Novel contour-based registration algorithm for VBM pre-processing

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Introduction

The performance of registration algorithms is one of the limiting factors of automated morphology methods. It is known that the discrete cosine transform (DCT) based registration used in SPM5 (http://www.fil.ion.ucl.ac.uk/spm/), and hence for most voxel-based morphometry (VBM) studies, can fail in some brain regions [1]. As such, VBM analyses are hindered due to the nuisance effect of such variability, masking out potentially relevant regions which may suffer from poorer registration (e.g. hippocampi). One of the crucial restrictions of SPM5's registration method is that it is volume-based, which entails a poor performance in surface areas such as the cortex and the ventricles. The present work aims at reducing the residual variability. An algorithm was developed in which the normalised segments of grey matter and white matter are used as inputs from which the contours of the main edges are extracted. This contour information is then used as the driving force of a viscous-fluid registration algorithm [2].

Methods

Ten controls (5 male, 5 female, average age 69.7 years) and ten Alzheimer's disease (AD) subjects (4 male, 6 female, average age 68.8 years) were used to evaluate the performance of the algorithm on both healthy and non-healthy brains. All scans were acquired using a 1.5T GE MRI scanner. The images were acquired using a coronal T1 weighted 3D spoiled gradient echo sequence with echo time of 4.2 ms, inversion time of 650 ms and flip angle of 20º. SPM5 was used to perform a first registration and to find the modulated normalised grey matter (GM) and white matter (WM) segments, used as input for the proposed algorithm. Both segments were then added together in order to have information about surface areas, whose contours were extracted and labelled in order to have a structure of several curves for each scan. Using one of the controls as a randomly chosen target, all scans were registered to it in two stages. Firstly, a curve matching procedure was performed in order to find corresponding contours. This was achieved minimising a weight matrix, whose entries w_{ij} were calculated using the size and centroid difference between curves i (from the subject) and j (from the target): $w_{ij} = ((size_i - size_j)/size_j + 1) \times ||centroid_i - centroid_j||$. With the matching information and centroid difference, a translation vector was computed ($centroid_i - centroid_j$) and used as driving force for each curve voxel, for each curve separately. Non-matching curves were discarded from this step. That information was then used to drive an elastic based registration (translation), in which the force equalled the translation vector, which was then convolved with a 5×5 gaussian kernel via Fourier transformation to extract the deformation field. The second step consisted in using an implementation of Thirion's demons (linear functions, [3]) to drive a viscous-fluid registration using the approximation seen in [4], again implemented with Fourier transforms (all in 2D, for each slice). Entropy assessment of contour points was performed in order to evaluate if it was worth registering the associated region [5]. Topology preservation was enforced by regridding the deformation matrix whenever the minimum of the determinant of the local deformation jacobian dropped below 0.5. All functions were implemented using Matlab7 (Mathworks Inc., Natick, MA, USA). The main steps of the algorithm can be seen in Figure 1, together with examples of particular slices. This method was assessed by contrasting the root mean square error (rmse) between target and scan GM before and after this novel supplementary registration.

Results and Discussion

As seen in Table 1, this algorithm was able to increase similarity between target and subject by an average of 7.5%, for both controls and AD subjects, as measured by the rmse. This performance was shown to be consistent throughout the cohorts. A visual assessment of differences (not shown here) shows that, as expected, the improvement lies in the cortical areas, which SPM5 method is unable to account for. As can be seen from Figure 1 (a), the registration method used in SPM5, although in 3D, produces broadly varying deformation fields spanning the whole volume. The proposed method produces subtler deformation fields (Figure 1 (c), (e)) which are able to better compensate minor differences between scans. The main issue of this method is time consumption, as it takes an average of 3.5 hours per subject on a Dual Xeon 3.2 GHz Intel X86 64 bit processor with 4GB RAM. This may be because of the non-optimal Matlab implementation.

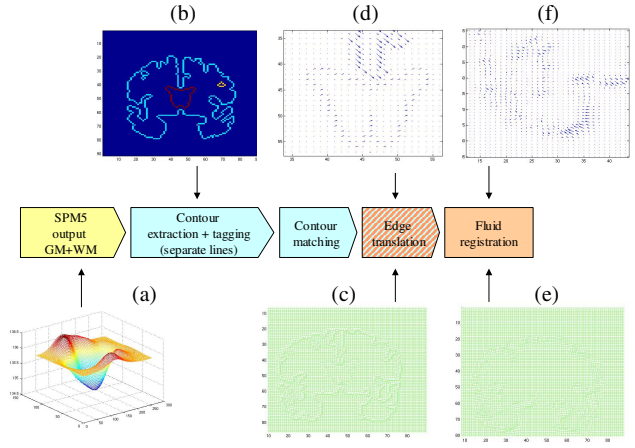

Figure 1: Proposed algorithm pipeline. SPM5 deformation field is seen in (a). Contour extraction and tagging is performed (b), followed by curve weight matching and edge translation, with the resulting deformation field seen in (c) and details of the forces in (d). Finally, fluid registration is used: deformation field (e) and forces detail (f) are shown. All examples are from a random slice.

		Initial rmse	Final rmse	Difference	% Difference
Controls	***mean***	0.123	0.114	-0.009	-7.48
	std deviation	0.011	0.008	0.003	1.69
AD	***mean***	0.125	0.116	-0.009	-7.46
	std deviation	0.013	0.011	0.002	1.01

Table 1: Mean and standard deviation of performance values for Control and AD cohorts. Rmse for GM segments is shown before (initial) and after (final) using the proposed algorithm. Absolute and percentage differences are shown.

Conclusions and Future Work

The proposed algorithm performs as expected, reducing the residual variability around surface areas for both controls and AD subjects. If this method is performed after SPM5's segmentation, the increased similarity will aid the localization problems seen for voxel-based morphometry (VBM) studies. Future work will include the optimization of this method for faster processing, and its application in VBM studies. A single iteration per slice method is also being developed, which attempts to provide an explicit point-to-point correspondence of different contours, avoiding computing driving forces in several iterations.

References

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