University College London

Information Processing in Medical Imaging - Coursework Report

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Task I - Full brain segmentation

Proposed pipeline

Segmentation propagation (`p1reg.py`) has been performed on the extra 5 AD and 5 controls, both baseline and followup images, using the tutorial instructions from the CMIC TIG website. This means that we needed to propagate segmentations for 20 different images, and since we had 10 source templates available, this meant 200 propagations. As each propagation took around 1.5 minutes on an Intel(R) Xeon(R) CPU @ 3.60GHz, a careful balance between computation time and accuracy had to be obtained. The parameters chosen were:

- `reg_aladin`: –speeeed (parameter that speeded up the affine registration)
- `reg_f3d`: number of levels: 4, number of iterations: 200

A discussion about how I chose these parameters is given at the end of this section. After performing the

Parameters

Task II - Atrophy measurement

The BSI has been computed using the method described in Leung et al. [1]. First, the baseline and followup images have been aligned using the 9DOF affine registration. Then, the union and intersection regions of the images is computed. The union is dilated once, while the intersection is eroded once using a structure that looks like a 3x3x3 sphere. The brain boundary shift region is then given by the XOR of the dilated union and eroded intersection. The intensity of both images is then normalised by dividing by the mean intensity inside the intersect region. Finally, the BSI is computed using a manually chosen intensity window of [0.45,0.65] recommended by Freeborough and Fox, 1997. [2].

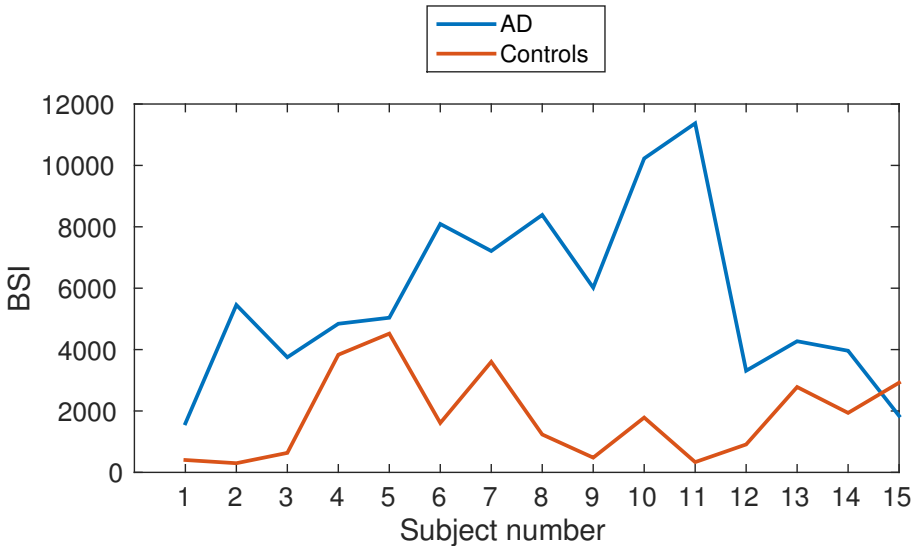

Figure 1: BSI measurements for all AD and control subjects. Each AD patient is paired with an age-matched control, typically a spouse or carer. [3] There is visibly more atrophy (as measured by BSI) for AD subjects compared to control subjects. The only exception is subject 15, which might be an outlier.

