MULTI-CONTRAST PATCHMATCH ALGORITHM FOR MULTIPLE SCLEROSIS LESION DETECTION

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ABSTRACT

Due to their abnormal appearance, Multiple Sclerosis lesions can influence the results of various image analysis techniques such as segmentation and registration. As the multi-modal characteristic intensity of the Multiple Sclerosis lesions is different that of non-pathological tissues, a local multi-modal intensity similarity can be used to classify and segment lesions. In this work, lesions are segmented using a fast patch matching approach, namely the optimised PatchMatch label fusion algorithm. The optimised PatchMatch label fusion algorithm is here extended to multimodal data, enabling an accurate Multiple Sclerosis lesion segmentation.

***Index Terms*—** patch-based, multimodal, lesion detection, mri, patchmatch

1. INTRODUCTION

Automatic detection and segmentation of Multiple Sclerosis (MS) lesions can help diagnosis and patient follow-up, providing quantitative assessment of inflammatory activity and lesion load. MS lesions appear with different intensities depending on the MRI sequence and have considerable shape variability, making automatic segmentation a challenging task. Several automated segmentation techniques have been developed, including some intensity-based k-nearest neighbor algorithms [1]. Traditionally, these intensity-based approaches were computationally expensive to solve this problem and needed a learning set reduction to reduce the computation time [2]. Recently, Ta et al. [3] presented a very quick patch-based algorithm using PatchMatch technique. PatchMatch was designed to look for similarities between two 2D images [4]. Shi et al. [5] extended it to 3D MRI images and applied it to cardiac images. Later, Ta et al. [3] presented an optimised version of the PatchMatch algorithm, named Optimised PAtchMatch Label fusion (OPAL), producing accurate and fast segmentation of the hippocampus using a library of associated segmented images and speeding up the process of multi-atlas label fusion.

In this work, we propose to use the PatchMatch algorithm for MS lesion detection. The main contributions of this work are the generalisation of the optimised PatchMatch algorithm to this context and its extension to multimodal data.

2. METHOD

The original PatchMatch algorithm was designed to look for similarities between two 2D patches within the same image [4]. Later, OPAL extended patch correspondences between a target 3D image and a reference library of 3D training templates [3]. Here, the PatchMatch algorithm is used to locate pathological regions through the use of a template library comprising a series of multimodal images with manually segmented MS lesions. By matching patches between the target multimodal image and the multimodal images in the template library, PatchMatch can provide a rough estimate of the location of the lesions in the target image.

We extend the OPAL algorithm to match patches between multiple image modalities at the same time. In order to do so, for each subject, we first register all the available modalities to a common space and stack them to form a 4D volume of multimodal intensities. Patches are defined as in the OPAL method, with the only difference being the estimation of the patch similarity. Rather than calculating the sum of the squared differences (SSD) between two patches over one single modality, we estimate the l_2-norm between multimodal patches. While this extension is trivial, as it is equivalent to the sum of the SSDs for each image modality independently, it provides a crucial improvement in discrimination when distinguishing between pathological and healthy intensity patterns. To improve computational speed, as in the original OPAL method, we stop the computation of the patch similarity if the current sum is superior to the previous minimal multimodality SSD. Also of note is the fact that this Patch-

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	Split	Union	Inter.
TNR	99.84 (0.04)	99.77 (0.07)	99.92 (0.02)
TPR	78.48 (9.73)	81.43 (9.75)	72.33 (10.30)
FPR	0.16 (0.04)	0.23 (0.07)	0.08 (0.02)
PPV	38.91 (23.13)	33.47 (22.56)	49.87 (22.83)
VO	33.11 (16.75)	29.38 (17.23)	39.26 (13.43)
VD	201.3 (191.9)	282.7 (260.9)	97.5 (93.0)
SD	1.65 (0.16)	1.70 (0.17)	1.56 (0.12)
DSC	0.47 (0.19)	0.43 (0.20)	0.55 (0.14)
Score	1.86 (0.35)	1.50 (0.93)	2.64 (0.74)

Table 1. Evaluation results using different template libraries. Mean (standard deviation) for each metric. True negative rate (TNR), true positive rate (TPR), false positive rate (FPR), positive predictive value (PPV), volume overlap (VO), volume difference (VD), average symmetric surface distance (SD), mean dice score coefficient and mean global score.

