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Original Article

Alzheimer's Disease: Diagnosis by Different Methods of Voxel-Based Morphometry

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Abstract *Purpose* : The purpose of this study was to determine the optimal computational options in voxel-based morphometry (VBM) for discrimination between Alzheimer's disease (AD) patients and healthy control (HC) subjects.

Materials and Methods : Structural magnetic resonance images of 24 AD patients and 26 HC subjects were analyzed using VBM to determine brain regions with significant gray matter (GM) loss due to AD. The VBM analyses were performed with 4 different computational options : gray matter concentration (GMC) analysis with and without global normalization, and gray matter volume (GMV) analysis, with and without global normalization. Statistical maps calculated with the 4 computational options were obtained at 3 different P-value thresholds ($P < 0.001$, $P < 0.0005$, and $P < 0.0001$, uncorrected for multiple comparisons), yielding a total of 12 sets of maps, from which regions-of-interest (ROI) were generated for subsequent analyses of performance in terms of discrimination between AD patients and HC subjects as based on the mean value of either the GMC or GMV within the ROI for each of the 12 maps. Discrimination performance was evaluated by means of comparing the area-under-the-curve derived from the receiver-operating characteristic analysis as well as on the accuracy of the discrimination.

Results : Discrimination based on GMC analysis resulted in better performance than that based on GMV analysis. The best discrimination performance was achieved with GMC analysis either with or without proportional global normalization.

Conclusion : The findings suggested that GMC-based VBM is better suited than GMV-based VBM for discrimination between AD patients and HC subjects.

Key words : MRI, Alzheimer's disease, Voxel-based morphometry

Introduction

In the majority of developed countries, Alzheimer's disease (AD) is the most common progressive illness leading to dementia^{1)–3)}. Although in the clinical practice, the role played by structural magnetic resonance (MR) imaging of

the brain has been confined primarily to ruling out alternative causes of dementia, MR imaging has been increasingly recognized as a tool for the early diagnosis of AD. With the advent of new therapeutic agents, such as cholinesterase-inhibitors, which have been shown to be efficacious in the early AD stages^{4)–6)}, the identification of AD-compatible morphological features prior to the onset of severe clinical dementia is a crucial component of clinical decision-making and is relevant for the assessment of promising therapies in the context of clinical trials⁷⁾. Fully

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automated voxel-based morphometry (VBM)⁸⁾ objectively detects disease-related alterations in regional brain tissue morphology and offers independence from the expertise of individual neuroradiologists. VBM has been used for group-wise studies of AD, as well as for distinguishing between individuals with AD from those without^{9)–12)}. Recently, VBM was adopted into a dedicated software package for AD screening¹¹⁾. VBM consists of several steps of image processing, each of which has different computational options that may critically affect the final diagnostic results. Scarce number of publications on the assessment of the effects of variations in image processing as well as the divergent manner of reporting VBM results and the differences between applied VBM protocols make the tracing of such effects difficult and render it necessary to systematically evaluate VBM performance. The purpose of this study was to determine the optimal computational options in VBM for discrimination between AD patients and healthy control (HC) subjects.

Materials and Methods

The study was approved by the regional institutional review board, and informed consent was obtained from each HC subject. Clinical and imaging data for the AD patients were reviewed retrospectively, and the need to obtain informed consent was waived.

Subjects

Among those who visited the memory clinic at our hospital, 83 consecutive patients were identified respectively. Among these patients, those, who fulfilled the clinical criteria for AD were considered for inclusion in the study population. Each patient was diagnosed based on case conferences by both experienced neurologists and psychiatrists at our hospital, according to the criteria of the National Institute of Neurological and Communicative Disorders and Stroke, in concert with the criteria defined by the Alzheim-