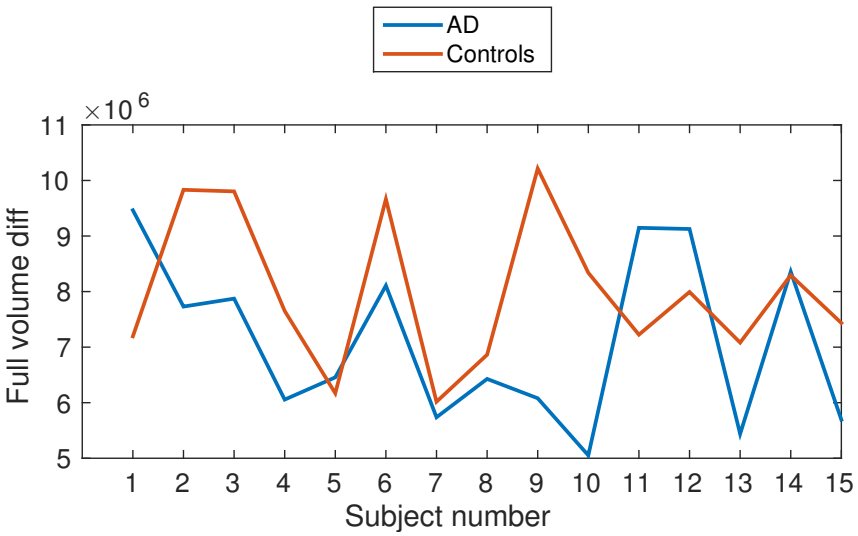

Figure 2: Full volume difference for all AD and control subjects. There is considerable more overlap between AD and controls

Task III - Statistical Analysis

T-tests

A two-sample t-test has been performed for AD and control groups using the BSI, in order to see if there is a statistically significant difference in atrophy. Since each AD patient had an age-matched control (normally a spouse or carer) [3], this allows us to also perform a paired t-test, checking for a pairwise difference in atrophy. A similar analysis has been made using the full-volume difference. Results are presented in the following table:

Metric	paired-sample t-test		two-sample t-test	
	H_0	p-value	H_0	p-value
BSI	rejected	5.23e-04	rejected	6.45e-05
Full-volume	not rejected	0.0844	not rejected	0.1062

For the BSI metric, both t-tests rejected the null hypothesis H_0, while for the full-volume metric, H_0 could not be rejected. We therefore conclude that there is a significant difference of atrophy between AD and control groups, as measured by the BSI. Furthermore, we also conclude that BSI is better than the full-volume difference at discriminating between AD and control subjects.

Sample size analysis

MATLAB function `samplesizepwr` has been used to calculate the sample size required to detect a 25% atrophy rate with an 80% power (file `p3.m`). For the BSI, minimum sample sizes of 34 and 77 are required to detect an atrophy reduction relative to AD and normal ageing respectively. Similarly, for the Full brain volume, minimum sample sizes of 8 and 6 are required to detect an atrophy reduction relative to AD and normal ageing, respectively. The reason for the lower sample size required using the full volume atrophy is because the standard deviation of the groups was much lower relative to the mean.

Future improvements

In order to improve the statistical power of this technique, there are several things one could do:

- **Data acquisition**: Obtain higher-resolution MRI data using 7T or 9T scanners. In our MIRIAD dataset [3], a 1.5T scanner was used.

- **Registration**: Calculate the transformation using more levels and iterations at the free-form deformation step.
- **Segmentation**: using more templates, or by implementing smarter fusion methods such as weighted majority voting or probabilistic methods such as Non-local-STAPLE or STEPS. One other limitation of this method is that the templates might produce similar labeling errors, but this can be overcome with the method proposed by Wang et al, 2013 [4]. One could also combine the segmentation propagation method with other methods based on level sets [5], fuzzy c-means [6], Gaussian mixture models using EM, Markov random fields, Self organising maps [7] or Learning vector quantization [8].
- **Atrophy estimation**: Perform a bias field correction before BSI computation and do a more robust intensity normalisation and automatic parameter selection based on the intrinsic tissue contrast of the MR images, as described in Leung et al, 2010 [1].

Demographic information could also be included in order to improve the statistical analysis. For example, one could compensate for age in the atrophy measurement using the BSI by fitting a linear or polynomial model over the age BSI data. The two-sample t-test should show improvements after this change, while the paired t-test shouldn't be affected too much, as the AD and control pairs are already age-matched. If gender information is also available, one could use that to perform a t-test on male and female groups in order to see if the atrophy rate is statistically different. Other demographic information could be used in a similar manner. If multiple types of demographic data is used, one could perform *Canonical Correlation Analysis* in order to find out how much each of these demographic factors are correlated with increased atrophy rate and full volume difference.

Bibliography

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