Using Diffusion and Structural MRI for the Automated Segmentation of Multiple Sclerosis Lesions

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Abstract. This work proposes to use scalar features calculated from diffusion MR data alongside structural MR intensities in the automated segmentation of Multiple Sclerosis (MS) lesions. We acquired and processed multi-contrast MR data from 7 MS patients, used random forests to segment lesions, and evaluated our method via DICE scores, achieving scores over 0.65. Finally, we made use of the random forest framework to assess the discriminative power of the estimated features. We show that diffusion features estimated from the diffusion tensor are as discriminative as T1 and T2 intensities for the classification task.

1 Introduction

Current clinical settings use multi-contrast MRI, including T1, T2 and FLAIR, as part of the radiological assessment of Multiple Sclerosis (MS) [7]. Despite their diagnostic ability, these contrasts remain unspecific to underlying pathological processes that often over- lap, such as axonal damage and demyelination. In recent years, diffusion MRI has appeared as a quantitative technique with the potential of providing markers with increased pathological sensitivity and specificity [3] Furthermore, with the introduction of Compressed Sensing to Diffusion Spectrum Imaging (CS-DSI) [6], acquisition times were reduced to clinically feasible ranges (<30 min.). We present preliminary results of an ongoing MS patient study, focusing on the automated segmentation of MS lesions with multi-contrast MRI. Segmentation is performed by using intensities from the structural T1, T2, and FLAIR channels alongside diffusion features calculated from a CS-DSI protocol.

2 Theory

The task of automatically segmenting MS lesions with multi-channel data has already been undertaken[1,8]. In [8] tissue classification is achieved using a stochastic model with an expectation-maximization algorithm and lesions are detected

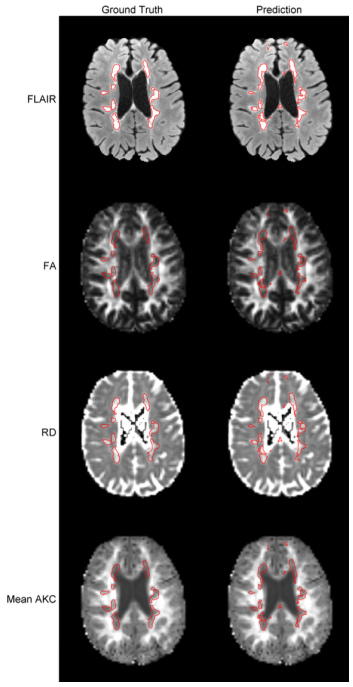

Fig. 1. Left: ground truth obtained by manual labeling. Right: Automatic segmentation results using random forests. Every column displays a different contrast.

as model outliers. In [1] lesions are automatically classified using discriminative random decision forests. We also use random forests for the classification task, but replace the context-rich features used in [1] and introduce the use of diffusion features. Diffusion features are estimated by fitting data acquired with a CS-DSI protocol to the diffusional kurtosis equation presented in[5].

3 Methods

Seven MS patients were scanned with a CS-DSI acquisition protocol using a GE MR750 scanner (GE Medical Systems, Milwaukee, WI). The CS-DSI protocol comprised of 150 volumes acquired on a Cartesian grid with maximal b-value = 3,000 s/mm^2. Additionally, high resolution T1, T2, and FLAIR contrasts were acquired. DSI volumes were co-registered to the first b=0 image and corrected for motion using FLIRT and FNIRT [4]. Scalar metrics were derived from the Eigenvalue decomposition of the diffusion tensor and from projections of the fourth order kurtosis tensor into spherical and elliptical coordinates [2]. The derived metrics were up-sampled and co-registered to the high resolution T1 image with FLIRT [4]. T2 and FLAIR volumes were also co-registered to the T1 volume and a brain mask was obtained using BET [4]. For every patient,

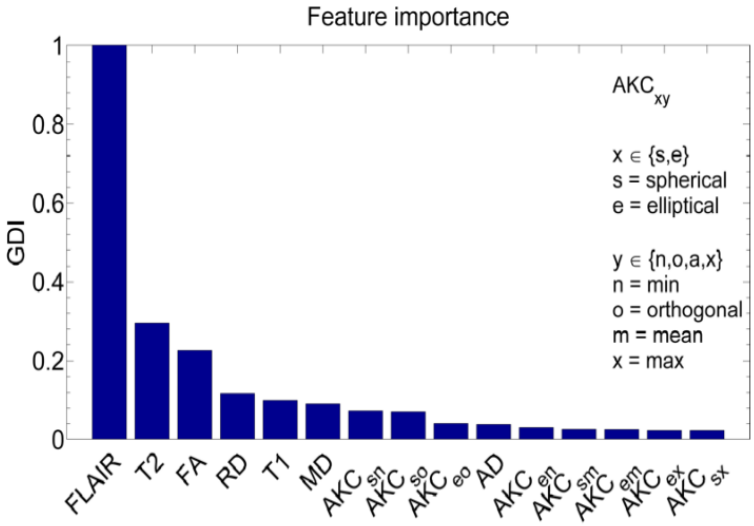

Fig. 2. Feature importance as given by the Gini Diversity Index (GDI) within the random forest framework.

11 slices were selected and lesions were manually labeled using a region growing algorithm based on thresholding FLAIR intensity values. The classification task with random forests was accomplished using Matlab's (The Mathworks, Inc.) Statistics Toolbox. A total of 10 trees were grown, where each tree received a randomly subsampled dataset of voxels. Every randomly subsampled dataset contained the same amount of lesion and non-lesion voxels, and every voxel consisted of 15 input features: three intensity channels, four diffusion features, and eight kurtosis features.

4 Results

Figure 1 shows the segmentation performance of an exemplary slice from one patient. For this particular set, the average DICE score over 10 iterations was 0.67. Repeating the experiment with different forest configurations and training sets yielded DICE scores in the range from 0.60 to 0.70 (results not shown). Figure 2 displays the feature importance, as ranked by the Gini Diversity Index (GDI) (values normalized to the score of the highest ranking feature). The ranking shows that most of the classification is achieved by FLAIR, followed by T2, diffusion features fractional anisotropy (FA) and radial diffusivity (RD), and T1. Mean diffusivity (MD) is ranked similarly to T1 intensities, while kurtosis features and axial diffusivity (AD) were ranked lowest.

5 Discussion

Random forests provide insight on the discriminative power of separate image based channels. In our analysis, diffusion features such as RD and FA are more discriminative than T1 intensity channels. On the other hand, kurtosis features and the diffusion feature AD did not significantly support the classification task. Although the ground truth was obtained from lesions clearly visible in FLAIR, the multi-contrast and longitudinal nature of the ongoing study will enable the definition of different types of lesions. Therefore, future work will focus on identifying intermediate lesion types not detectable on standalone FLAIR or T2 images.

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