er's Disease and Related Disorders Association¹³⁾ and the Diagnostic and Statistical Manual of Mental Disorders, 4th edition¹⁴⁾. All patients received the Japanese version of the Mini-Mental Scale Examination (MMSE) test¹⁵⁾. The interval between MMSE test and MR imaging ranged from 0 to 53 days (mean 26 days). Additionally, Raven's Colored Progressive Matrices and the Miyake's paired verbal associate learning test were routinely performed. During the diagnosis, both structural MR imaging results and single-photon emission tomography (SPECT) findings were taken into consideration. In addition, MR imaging was used to carefully exclude vascular dementia, according to the criteria of the National Institute of Neurological and Communicative Disorders and Stroke - Association Internationale pour la Recherche et l'Enseignement en Neuroscience¹⁶⁾. All MR images of the patients were screened by a board-certified radiologist (T. Y.). Patients with a space-occupying lesion were excluded, since VBM has not been validated under such conditions. In addition, patients were excluded when artifacts degraded their MR images. Twenty-four patients (10 men and 14 women; mean age \pm SD, 74.4 \pm 8.9 years) met the inclusion/exclusion criteria, and were included in this study. The MMSE scores of these patients ranged from 11 to 29 (mean \pm SD = 21.2 \pm 4.3).

The HC subjects were recruited from the general population. They had no history of hypertension, diabetes mellitus, cardiovascular disease, stroke, brain tumor, epilepsy, Parkinson's disease, dementia, depression, drug abuse, or head trauma. These candidate control subjects also received the MMSE. Only those recruited subjects who achieved 27 points or more were included in the study. The HC subjects were also assessed using the self-rating depression scale¹⁷⁾ in order to screen for depression, and those who scored 40 points or more were excluded from the present study. Twenty-six HC subjects (12 men and 14 women; mean age \pm

SD, 73.6 ± 6.8 years; mean MMSE score \pm SD, 29.4 ± 0.9) were included in the study.

MR imaging procedures

All images were acquired using a 3T MR imager (Achieva Quasar Dual ; Philips Medical Systems, Best, Netherlands) and an 8-channel head array coil. High-resolution T1-weighted images for morphological analysis were obtained using the following settings for three-dimensional (3D) magnetization-prepared rapid gradient-echo (MPRAGE) : repetition time = 8.3 ms, echo time = 3.8 ms, inversion time = 240 ms, flip angle = 8° , sensitivity encoding factor = 2, number of signal-intensity acquisitions = 1, field of view = 240 mm, matrix size = 240×240 , slice thickness = 1 mm, imaging time = 5 min 20 s. The images were reconstructed into 1-mm-thick consecutive transverse images.

Image analysis

VBM analysis was performed using SPM8 software (Wellcome Trust Center for Neuroimaging, London, UK, <http://www.fil.ion.ucl.ac.uk/spm/software/spm8/>). The images were segmented into gray matter (GM) and white matter (WM) images. Next, roughly aligned isotropic

($1.5 \times 1.5 \times 1.5 \text{ mm}^3$) GM images were obtained such that the images could be imported for subsequent non-linear registration based on an algorithm referred to as “diffeomorphic anatomical registration through exponentiated lie algebra” (DARTEL)¹⁸. The GM images of all subjects were non-linearly registered to the “template” images, which were initially created by averaging GM images from all subjects, i.e. all HC subjects and AD patients. The GM images of each subject registered to the template by iterative calculations were spatially normalized into a common stereotactic space. Finally, the images were smoothed using an 8 mm full-width-at-half-maximum isotropic 3D Gaussian kernel. For each subject, we prepared two sets of GM images, including those obtained with and without “modulation”, which was applied to correct for volume alterations due to deformation during spatial normalization¹⁹. Specifically, such modulation involves multiplying voxel values by the Jacobian determinants derived from the spatial normalization step. In images obtained without the modulation, the value of each voxel represents the local GM concentration (GMC), whereas it represents the local GM volume (GMV) in images obtained with the modulation. In