Match algorithm can propagate more than one label at the same time.

As the PatchMatch output is non-binary, we apply an adaptive threshold value to binarise the probabilistic mask obtained by the PatchMatch algorithm. For this purpose, the robust range (assuming 2% outliers on both sides) of all voxels with non-zero probabilities is calculated, and then the mean of the values inside the robust range is computed. This mean is then used as a threshold to binarise the probabilistic segmentation. The algorithm also detects healthy controls by taking into account the robust range obtained values: if the highest probability within the robust range is below 0.1 we consider that no lesions have been detected, meaning that the patient is lesion free.

3. VALIDATION AND RESULTS

In our experiments, we used the parameters suggested by Ta et al. [3]; the patch size was $5 \times 5 \times 5$, the number of inner iterations 5, and the number of threads and the number of best-matches both 10.

For the sake of comparison and tuning, three template libraries were built. For each subject the T1, T2, PD and FLAIR images were stacked as 4D images. All libraries start with 21 training datasets. In order to increase the size of the libraries, all the scans were left-right flipped, resulting in 42 datasets in each template library. As multiple rater segmentations were available, a consensus segmentation was estimated in two different ways: the first template library used the intersection of the segmentations of both raters, while the second used the union mask of both raters. Finally, rather than estimating a consensus, a third database was obtained by using the segmentations from both rater 1 and rater 2 independently, resulting in a template library with 84 datasets.

In order to compare the results, we used the evaluation metrics proposed in the MICCAI MS Segmentation Challenge [6], the average Dice score coefficient (DSC) when compared to each of the human raters, and a compound score ranging from 1 (worst) to 3 (best) (see Table 1). In order to remove possible bias, a leave one out strategy was used for the proposed method, i.e. when segmenting an image, all the time-points of this image and their left-right flipped versions were removed from the template library.

The best segmentation results, found to be the ones using the intersected rater consensus database, were submitted to the Challenge.

4. DISCUSSION AND CONCLUSIONS

The proposed generalised PatchMatch algorithm demonstrated good performance for single time-point MS lesion detection. It is important to note that, due to the patch search nature of the proposed methodology, the template database needs to encode several degrees of lesion severity and spatial locations in order to appropriately capture the population appearance variability. Future work will not only expand the size and variability of the database but will also explore a multi-time-point extension of the proposed algorithm.

5. REFERENCES

[1] X Lladó, A Oliver, M Cabezas, J Freixenet, JC Vilanova, A Quiles, L Valls, L Ramió, and A Rovira, "Segmentation of multiple sclerosis lesions in brain MRI: A review of automated approaches," *Information Sciences*, vol. 186, no. 1, pp. 164–185, 2012.

[2] Petronella Anbeek, Koen L. Vincken, Matthias J.P. van Osch, Robertus H.C. Bisschops, and Jeroen van der Grond, "Probabilistic segmentation of white matter lesions in MR imaging," *NeuroImage*, vol. 21, no. 3, pp. 1037 – 1044, 2004.

[3] VT Ta, R Giraud, DL Collins, and P Coupé, "Optimized PatchMatch for near real time and accurate label fusion," *MICCAI 2014, LNCS*, vol. 8675, pp. 105–112, 2014.

[4] C Barnes, E Shechtman, DB Golman, and A Finkelstein, "The generalized patchmatch correspondence algorithm," *ECCV 2010, Part III. LNCS*, vol. 6313, pp. 29–43, 2010.

[5] W Shi, J Caballero, C Ledig, X Zhuang, W Bai, K Bhatia, A De Marvao, T Dawes, D O'Regan, and D Rueckert, "Cardiac image super-resolution with global correspondence using multi-atlas PatchMatch," *MICCAI 2013, Part III. LNCS*, vol. 8151, pp. 9–16, 2013.

[6] M Styner, J Lee, B Chin, M Chin, and O Commowick, "3D segmentation in the clinic: A grand challenge II: MS lesion segmentation," *MIDAS Journal*, pp. 1–6, 2008.