Deep Convolutional Encoder Networks for Multiple Sclerosis Lesion Segmentation

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Introduction

- Multiple sclerosis (MS) is an inflammatory and demyelinating disease of the central nervous system, and is characterized by the formation of lesions, primarily visible in the white matter on conventional MRIs.
- Imaging biomarkers based on the delineation of lesions, such as lesion load and lesion count, have established their importance for assessing disease progression and treatment effect.
- We propose a new method for segmenting MS lesions that processes entire MRI volumes through a neural network to automatically learn features tuned for lesion segmentation.

Contributions

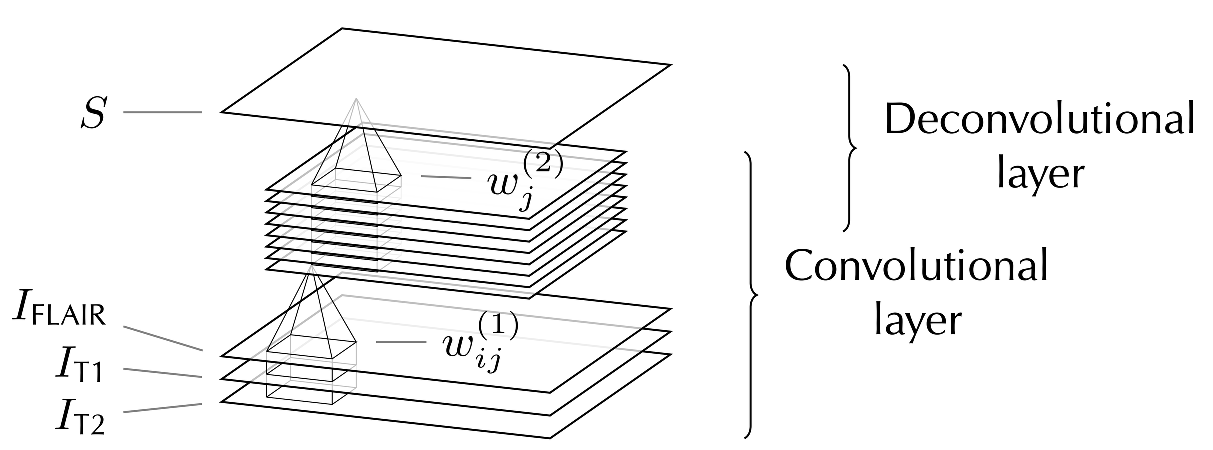
- Our network processes entire volumes instead of patches, which removes the need to select representative patches, eliminates redundant calculations where patches overlap, and therefore scales up more efficiently with image resolution.
- Our approach combines feature learning and segmentation in a single model, which allows for the automatic learning of features that are tuned towards lesion segmentation.
- We propose a new objective function based on a weighted combination of sensitivity and specificity, designed to deal with unbalanced classes, as is the case for lesions, which typically comprise less than 1 % of the image voxels.

Method

- The task of segmenting MS lesions is defined as finding a function s that maps multi-modal images I, e.g., $I = (I_{\text{FLAIR}}, I_{\text{T1}}, I_{\text{T2}})$, to corresponding lesion masks S.
- Given a training set (I_n, S_n), finding s is modeled as an optimization problem of the following form

$$\hat{s} = \arg\min_{s \in \mathcal{S}} \sum_n E(S_n, s(I_n)) \tag{1}$$

where $\mathcal{S}$ is the set of possible segmentation functions, and E is an error measure.
- The set of possible segmentation functions, $\mathcal{S}$, is modeled by the following 3-layer convolutional encoder network:



- The input layer is composed of the image voxels of different modalities.
- The convolutional layer extracts features from the input layer at each voxel location.
- The deconvolutional layer uses the extracted features to predict a lesion mask and thereby classify each voxel of the image in a single operation.
- The error measure, E, is a weighted sum of the mean squared difference of the lesion voxels (sensitivity) and non-lesion voxels (specificity), reformulated to be error terms.

$$E = r\frac{\sum_{\vec{p}}\left(S(\vec{p}) - y^{(2)}(\vec{p})\right)^2 S(\vec{p})}{\sum_{\vec{p}} S(\vec{p})} + (1-r)\frac{\sum_{\vec{p}}\left(S(\vec{p}) - y^{(2)}(\vec{p})\right)^2 \left(1 - S(\vec{p})\right)}{\sum_{\vec{p}}\left(1 - S(\vec{p})\right)} \tag{2}$$