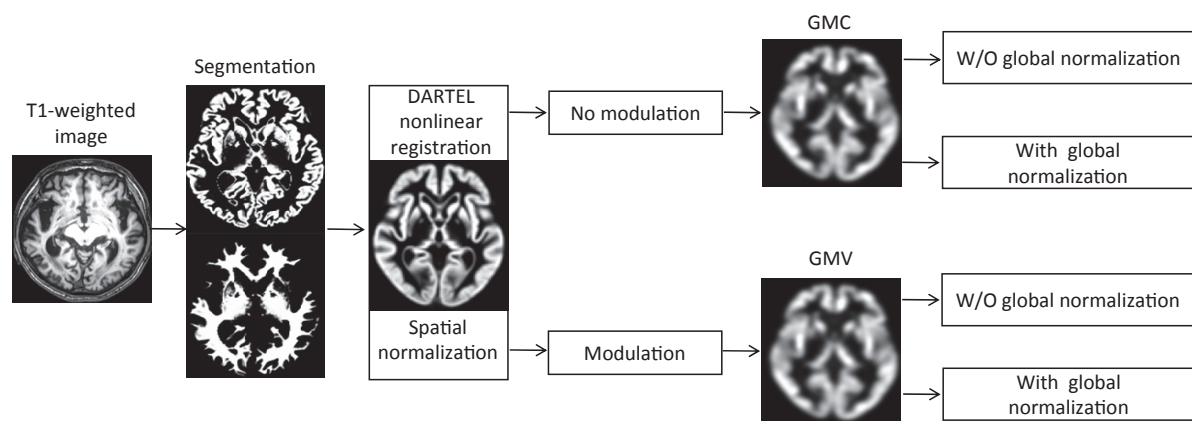


Fig. 1 Voxel-based morphometric (VBM) analysis of structural magnetic resonance images. T1-weighted images of each subject were first segmented into gray matter (GM) and white matter images. The GM images were then spatially normalized using a non-linear registration algorithm rendering to as “diffeomorphic anatomical registration through exponentiated lie algebra” (DARTEL). The voxel values of the spatially normalized GM image represent the local gray matter concentration (GMC). By applying a modulation to the spatially normalized GM image, the voxel values represent the local gray matter volume (GMV). For both GMC and GMV images, there was the option of either using or not using proportional global normalization. Thus, there were 4 different computational options in the VBM analysis.

addition, for both GMC images and GMV images, there was another option of performing the analysis either with or without proportional global normalization to control for individual variation in the global mean, where the value of each voxel was normalized by the proportional scaling to the global mean value. Thus, there were 4 different computational options in the VBM analysis (Fig 1).

Statistical analysis

A two-sample *t*-test was conducted using SPM8 to determine areas with significantly reduced GMC or GMV in AD patients as compared to HC subjects. Absolute threshold masking was employed to exclude voxels outside of GM regions. The statistical maps were generated at different voxel-wise significance levels of $P < 0.001$, $P < 0.0005$, and $P < 0.0001$, uncorrected for multiple comparisons. Finally, we generated 12 sets of statistical maps, including those for GMC and GMV obtained with and without global normalization at 3 different *P* value thresholds. Each of the 12 statistical maps was binarized and was used as a region-of-interest (ROI) in the subsequent analysis of the discrimination performance.

Discrimination between AD patients and HC subjects was attempted based on the mean values of either the GMC or GMV within the ROI generated from each of the 12 statistical maps in the previous step. The discrimination performance of each approach was evaluated by the area-under-the-curve (AUC) values derived from the receiver-operating characteristic (ROC) analysis using ROCKIT 1.1 B2 software (Kurt Rossmann Laboratories for Radiologic Image Research, The University of Chicago, Chicago, IL, USA), as well as from the sensitivity, specificity, positive predictive value, negative predictive value, and accuracy of the discrimination calculated using the linear discriminant analysis on JMP8.0 (SAS Institute, Cary, NC, USA).

Results

VBM analysis

The results of the VBM analyses of GMC with and without the proportional global normalization at three different *P*-value threshold settings ($P < 0.001$, $P < 0.0005$, and $P < 0.0001$, uncorrected for multiple comparisons, respectively) are shown in Fig. 2. Comparison of the GMC without global normalization revealed areas of significant GM loss due to AD which were distributed in a scattered pattern in both cerebral and cerebellar hemispheres with *t*-value peaks in the bilateral hippocampi (Fig. 2a). When proportional global normalization was added to the analysis, the areas of significant GM loss due to AD were reduced to areas of the bilateral hippocampi, bilateral temporal lobes, bilateral frontal lobes, right anterior insula and left inferior parietal lobule (Fig. 2b).

