Segmentation

The purpose of image segmentation is to separate tissue into different types. Usually a 3DT1 is used since it has good contrast between grey matter, white matter, CSF. Most of the tools mention are from the fsl toolbox and their wiki (https://fsl.fmrib.ox.ac.uk/fsl/fslwiki) has lots of information.

First we must remove the skull otherwise the segmentation tool will place it in its own category. I use BET (fsl's brain extraction tool).

- bet filename.nii.gz filename_brain.nii.gz -f 0.3

The f factor changes how aggressively the extraction is done. If you find that too much of the outer brain is removed then decrease this number.

The next step is to segment the brain into 3 classes. (I've tried more than 3 classes to attempt to separate lesions as well but then the csf tissue is just separated into 2 rather than capturing lesons.) I use FAST (fsl toolbox).

- fast -t 1 -n 3 -p -g -o filename_brain filename_brain

Here the -t indicates the image type (1=T1-weighted), n is number of classes, -p creates probability images, -g separates each tissue into its own image, o is output basename. The probability maps (labeled _pve_) give the probability of the tissue belonging to each of the 3 tissue types. From a 3DT1 image:

pve_0=CSF

pve_1=GM

pve_2=WM

We then want to erode and binarise our images since we want to avoid the tissue edges where there are partial volume issues. Exactly how you do this depends on the purpose of your mask. For a WM mask, you want to make sure that the tissue included truly is WM so I use

- fslmaths filename_brain_pve_2 -thr 0.99 -bin -kernel 2D -ero WMmask

So, I've thresholded to only include tissue with 99% probability of being WM and then eroded by a voxel around the edges. You can then get some results (here mean and standard deviation) using this mask with

- fslstats quantitative_image -k mask -m -s

I will note here that FAST is not great at segmenting deep grey matter and often parts of the putamen are included in the WM mask. For DGM segmentation, there is another fsl tool called FIRST.

- run_first_all -i t1_image -o output_name

This will output an image with segmented putamen, caudate, thalamus and pallidum (and probably more).

Another tool that does segmentation is freesurfer. I've only ever run the entire pipeline with

- recon-all -all -s subjectdir -I 3DT1_filename

This produces a whole bunch of directories and files with tons of data. (It also takes a very long time to run.) I've grabbed volumetric data from aseg.stats but there's a lot more data produced.

Finally, I've also done a bit of segmentation using ANTs. First, a bias field correction is applied to the 3DT1.

- N4BiasFieldCorrection -d 3 -i 3DT1file -o 3DT1file_N4.nii.gz

Then we extract the brain which also creates segmented tissue maps for whole brain, GM, WM and CSF.

- antsBrainExtraction.sh -d 3 -k 1 -z 0 -a 3DT1file_N4.nii.gz -e …/ANTs/OASIS/T_template0.nii.gz -m …/ANTs/OASIS/T_template0_BrainCerebellumProbabilityMask.nii.gz -f …/ANTs/OASIS/T_template0_BrainCerebellumRegistrationMask.nii.gz -o 3DT1file_N4

This tool uses a segmented brain template to then match tissue types.

Another aspect of segmentation that is often wanted is delineation of pathology (e.g. MS lesions). There's still no definitive way of doing this. For MS lesions, we have a semi-automated approach where a trained radiologist places seed points on all the lesions and then an algorithm grows the lesions. However, this is very time consuming. We've been exploring more automated ways and have tested Mimosa which seems to be doing a decent job.

To conclude, I want to emphasise that it is always important to **check your work**. So, always make sure that your segmentation is aligned with your image and hasn't gone horribly wrong.