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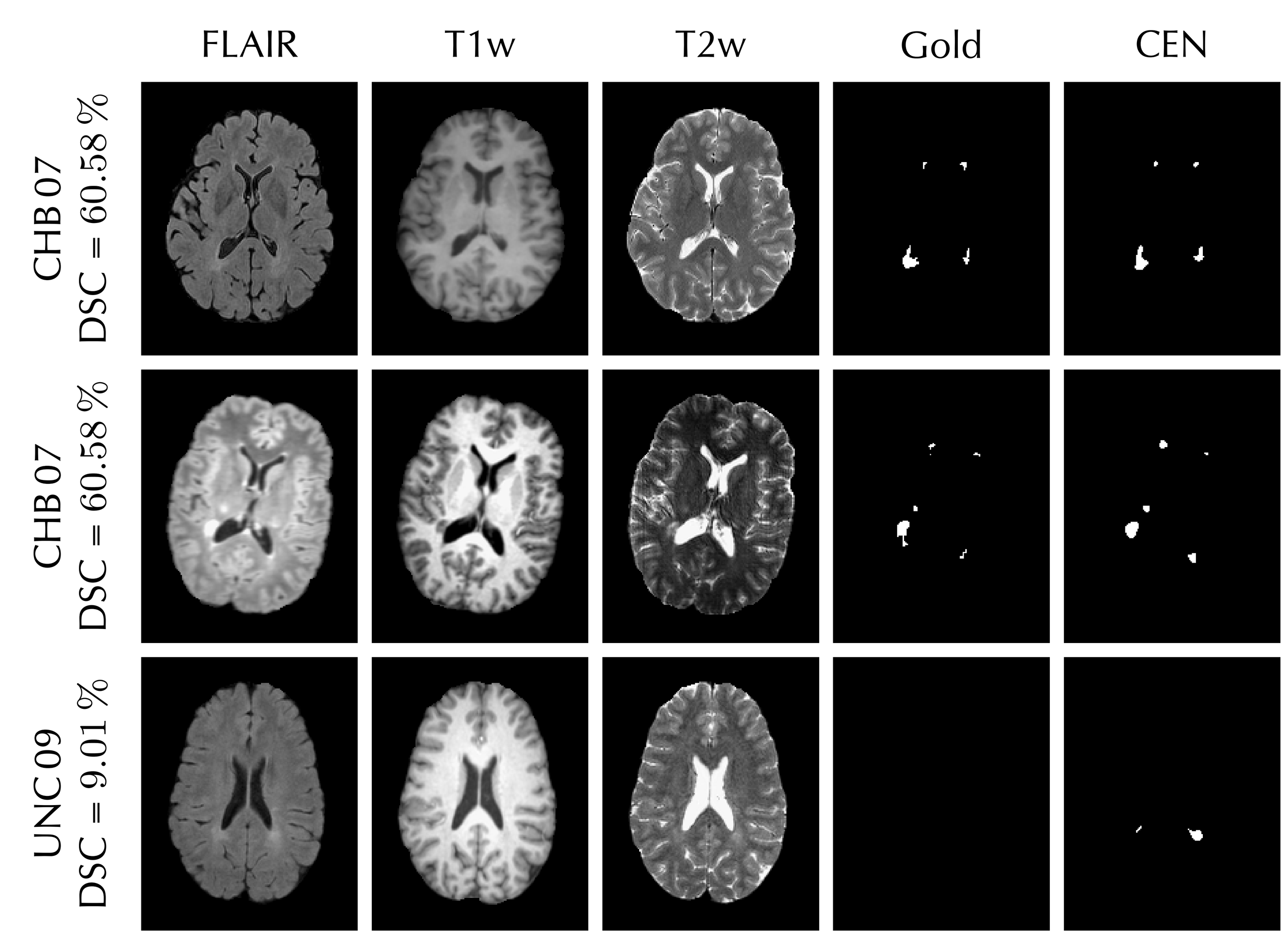
Evaluation

▸ Evaluation on Public Data

Dataset FLAIR, T1-, and T2-weighted MRIs of the 20 publicly available labeled cases from the MS lesion segmentation challenge 2008 [?].

Pre-processing Downsampled from the original isotropic voxel size of $0.5\,\text{mm}^3$ to an isotropic voxel size of $1.0\,\text{mm}^3$

- Example segmentations of our method for three different subjects.
- Our method performed well and consistently despite the large contrast differences seen between the first two rows.
- In the third row, our method also segmented regions that have similar contrast, although these regions had not been identified as lesions by the manual rater.