Figure 3 shows the results for the GMV analysis. In general, the areas of significant GMV loss due to AD were found to be more localized than the areas of significant GMC loss obtained at the same *P*-value thresholds as those shown in Fig 2. The areas of significant GMV loss were distributed in the bilateral hippocampi, right medial temporal lobe, right orbitofrontal region and left inferior parietal lobules (Fig. 3a). As seen in the GMC results, the inclusion of proportional global normalization resulted in a reduction in areas revealing significant differences (Fig 3b).

Analysis of discrimination performance

The results of the discrimination performance evaluation are summarized in Table 1. In general, discrimination based on GMC analysis (AUC range, 0.716–0.817) tended to be associated with better performance than that based on GMV analysis (AUC range, 0.624–0.745). The best discrimination performance was achieved either when the unmodulated data (GMC) were analyzed with proportional global normalization at a threshold of $P < 0.0005$ (AUC = 0.816, accuracy =

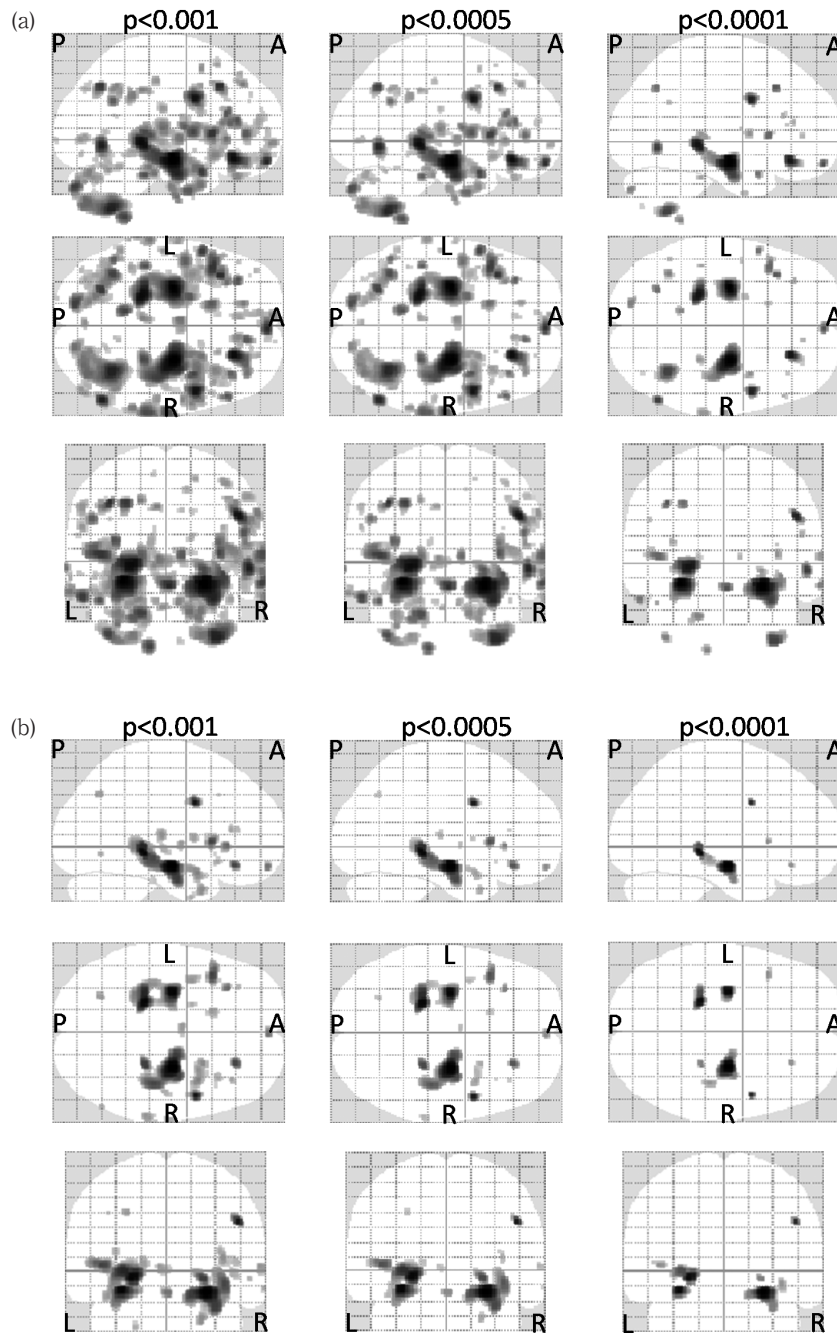


Fig. 2 Results of the group-wise VBM analysis of GMC obtained without (a) and with (b) proportional global normalization at three different P-value threshold settings ($P < 0.001$, $P < 0.0005$, and $P < 0.0001$, uncorrected for multiple comparisons). In each map, the gray scale reflects t value. P, posterior ; A, anterior ; L, left ; R, right.

