

LONGITUDINAL MULTIPLE SCLEROSIS LESION SEGMENTATION CHALLENGE: MODEL OF POPULATION AND SUBJECT (MOPS) SEGMENTATION

X. Tomas-Fernandez and S.K. Warfield

Computational Radiological Laboratory, Boston Children’s Hospital.

ABSTRACT

Due to the substantial overlap between the whole brain signal intensity distribution of lesions and normal tissue in magnetic resonance images (MRI), the sensitivity and specificity of fully automatic lesion segmentation algorithms have been inadequate. Inspired by the ability of experts to detect lesions based on their local signal intensity characteristics, we propose a new algorithm that achieves lesion and brain tissue segmentation through simultaneous estimation of a spatially global within-the-subject intensity distribution and a spatially local intensity distribution derived from a healthy reference population.

1. INTRODUCTION

The development of fully automated multiple sclerosis (MS) lesion segmentation methods has been an area of vigorous research in the medical imaging community over the past 20 years. Techniques for automated MS lesion segmentation generally modify intensity-based classifiers (originally applied to tissue segmentation in the healthy adult brain) to model brain abnormalities on MRI as an additional class. Tissue classification relies on contrast between tissue types (e.g. normal brain tissue and MS lesions) on a particular feature space. It has been previously described how the MS lesion intensity distribution overlaps with that of healthy tissue. This limitation, in turn, results in MS lesion segmentation that is generally inaccurate.

Approaches aimed at reducing the extent of lesion false positives are usually based on post-processing steps. Due to the heterogeneous intensity distribution of MS lesions, these post-processing steps may have to be re-tuned based on the individual features of each case, or tailored to different subjects for varying degrees of lesion burden. To address these limitations, we proposed augmenting the imaging data used to identify lesions to include both an intensity model of the patient under consideration and a collection of intensity and segmentation templates that provide a model on normal tissue. We called this combination a Model of Population and Subject (MOPS) intensities [1]. Unlike the classical approach where lesions are characterized by their intensity distribution compared to all brain tissues, MOPS aims to distinguish locations in the brain with an abnormal intensity level when

compared with the expected value at the same location in a healthy reference population.

2. MATERIAL AND METHODS

In this section, we first introduce the reference population composed of healthy volunteers. Later, we introduce a brief description on how our MOPS intensity model is formed by combining the global intensity information from the target subject with the local intensity model derived from the reference population.

2.1. Reference Population

Fifteen healthy volunteers underwent MRI acquisition. The imaging protocol consisted in a T1-weighted; T2-weighted FSE (Fast spin echo); FLAIR-FSE; and diffusion weighted images on a 3T clinical MR scanner from GE Medical Systems (Waukesha, WI, USA) using an 8-channel receiver head coil. The T1w images were acquired sagittally with a matrix size of 256x256 and a field of view of 24 cm. Slice thickness was 1.3 mm and the T1w acquisition parameters were TR 10/TE 6/TI 725 ms with a flip angle of 8. After image acquisition, the T2w and FLAIR images were aligned to the T1w scan. Last, a trained expert manually segmented the intracranial volume, CSF, GM and WM tissues.

To achieve accurate alignment between healthy volunteers and a patient with MS, we used a nonlinear registration algorithm proposed in [2], which, although not intrinsic to our method, was selected because it is robust to the presence of WM lesions.

2.2. Model of Population and Subject

The MOPS MS lesion segmentation algorithm [1], combines a local intensity gaussian mixture model derived from the reference population previously described with a global intensity gaussian mixture model estimated from the imaging data (i.e. T1w, T2w and FLAIR) of the MS patient.

