

# HIERARCHICAL MRF AND RANDOM FOREST SEGMENTATION OF MS LESIONS AND HEALTHY TISSUES IN BRAIN MRI

Andrew Jesson, Tal Arbel

Centre For Intelligent Machines, McGill University

## ABSTRACT

In this paper, we present an automatic hierarchical framework for the segmentation of a variety healthy tissues and lesions in brain MRI of patients with Multiple Sclerosis (MS). At the voxel level, lesion and tissue labels are estimated through a Markov Random Field (MRF) segmentation framework that leverages spatial prior probabilities for 9 healthy tissues through multi-atlas fusion (MALF). A random forest classifier then provides region level lesion refinement. Validation is performed on the data provided by the ISBI 2015 Longitudinal Multiple Sclerosis Lesion Segmentation Challenge.

**Index Terms**— Segmentation, Multiple Sclerosis, MRI, MAP-MRF, MALF, Random Forest

## 1. INTRODUCTION

Automatic segmentation of Multiple Sclerosis (MS) lesions in patient brain MRI is a challenging task due to their wide variability in texture, shape, size, and location. A variety of MS lesion segmentation strategies have been developed [1–4]. The premise of this work is that by carefully modelling a variety of healthy structures in the presence of pathology, lesion segmentation can be further improved. The framework consists of building atlases for lesions and a wide variety of healthy tissues off-line during training. Multi-atlas label fusion (MALF) is then performed from the atlases to patient images to use as spatial priors for a voxel-based Markov Random Field framework that leverages intensity distributions and local contextual constraints. A Regional Random Forest (RRF) classifier then refines candidate lesions segmentations. The method was tested on the MICCAI 2008 MS Lesion Segmentation Challenge (MSLSC) [5] where it is currently the top performing methods on the leader board. The strategy has been tested in a leave-one-out fashion on the training data provided by the ISBI 2015 Longitudinal Multiple Sclerosis Lesion Segmentation Challenge, and show comparable results to the manual raters.

## 2. METHOD

We now describe the details of the method, including the implementation details.

### 2.1. Training

Training consists of three stages: Stage one involves building a set of lesion and healthy tissue atlases, referred to as *pathological atlases* as they are based on MS patient data. These are to be used as spatial priors for new test data. Stage two involves performing an initial segmentation of 9 healthy tissue structures in each of the patient training cases in order to build proper healthy and lesion intensity distributions. Stage three involves training the Random Forest. We now describe each of these stages in detail.

For the purposes of the ISBI challenge, stage one consists of building 25 multi-modal (T1, T2, and FLAIR) pathological atlases: 5 from each provided training subject (intensity values averaged over several timepoints), and 20 from the training set provided by the MSLSC [5]. Healthy labels for each pathological atlas are generated through MALF from multiple labels from 35 subjects from the 2012 MICCAI Challenge on Multi-Atlas Labelling (CMAL). Here the 134 labels provided are concatenated into 9 healthy structures: cerebrospinal fluid, lateral ventricle, other ventricle, deep gray matter, cortical gray matter, cerebellar gray matter, white matter, cerebellar white matter, and brainstem. Healthy labels are merged with the ground truth lesion segmentations provided from each dataset in order to create the complete atlases.

Stage two involves performing the same procedure as in stage one on the 21 training time points provided. This leads to a set of healthy and lesion labels and associated weights, which are used to guide voxel sampling used for building healthy tissues and lesion intensity distributions. Here intensity distributions of each class are modelled as Gaussian mixture models (GMM).

Stage three involves determining the labels at each voxel for each time points of each training subject using the models determined in stages one and two. The resulting segmentations are used to group together lesion voxels into lesion candidates. A regional random forest model (RRF) is then trained using the distance minimum, mean, and variance of

each candidate lesion to each healthy tissue, the size, volume, and solidity of each candidate lesion, and the principal moments and inertia matrix of the ellipse estimating the shape of each candidate lesion, as features.

## 2.2. Classification

For each test case, tissue priors are first generated through MALF of the 25 pathological templates in a MALF framework. The MRF incorporates these tissue priors, the intensity distributions, and a Potts model to perform voxel level inference. The MRF solution is then refined by the RRF.

## 2.3. Implementation Details

For the MALF estimation of spatial tissue priors, all rigid and affine transformations are determined through the antsRegistration tool [6], and deformation fields are computed using the deeds/MIND non-linear registration framework [7,8]. Label fusion is performed through a regional similarity method, and lesion priors are augmented through outlier detection. In addition to the pre-processing provided by the challenge, intensity normalization uses a sigmoidal function, where the parameters are determined by the mean and variance of intensities over several regions of interest. De-noising is based on a non-local means method [9].

## 3. RESULTS

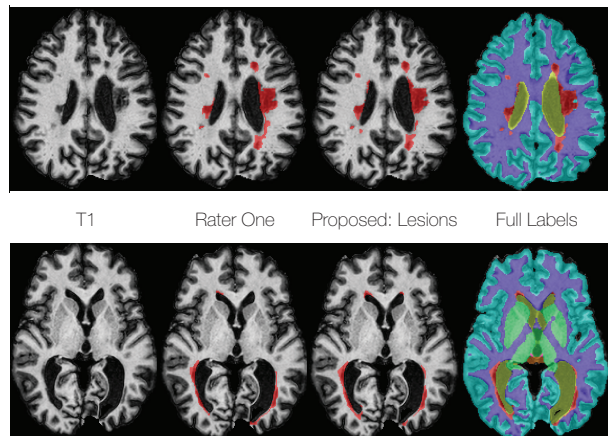
In order to validate our results, we performed leave one out cross validation on the five training subjects provided. Tables 1 and 2 show the averaged results over the 21 timepoints for the proposed method and compares them against the inter-rater results. Metrics used are the Dice and Jaccard coefficients, voxel and lesion-wise true positive rate (TPR and LTPR), and lesion-wise false positive rate (LFPR). Figure 1 shows slices from a typical output segmentation.

**Table 1.** Training Data Results: Proposed Method Segmentation Results against Rater One Results

	Dice	Jaccard	TPR	LTPR	LFPR
Proposed	0.704	0.550	0.812	0.610	0.135
Rater Two	0.734	0.589	0.808	0.832	0.348

**Table 2.** Training Data Results: Proposed Method Segmentation Results against Rater Two Results

	Dice	Jaccard	TPR	LTPR	LFPR
Proposed	0.681	0.528	0.721	0.501	0.127
Rater One	0.734	0.589	0.687	0.652	0.168



**Fig. 1.** Top to Bottom: Slices 76 and 98 from subject training01\_04. Left to Right: MPRAGE T1, rater one ground truth lesions, proposed lesion segmentation, proposed healthy tissue and lesion segmentation. Color coding for the full label segmentation: lesion, red; white matter, purple; cortical gray matter, cyan; deep gray matter, green; lateral ventricles, yellow; other ventricles, light green

## 4. CONCLUSION

These preliminary results show that our method performs similarly to a human rater. This is promising considering the relatively small training data set. While our method produces excellent Dice/Jaccard, TPR, and LFPR scores, we seem to be under performing in LTPR. The majority of missed lesions occur near cortical gray matter, within deep gray matter structures, and in the posterior fossa. Further work will examine modelling these lesions as distinct classes, increasing the size of our atlas database, and increasing the size of training dataset.

## 5. REFERENCES

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