

Brain structure and image segmentation: Hints

July 11, 2017

The aim of this case study is to introduce you to the structure of the brain and to segment the three main tissues in the brain (e.i. White Matter (WM), Grey Matter (GM) and Cerebrospinal fluid (CSF)). In addition to the tasks in the exercise sheet the following hints will be helpful in understanding the concepts and the tools employed.

1. **Brain Extraction.:** Here investigate the different parameters of the `fsl.BET` nipype interface. You can get the documentation of the interface in python by using the code below

```
import nipype.interfaces.fsl as fsl
fsl.BET.help()
```

this will provide help on the needed parameters. Try to understand what these parameters are by playing around them. That is, by changing the values where possible to see the effect it has on the final outputs. In each case visualize the **mask_file** volume to see if the brain mask has been successfully created. you can visualize 3D volumes in **itk-snap** (Download itk-snap at <http://www.itksnap.org/pmwiki/pmwiki.php>)

2. **Registration.:** There are two main registration tasks involved in the case study. The first task involves aligning `flair` and `t1` volumes. This has been implemented in the solution scripts. The second registration task involves registering the 3 atlas volumes for WM, GM, and CSF to the input image (e.i. either `flair` or `t1` volume). You may checkout the help string in python by using the code below.

```
from nipype.interfaces.ants import Registration
Registration.help()
```

Again play around with the parameters and checkout the effect of these parameters on the registration task. Note some of these parameters especially where it has noticeable effect on the task. You can again use **itk-snap** to visualize the 3D volumes.

3. **Segmentation.**: The third task involves using the registered tissue maps to segment the corresponding tissues in the flair and t1 images. This is implemented using Expectation-Maximisation (EM) algorithm. In this task you can invest some time in understanding the various steps in the EM algorithm. You can also alter the code a bit to visualize (or save) the tissue maps after each iteration so that you can see the progression of the segmentation task after each iteration.

Finally, if you have some more time you can spend some time in finding out how to carry out the segmentation task using the nipyne ants interface : **nipyne.interfaces.ants.segmentation**