also the python file preprocess\_data\_template.py to generate the files you just created from scratch and whithout having to restart this painfull process (again, for both contrast.