

# Information Processing for Medical Imaging Module MPHYGB06

## Coursework 2016-2017

You are expected to write-up the results of the coursework in a single combined report. (expected length between 2,500 and 4,000 words). You are also expected to submit any source files of code you wrote specifically for this coursework. Submit a single file (compressed file containing both report and source files) through Moodle by the 14th April 2017 at 17:00.

[Anticipated marks for each section are in square brackets]

The aim of this coursework is to extract features from structural magnetic resonance images and use them to classify healthy subjects from subjects diagnosed with dementia.

Three steps are required to perform this analysis:

- Brain tissue segmentation using prior information from an atlas
- Extraction of subject specific regional information using Jacobian integration
- Statistical analysis

20 MRI images will be used for this coursework. 10 scans from healthy subjects and 10 scans from subjects diagnosed with Alzheimer's disease. For each scan, the following information is encoded in the file name:

- gender [M/F]
- age at the time of the acquisition [age]
- disease status, Alzheimer's disease or healthy control [AD/HC]

You are also provided with a template image and associated tissue probability maps and brain parcellation.

You will need to implement some of the algorithms required for this coursework. You can use either Python, Matlab or C/C++. For all the required medical image registration tasks, you can use the NiftyReg software, or any other tool. For the statistical analysis, you can also use any software or library.

The instruction to compile the NiftyReg code can be found here: [http://cmictig.cs.ucl.ac.uk/wiki/index.php/NiftyReg\\_install](http://cmictig.cs.ucl.ac.uk/wiki/index.php/NiftyReg_install). Use the source code provided with this coursework. Tutorials to run the NiftyReg tools can be found here: [http://cmictig.cs.ucl.ac.uk/wiki/index.php/NiftyReg\\_documentation](http://cmictig.cs.ucl.ac.uk/wiki/index.php/NiftyReg_documentation)

### Step 1: Tissue segmentation [30].

The aim of the first step is to segment the brain scans into grey matter, white matter and cerebrospinal fluid. Using medical image registration (using *reg\_aladin*, *reg\_f3d* and *reg\_resample* if using NiftyReg), propagate the provided probabilistic tissue maps to all individual subject scans and use them as priors [10]. You are expected to use a Gaussian Mixture Model, as described during the module lecture and implemented during the coursework, including the Markov Random Field regularisation [15]. Try different regularisation level (beta-value) and comment on your final choice [5].

### Step 2: Extraction of regional volume change [30].

*For any question about this coursework, please contact Marc Modat, [m.modat@ucl.ac.uk](mailto:m.modat@ucl.ac.uk)*

The aim is to quantify the regional volume differences between the provided template image and all individual scans. First, you will need to align all subjects' scans independently to the provided average template image (using *reg\_aladin* and *reg\_f3d* if using NiftyReg) [5]. You will obtain the **transformations** that maps the average image to all other scans. Second, you can generate the Jacobian determinant maps for all subject (using *reg\_jacobian* if using NiftyReg) [5]. Third using the provided average image parcelation, you can compute the average Jacobian determinant values for all regions of interest [5]. What are the desired properties for the Jacobian determinant maps? [5] Explain how you promoted them when running the registration? [5] How did you check that these properties were enforced? [5]

### Step 3: Statistical analysis [30].

From the tissue segmentation, extract for each subject the ratio between the grey matter volume and the white matter volume [5]. Correlate the ratios with age with age for each sub-group separately. Discuss the findings [5].

Use age, gender, grey matter volume, white matter volume and total intra-cranial volume (white matter, grey matter and cerebro-spinal fluid combined) as features of a classifier, motivate your choice(s) and explain your evaluation strategy [10].

Using the regional Jacobian determinant information as features of a **logistic regression classifier**, find the regions of interest that are best to differentiate the two sub-groups [5]. characterise the classifier performance when using only the best regions, comment on the results. [5]

### Step 4: Potential improvements [10].

For each of the previous section (step 1 [3], step 2 [3] and step 3 [4]), discuss potential ways to improve the classification performance.

Use all features. non-linear, more data (patients, terms). Use GMM segmentation

### Compressed folder

The compressed folder contains:

- Template image: average T1w MRI and associated tissue segmentation and parcelation.
- 20 input images for analysis.
- Gaussian Mixture Model for brain tissue segmentation publications.
- NiftyReg source code.

### Extra tools

Nifti library (read and write nifti images (.nii)):

- *Python*:  
[http://sourceforge.net/projects/niftilib/files/pynifti/0.20100607.1/pynifti\\_0.20100607.1.tar.gz/download](http://sourceforge.net/projects/niftilib/files/pynifti/0.20100607.1/pynifti_0.20100607.1.tar.gz/download)
- *Matlab*:  
<http://sourceforge.net/projects/niftilib/files/niftimatlib/niftimatlib-1.2/niftimatlib-1.2.tar.gz/download>
- *C*:  
[http://sourceforge.net/projects/niftilib/files/nifticlib/nifticlib\\_2\\_0\\_0/nifticlib-2.0.0.tar.gz/download](http://sourceforge.net/projects/niftilib/files/nifticlib/nifticlib_2_0_0/nifticlib-2.0.0.tar.gz/download)

Medical image cross-platform viewers:

- *itk-SNAP*: <http://www.itksnap.org/pmwiki/pmwiki.php?n=Downloads.SNAP3>
- *MRIcron*: <http://www.mccauslandcenter.sc.edu/mricro/mricron/install.html>
- *3DSlicer*: <http://download.slicer.org>