80.0%), or when the GMC was analyzed without proportional global normalization at a threshold of $P < 0.0001$ (AUC = 0.817, accuracy = 74.0%) (Table 1).

Discussion

The present series demonstrated that the

selection of different computational options for VBM gave different results, and the influence of the various options applied both to group comparisons and analyses of discrimination performance.

In both the GMC and GMV analyses, a significant loss of GM due to AD was consistently identified in the temporal lobe, including the

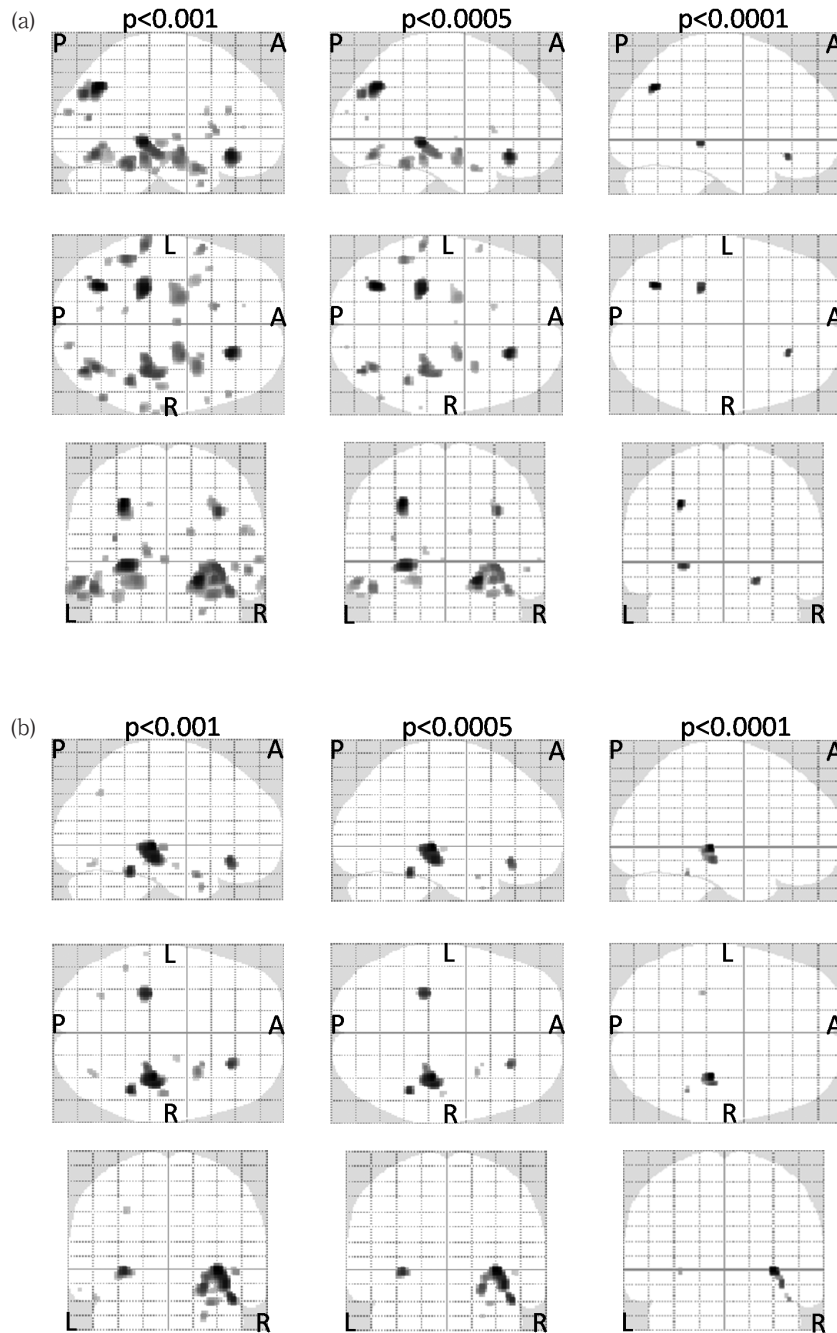


Fig. 3 Results of the group-wise VBM analysis of GMV obtained without (a) and with (b) proportional global normalization at three different P-value threshold settings ($P < 0.001$, $P < 0.0005$, and $P < 0.0001$, uncorrected for multiple comparisons). In each map, the gray scale reflects t value. P, posterior ; A, anterior ; L, left ; R, right.

hippocampus (Figs. 2 and 3). This finding was in agreement with those of previous morphometric studies^{20)–26)} as well as with those of neuropathological studies^{27)–29)}. On the other hand, a substantial difference was noted between the VBM results for the GMC and the GMV. In our study, at a given P-value threshold, the GMV

analyses (Fig. 3) detected less extensive areas of significant GM loss than did the GMC analyses (Fig. 2). Such discrepant results in a group-wise comparison between GMC and GMV analyses have been reported frequently in studies of various neurological and neuropsychiatric diseases^{30)–33)}. For example, a meta-analysis

Table 1 Analysis of discriminating performance

Gray matter measure	P-value	SE %	SP %	PPV %	NPV %	Accuracy	AUC
GMC W/O global normalization	< 0.001	54.1	69.2	61.9	62.1	62.0	0.716
	< 0.0005	58.3	73.1	66.7	65.5	66.0	0.744
	< 0.0001	66.7	80.8	76.2	72.4	74.0	0.817
GMC With global normalization	< 0.001	70.8	80.8	66.7	60.7	76.0	0.797
	< 0.0005	70.8	88.5	66.7	60.7	80.0	0.816
	< 0.0001	62.5	88.5	66.7	60.7	76.0	0.811
