

A novel framework for sub-acute stroke lesion segmentation based on random forest

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Abstract. Neuroimaging in the context of stroke is becoming more and more important. Quantifying and characterizing stroke lesions is still an open challenge. In this paper, we propose a novel framework to solve this problem. The features we use are intensities of patches from multiscale multimodal magnetic resonance (MR) images. We have built random forest classifiers for different parts of the whole brain. A leave-one-out cross-validation result on SISS training data yields 0.55 in Dice score.

1 Introduction

Stroke is a cerebrovascular accident, in which part of the function of the brain is lost through a decrease of the blood supply [3]. It is the second major cause of death and it may lead to long-term disability [2]. Advanced neuroimaging techniques have been widely used in the diagnosis of stroke. It is normally recommended that patients should undergo either MR or computer tomography (CT) imaging [4]. Diffusion-weighted imaging (DWI), T2-fluid attenuated inversion recovery (FLAIR), T1-weighted imaging, and T2-weighted imaging should be included in the MR sequences, which are regarded as the gold standard in stroke treatment since they are able to show different types of lesions.

Based on MR images, quantifying lesions is important for assessing the progression of the disease and predicting the functional outcomes for patients. However, manual delineation of lesions is extremely time-consuming and the inter-expert consistency is not satisfactory. In this paper, we propose a novel framework for sub-acute stroke lesion segmentation based on the data from the ISLES challenge, MICCAI 2015.

2 Methods

The ISLES challenge released 28 cases for model training, each of which consists of T1-weighted, T2-weighted, diffusion-weighted, and FLAIR images and a corresponding manual delineation of the actual lesions. The overview of our framework is shown in the Figure 1. It consists of six steps.

In the first stage we normalize all images in terms of intensity. For each image X , we apply the formula $\frac{X-\mu}{s}$, where μ is the mean intensity of the tissue in

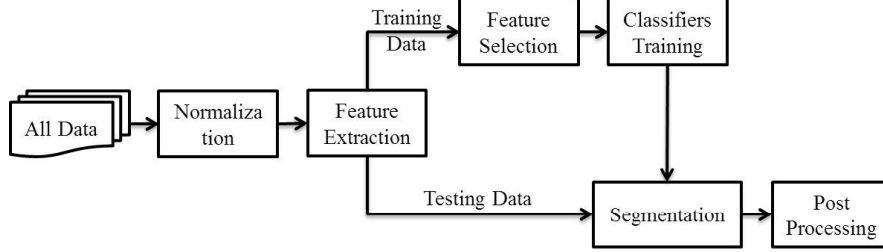


Fig. 1: Overview of the segmentation process.

X and s is its standard deviation. Notably, we exclude 5% outlier voxels with minimum and maximum intensities of the tissue, respectively.

Secondly, we extract features from all images. Intensities of multi-scale patches in each modality are extracted. Specifically, we blur all images at the lower resolutions using Gaussian kernels $\sigma = 1$ and $\sigma = 2$. 5×5 patches are extracted at each scale of each modality. Finally, all patches are converted to vectors and concatenated into a long vector of dimension 300. In a real clinical scenario, the acquired axial slices are typically thick and their thickness can vary significantly. Resampling them into thin slices leads to additional errors. Therefore we prefer pixels, rather than voxels as our features. We parcellate the whole brain into three parts (see Figure 2), including top, middle, and bottom. In the given dataset, there are 65, 40, and 49 slices in the bottom, middle, and top part, respectively. Patches are separated according to their locations and classifiers will be trained for each part individually. The main reason for this is that each part of the brain contains different anatomical structures. The top part contains relatively homogeneous structures. The middle part contains the ventricles and the bottom part contains complicated structures such as the cerebellum. Another reason is that strokes occur most frequently in the middle part of the brain because the main arteries are located there so that the numbers of lesion and normal patches are extremely unbalanced in the top and the bottom part.

In the third step, the data is divided into training and testing sets. In this work, as we will perform the leave-one-out cross-validation, one patient is left out for validation in each round. The remaining training patches will be selected to train classifiers. Since we have a limited number of subjects and not all images contain large lesions, there are significantly less lesion patches than normal ones. If we sample the same number of normal patches as the lesion ones globally, there will be many normal patterns that will be excluded and therefore the test performance will not be satisfactory. We propose to sample different numbers of normal patches for different parts of the brain. In the bottom part, we randomly select 5 times normal patches more than lesion ones since we would like to cover all kinds of normal patterns. For the middle and the top parts, the rates, where the number of normal patches versus lesion ones are 1.5 and 3, respectively.

