Information Processing for Medical Imaging Module
MPHYGB06

Coursework 2014-2015

You are expected to write-up the results of the coursework in a single combined report. 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) via Moodle. The submission deadline is available from the Moodle module page.

This coursework will take some time to complete. Please do not leave this until the last minute as you will not have time to generate your results!

[Anticipated marks for each section are in square brackets]

The aim of this coursework is to assess the (statistical) power of a longitudinal imaging biomarker routinely used in neurodegenerative disease analyses: full brain atrophy.

Three steps are required to perform this analysis:
- full brain segmentation
- atrophy measurement
- statistical analysis

20 pairs of images, from both subjects diagnosed with Alzheimer's disease (10) and age-matched control subjects (10), will be use for this coursework. Each pair consists of a baseline scan and a follow-up scan after 1 year. All images are a subset of the MIRIAD dataset. You can find more information about this dataset in [Malone, I. B., Cash, D., Ridgway, G. R., Macmanus, D. G., Ourselin, S., Fox, N. C., & Schott, J. M. (2013). MIRIAD-Public release of a multiple time point Alzheimer's MR imaging dataset. NeuroImage, 70, 33–36. doi:10.1016/j.neuroimage.2012.12.044].

You will need to implement some of the algorithms required for this coursework. You can use either python, matlab or C/C++.

I - Full brain segmentation

Within the compressed folder associated with this workshop, you will find 10 T1-weighted (T1w) brain MR images and their associated brain (grey and white matter) segmentations. Using these images as prior information, or template database, use segmentation propagation to segment the other images.

To obtain the required propagated segmentation, you can use the NiftyReg package (source code available in the compressed folder). Instruction to install the package can be found here:
http://cmictig.cs.ucl.ac.uk/wiki/index.php/NiftyReg_install
and a tutorial on how to use it for segmentation propagation can be found here:
http://cmictig.cs.ucl.ac.uk/wiki/index.php/NiftyReg_Segmentation_Propagation_Tutorial.
Note that segmentation propagation is a time consuming process, you will thus need to define parameters that give a good balance between computation time and accuracy. Discuss the proposed pipeline and comment on the parameters.

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Once multiple segmentations have been propagated through registration into the space of the MRI that you want to segment, use a label fusion technique to obtain a consensus segmentation

(majority voting, weighted majority voting or others). Implement the label fusion technique of your choice.
In the report, justify your parameter choices, using e.g. a leave-one-out approach on the template database by assessing the quality of the obtained segmentations with the Dice's Similarity coefficient (also known as Dice's Score or Dice's coefficient).

[25]

II - Atrophy measurement

Once the full brain for all input images have been segmented, compute the atrophy by implementing the Boundary Shift Integral (BSI) technique. Details about the BSI approach can be found in the lecture notes and the relevant literature: [Freeborough, P. A., & Fox, N. C. (1997). The boundary shift integral: an accurate and robust measure of cerebral volume changes from registered repeat MRI. IEEE Transactions on Medical Imaging, 16(5), 623–629. doi: 10.1109/42.640753].
A tutorial describing the required registration steps with NiftyReg to run BSI can be found here: http://cmictig.cs.ucl.ac.uk/wiki/index.php/NiftyReg_Boundary_Shift_Integral_Tutorial.

[25]

III - Statistical analysis

Using the obtained atrophy rates, run a Student's t-test to first assess if the rates of atrophy from the subjects diagnosed with Alzheimer's disease are statistically different from those of the age-matched controls. If you were to design a clinical trial for a new drug, using the full brain atrophy as an imaging biomarker, what would be the required sample size to detect a 25% absolute atrophy reduction with a 80% power? Compute the sample size to detect a 25% atrophy reduction relative to normal ageing. Compare the sample size results obtained from the BSI outcomes with the sample size obtained using segmentation volume differences (volume of the follow-up scan full brain segmentation minus the volume of the baseline full brain segmentation). Comment on these findings.

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What techniques could potentially be used to improve the statistical power of this imaging biomarker? (e.g. how to obtain a better segmentation? how to obtain a better atrophy estimation?) What statistical analysis could be performed to include demographic information (e.g. gender, age, …)?

[10]

IV - Compressed folder

The compressed folder contains:
- Template database. 10 T1w MRI and associated full brain segmentation.
- 40 input images for analysis. 20 baseline and 20 follow-up scans.
- MIRIAD publication.
- BSI publication.
- Label fusion publication.
- NiftyReg source code.

V - 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

- *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

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