GMV W/O global normalization	< 0.001	62.5	73.1	68.2	67.9	68.0	0.729
	< 0.0005	62.5	76.9	71.4	69.0	70.0	0.745
	< 0.0001	58.3	65.4	60.9	63.0	62.0	0.624
GMV With global normalization	< 0.001	58.3	73.1	85.0	76.9	66.0	0.660
	< 0.0005	54.2	76.9	85.0	76.9	66.0	0.712
	< 0.0001	54.2	76.9	85.0	76.9	66.0	0.705

Note. GMC, gray matter concentration ; GMV, gray matter volume ; SE, sensitivity ; SP, specificity ; PPV, positive predicting values ; NPV, negative predicting value ; AUC, area-under-the-curve.

reported by Fortino *et al.*³³⁾ describes such disagreement in schizophrenia studies, in which larger areas with GMC loss were distributed in a manner that differed areas showing GMV loss.

In the discrimination performance analysis, GMC-based discriminations tended to perform better than those based on GMV (Table 1). This tendency was consistent with that described in several previous reports. Wilke *et al.*³⁰⁾ used the VBM to detect GM malformation, and their GMV analysis demonstrated lower detection sensitivity and identified smaller lesion volumes than did analysis of the GMC. A more recent publication by Bruggermann *et al.*³²⁾ on the detection of dysplasia and neoplasia in childhood epilepsy showed greater sensitivity and specificity for GMC than GMV analysis. In the discrimination of AD patients from HC subjects, Matsunari *et al.*³⁴⁾ used VBM, and they reported better performance with GMC (AUC = 0.832, accuracy = 85 %) compared to GMV (AUC = 0.782, accuracy = 79 %). It should be noted that all of these previous studies were based on older VBM regimens, i.e. either the so-called “classical” or “optimized” VBM. In our VBM analysis, the spatial normalization of the images was performed using the DARTEL algorithm, which is a more advanced and robust registration method compared to that used in either the classical or

optimized VBM approach³⁵⁾. Our results suggest that the use of DARTEL registration does not change the advantage of GMC analysis over GMV analysis in terms of diagnostic performance.