- Comparison of our method with state-of-the-art lesion segmentation methods in terms of mean TPR, PPV, and DSC.

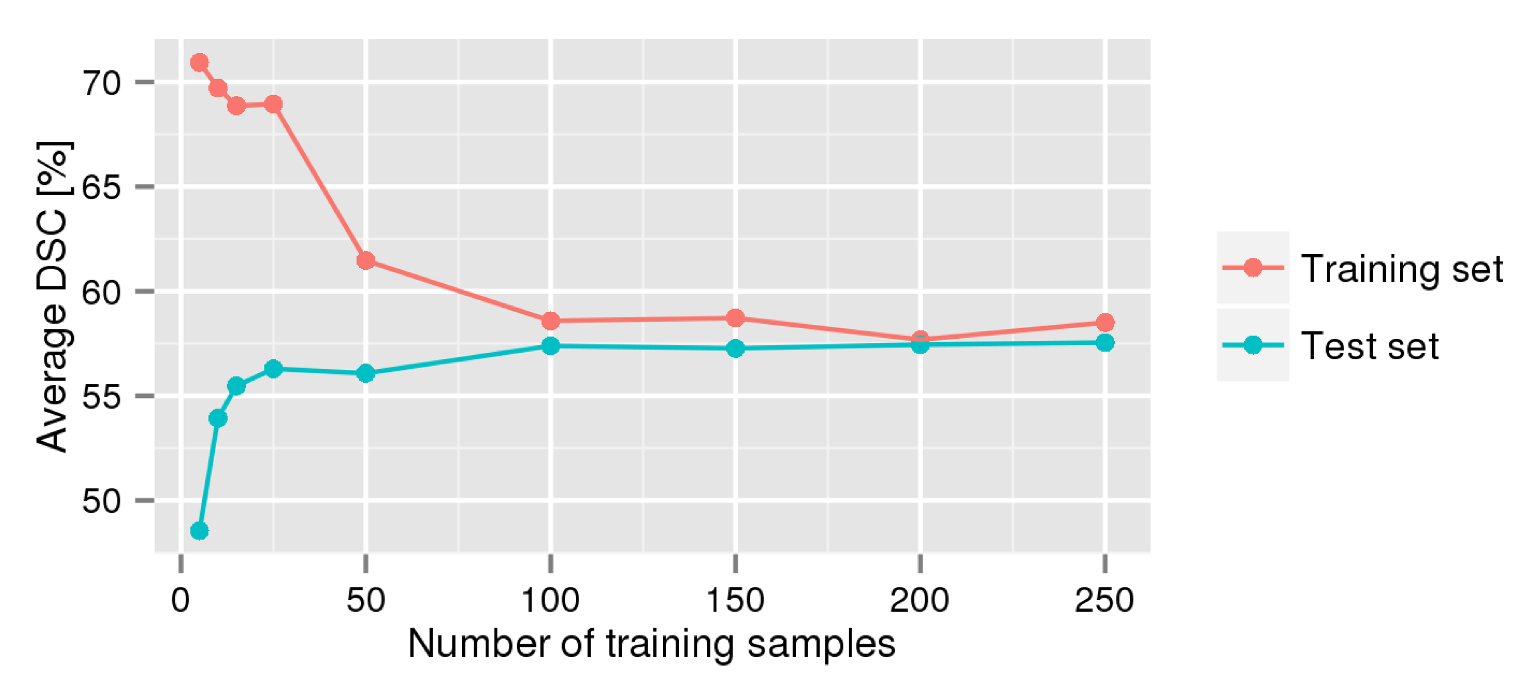
Method	TPR	PPV	DSC
Souplet et al. [?]	20.65	30.00	—
Weiss et al. [?]	33.00	36.85	29.05
Geremia et al. [?]	39.85	40.35	—
Our method	39.71	41.38	35.52

▸ Evaluation on a Large Data Set from an MS Clinical Trial

Dataset The T2- and PD-weighted MRIs of 500 subjects acquired from 45 different scanning were sites split equally into training and test sets.

Pre-processing Rigid intra-subject registration, brain extraction, intensity normalization, and background cropping.

- Comparison of DSC scores calculated on the training and test sets for varying numbers of training samples.
- At around 100 samples, the model becomes stable in terms of test performance.
- The small difference between training and test DSCs, indicating that overfitting of the training data no longer occurs.



Conclusions

- Our method performs comparably to the best methods reported on the MS lesion segmentation challenge data set.
- Performs can be much improved when a suitable training set is available.