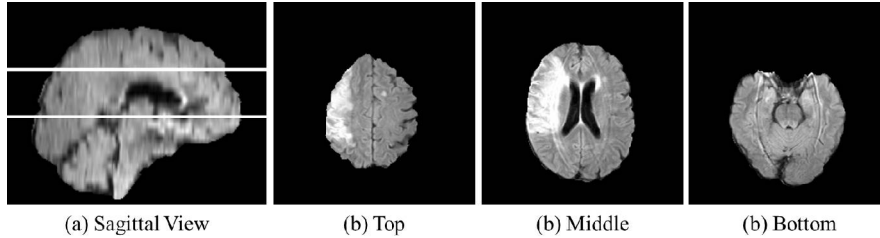


Fig. 2: Illustration of brain parcellation. This is a FLAIR example showing each part of the brain. The structure of the top part is relatively simple. The middle part has ventricles and more lesions. The bottom consists of more complex structures and less lesions.

Subsequently, we can train three classifiers based on the patches selected from three parts of the brain. In this paper, the standard random forests [1] are used as patch classifiers. In each forest, 100 trees are developed. Afterwards, the classifiers can be evaluated with the test data to distinguish how abnormal they are. The outputs of the classifiers are the probabilities that characterize the abnormality of the test patches.

Finally, we perform some post-processing operations. Considering that the lesions in the brain are typically continuous, we smooth the probabilities of the slice at the joint of bottom and middle part of the brain by averaging the probabilities of the neighbouring slices where the outputs given by the classifier of the bottom volume and the classifier for the middle volume have sharp difference occasionally. Based on the resulting probabilities, a threshold $\Theta = 0.6$ is applied to obtain the binary lesion map. For some patients with lacuna infarction, the lesion appearance on the FLAIR image used to be a hyperintense clot with a dark 'hole' inside, which can hardly be detected by the classifiers. Therefore we perform a morphological operation to fill up these 'holes'.

3 Experiments and Results

The method mentioned above is performed on the given training data and we achieve the results presented in Table 1. The leave-one-out cross-validation is used. It is obvious that the results are good if the subject have large lesions. The very small lesions shown in Case 26 and 27 can never be detected.

4 Discussion and Conclusion

We have presented a novel framework for sub-acute stroke lesion segmentation and we achieved an average Dice score of 0.55. In the future, we proposed to collect more data so that there are sufficient data for all kinds of lesions. As a result, different classifiers can be trained for different conditions, where the lesion sizes vary.

Table 1: The results on the SISS training data.

Case ID	ASSD	Dice	Hausdorff Distance	Precision	Recall
1	0.96	0.93	48.88	0.91	0.94
2	2.15	0.83	52.43	0.75	0.92
3	1.59	0.62	49.75	0.48	0.89
4	2.34	0.79	55.29	0.93	0.69
5	1.44	0.87	45.52	0.85	0.88
6	1.05	0.90	28.46	0.86	0.95
7	1.76	0.86	58.60	0.84	0.88
8	19.4	0.49	94.22	0.35	0.84
9	2.11	0.86	24.19	0.90	0.82
10	5.19	0.67	73.74	0.83	0.56
11	10.09	0.59	92.50	0.43	0.94
12	8.30	0.53	67.60	0.41	0.74
13	12.56	0.23	70.80	0.15	0.57
14	1.55	0.81	81.65	0.89	0.75
15	2.22	0.83	48.93	0.73	0.95
16	40.52	0.02	120.59	0.01	0.14
17	11.02	0.49	93.01	0.67	0.38
18	8.41	0.59	83.96	0.47	0.80
19	13.78	0.16	56.86	0.09	0.69
20	4.44	0.77	126.15	0.81	0.74
21	41.43	0.07	140.13	0.04	0.46
22	6.75	0.52	79.76	0.72	0.41
23	22.80	0.38	90.14	0.25	0.77
24	15.38	0.44	102.51	0.31	0.76
25	9.46	0.60	87.87	0.43	0.97
26	29.92	0	85.65	0	0
27	59.99	0	124.96	0	0
28	11.13	0.67	76.69	0.56	0.56
Average	12.42 ± 14.29	0.55 ± 0.29	77.17 ± 28.60	0.52 ± 0.32	0.68 ± 0.27

References

- [1] Breiman, L.: Random forests. *Machine learning* 45(1), 5–32 (2001)
- [2] Donnan, G., Fisher, M., Macleod, M., Davis, S.M.: Stroke. *The Lancet* 371, 1612–1623 (2008)
- [3] Sims, N.R., Muyderman, H.: Mitochondria, oxidative metabolism and cell death in stroke. *Biochimica et Biophysica Acta (BBA)-Molecular Basis of Disease* 1802(1), 80–91 (2010)
- [4] Wintermark, M., Albers, G.W., Alexandrov, A.V., Alger, J.R., Bammer, R., Baron, J.C., Davis, S., Demaerschalk, B.M., Derdeyn, C.P., Donnan, G.A., et al.: Acute stroke imaging research roadmap. *American Journal of Neuroradiology* 29(5), e23–e30 (2008)