Intuitively, the local intensity model downweights the likelihood of those voxels having an abnormal intensity given the reference population. Since MRI structural abnormalities will show an abnormal intensity level compared to similarly

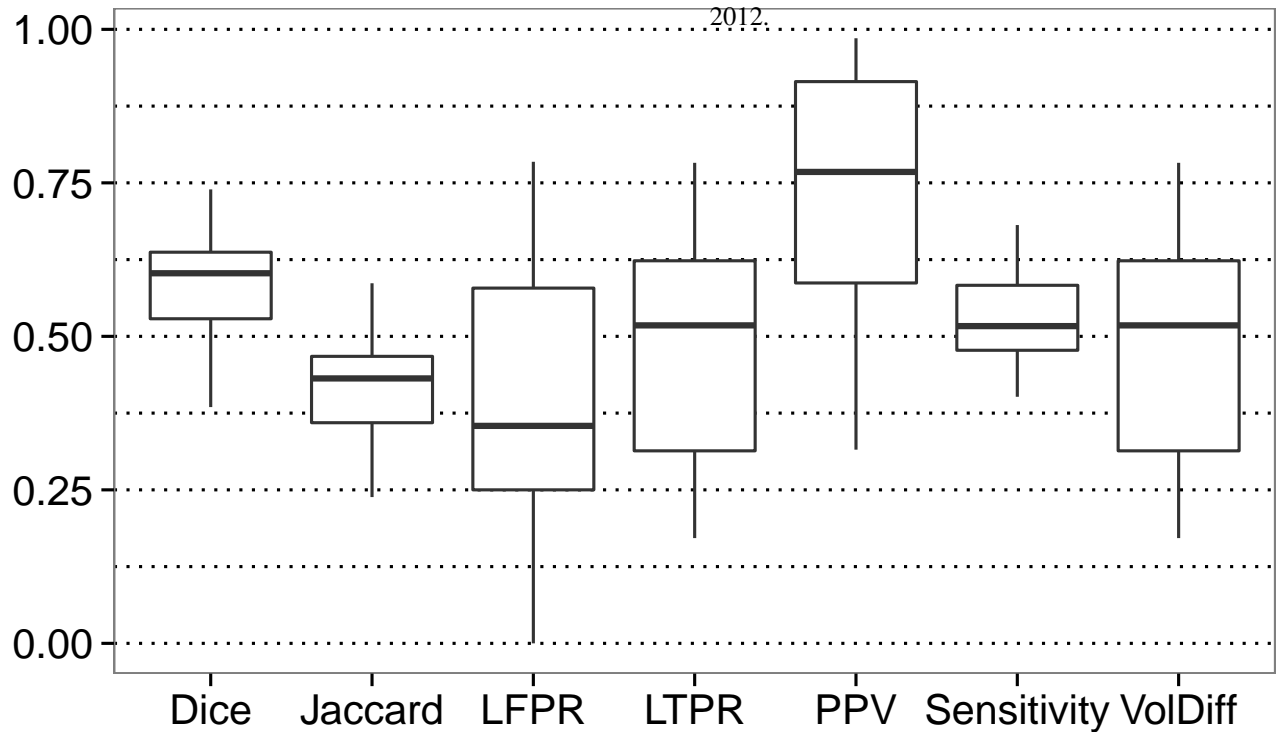


Fig. 1. Training dataset segmentation results.

located brain tissues in healthy subjects, we seek to identify MS lesions by searching for areas with low likelihood.

3. RESULTS

We evaluated MOPS lesion segmentation performance using the training dataset provided by the organizers of the Longitudinal Multiple Sclerosis Lesion Segmentation Challenge at ISBI 2015. Figure 1 show the boxplots of the Dice Score, Jaccard index, positive predictive value (PPV), sensitivity, lesion true positive rate (LTPR), lesion false positive rate (LFPR) and volume difference (VolDiff) achieved by the proposed algorithm.

4. REFERENCES

- [1] Xavier Tomas-Fernandez and Simon Keith Warfield, “A Model of Population and Subject (MOPS) Intensities with Application to Multiple Sclerosis Lesion Segmentation,” *IEEE Trans. Med. Imaging*, vol. 0062, no. c, pp. 1–1, 2015.
- [2] Ralph O Suarez, Olivier Commowick, Sanjay P Prabhu, and Simon K Warfield, “Automated delineation of white matter fiber tracts with a multiple region-of-interest ap-