Comparison of normalized DTI analytical methods: Detection powers of voxel-based analysis and sub-atlas based analysis

K. Sakai[1,2], S. Mori[2], K. Oishi[2], and A. Faria[2]
[1]Kyoto University, Kyoto, Kyoto, Japan, [2]Johns Hopkins University, United States

INTRODUCTION

The voxel-based group analysis (VBA) is one of the most effective examination methods of the entire white matter (WM) of brain. However, the VBA often suffers from low statistical power (high false discovery rate), which caused by embedded noise in voxels. To ameliorate this problem, the combination of the VBA with a pre-segmented WM has already been proposed [1]. On the other hand, 3D whole brain WM atlas (ABA: atlas-based analysis) was proposed to gain statistical power on the examination of the WM analysis [2]. In this paper, we attempted to further extend the ABA to obtain statistically stronger detection power than the VBA. We propose a sub-atlas-based analysis (SBA), which uses 3D plane made from the fitting curves to the WM atlas. We will compare detection power among the VBA and the SBA by using ICBM-152 normal brain artificially embedded abnormal values. From the results, we will consider the differences of these methods on the different kinds of abnormalities.

METHODS

Subjects: ICBM-152 normal subjects data (n=21) [3], which were randomly selected from data set, were used. We performed dual channel (b0 and FA) affine transformation and a large deformation diffeomorphic metric mapping (LDDMM) for alignment [2] and computed FA values. **Creation of a sub-atlas:** Fig.1 shows the sub-atlas creation steps of corpus callosum (CC) and a final WM sub-atlas. First, we fit a 3D plane to each portion of parceled WM atlas by using a cubic surface function [4]. Second, the hanging out portions of fitted plane was trimmed. We repeated the process to every parceled WM region. At the end of these steps, we combined all atlas planes to create whole brain WM atlas plane. All voxels within a parceled atlas were projected to the nearest voxel on sub-atlas plane. The averaged value of the all projected voxels was assigned as the value of voxel on the sub-atlas. **Embedding abnormal value:** We embedded abnormal values within the rectangle area which covers body of CC (Fig.2a). We set this rectangle was 100% abnormal area, which included 22 portions of parceled WM (fornix, anterior limb of internal capsule left (-L), right (-R), posterior limb of internal capsule-L, -R, cingulum-L, -R, superior fronto-occipital fasciculus-L, -R, superior frontal blade-L, -R, post-central blade-L, -R, CC, corona radiata-L, -R). We changed abnormality covering area based on this rectangle from 10 to 100%. We also changed FA value of each voxel from 10 to 100% based on original values. Fig. 2(b and c) shows slices of 60% abnormal area 60% decreased FA (b: randomly arranged abnormal values, c: cluster arranged abnormal values). **Comparison of detection power:** We detected abnormality as the outlier of FA values on the same spatial position across the subjects (VBM-style analysis [1]) by using Grubbs-Smirnov (GS) test. The detection power of each method was defined as percentage of detected outliers per embedded abnormalities.

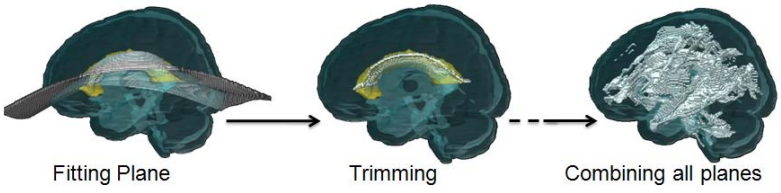

Figure 1. Steps of making a WM sub-atlas

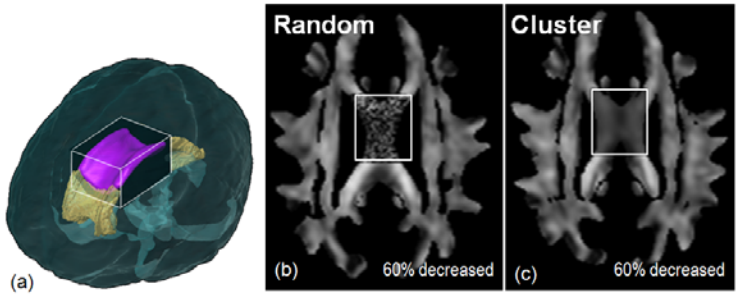

Figure 2. Embedded abnormal area (a) and arrangements of abnormality(b, c)

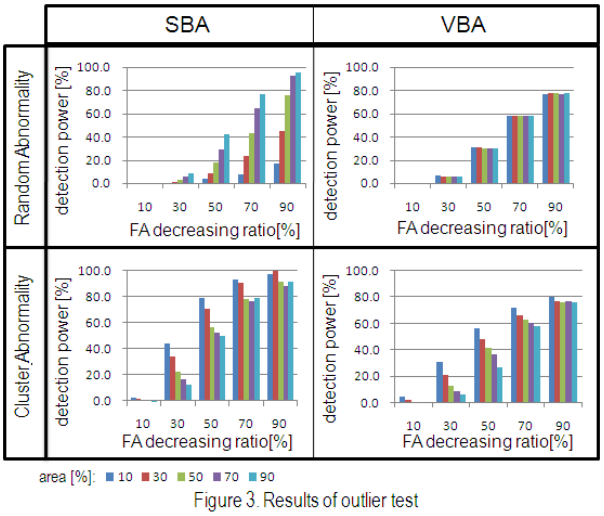

Figure 3. Results of outlier test

RESULTS AND DISCUSSION

Fig.3 shows the results of outlier test. The horizontal axis of the charts indicates the decreasing percentage of original FA value. Each bar shows the percentages of abnormal area, based on Fig.2a. The vertical axis shows the detection power. In the case of random abnormality, the detection power of SBA was clearly affected by both abnormal area and its value (Fig3, upper left). On the other hand, the detection power of VBA was not affected abnormal area and it was only affected by abnormal values (Fig3, upper right). In the case of cluster abnormality, the detection power of SBA was affected by both abnormal area and value (Fig3, lower left). The affection of abnormal area was opposite from random abnormality due to the difference of their arrangement. The detection power of VBA was also affected by both abnormal area and value (Fig3, lower right). From the results, these two methods showed better detection power on the cluster abnormal arrangement than the random abnormal arrangement. This means that the distribution of abnormal values affects the detection power of VBM-style examination methods. The extension of the area covered by abnormal values in the region of interest also affected the detection power of these methods. When abnormal values covered relatively narrow area, the detection power was relatively higher than the wide-covered area by abnormal value. The reason was the averaging, which decides each voxel value, on the SBA. On the VBA, when abnormal values cover relatively wide area, wide-value-distribution occurs. This wide-value-distribution range across the subjects make hard to detect the abnormality by GS test.

CONCLUSION

We proposed new method "SBA" to analyse abnormality within the white matter in brain. We compared our proposed method with conventional VBA. The SBA had a larger abnormality detection power than the VBA , when the abnormality arranged as a cluster .

References [1] Smith et al., NeuroImage 31(2006), 1487-1505, [2] Mori et al., NeuroImage 40 (2008), 570-582, [3] http://www.loni.ucla.edu/ICBM/Downloads/Downloads_Atlases.shtml, [4] http://www.mathworks.com/matlabcentral/fileexchange/8998