The reason for the discrepant results between the GMC and GMV analyses remains unclear. Fortino *et al.*³³⁾ raised the possibility that the modulation can increase inter-subject variability in the data. As noted earlier, the modulation is performed to correct for the volume alteration due to deformation during the spatial normalization. Since the modulation is dependent on the degree and nature of the deformation, it can introduce additional variability into the results, depending on the shape of the individual subject's brain, which may in turn reduce the statistical power of the analysis. In contrast, GMC analysis is conducted directly after spatial normalization, when the interindividual variability is minimized. Thus, GMC analysis may be more sensitive to systematic differences in the morphology of the local GM, while those “differences” may actually reflect alterations such as sulcal widening and displacement caused by AD pathology rather than true GM loss. It is conceivable that the better discrimination performance of the GMC analysis relative to that of the GMV analysis in this study (Table 1) was related to the greater sensitivity of the GMC analysis in the group

comparison.

As shown in Figs. 2 and 3, the use of proportional global normalization resulted in a more localized distribution of significant voxels within the medial temporal regions in both the GMC and GMV analyses. That finding is likely to have reflected a well-known distribution pattern for GM loss in AD patients, namely, rather than being diffusely distributed. GM loss in AD patients is limited to the medial temporal regions, especially during the early stages of disease¹⁰⁾¹¹⁾²⁰⁾. In the analysis of discrimination performance, the effect of proportional global normalization appears to be variable : in this series, global normalization appeared to have improved the performance in GMC analyses whereas no such effect was seen in the GMV analyses (Table 1). The underlying mechanism of this apparent differential effect of the global normalization on the discriminating performance of GMV and GMC analyses remains unexplained. This study has several limitations. The number of subjects included in the study was limited. In future studies, inclusion of a larger number of subjects will be desirable such that separate subject groups can be evaluated for the determination of discriminating criteria and the evaluation of overall performance. Although we found higher AUC values with GMC analysis than with GMV analysis (Table 1), we could not provide statistical significance for the differences of their AUC values due to the limited subject number. We used the DARTEL algorithm for spatial normalization, and we did not test other VBM regimens such as “classical” and “optimized” VBM. The effects of the normalization algorithm will still need to be clarified in future studies. In our study, discrimination was performed based on the averaged GMC/GMV within ROI. Averaged values were used in some previous reports³⁴⁾, while in other reports maximum Z-score within the ROI was used¹¹⁾. We did not include the latter method. AD patients used in this study were on average relatively mild cases

(mean MMSE score = 21.2). However, in clinical practice, diagnosis of even earlier AD or mild cognitive impairment is desirable. Further studies involving those patients are necessary.

Conclusion

We demonstrated that the choice of computational options in VBM can substantially affect both the results of group-wise comparisons as well as discrimination performance. Our findings suggested that VBM based on GMC analysis may be better suited for discrimination between AD patients and HC subjects than is VBM based on GMV analysis.

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(和文抄録)

Voxel-Based Morphometry に基づく Alzheimer 病の診断：解析法の影響

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目的：voxel-based morphometry (VBM) による脳形態解析に基づく Alzheimer 病患者と健常者の判別における、最適な解析法を明らかにすることが目的である。

対象と方法：24名の Alzheimer 病患者と26名の健常者を対象とした。それぞれの被験者の脳 T1 強調 MR 画像を VBM の手法に従って解析し、Alzheimer 病による有意な灰白質減少を示す脳領域を求めた。VBM 解析は、modulation を行わない灰白質濃度の解析と、modulation を行うことで得られる灰白質体積の解析の両者を、それぞれ全脳による正規化 (global normalization) を加えて行う場合と加えずに行う場合の、計4種類の解析法で行った。それぞれの方法において、3段階の P 値設定 ($P < 0.001$, $P < 0.0005$ および $P < 0.0001$) で statistical parametric mapping 解析を行い、得られた有意な灰白質減少を示す脳領域内での平均灰白質濃度または体積に基づいて、患者と健常者の判別を行った。receiver operating characteristic 解析と判別分析を用いて、異なる方法の間で判別能の比較を行った。

結果：灰白質濃度による解析は、灰白質体積による解析に比較して、判別能が高かった。global normalization の有無の影響は明らかではなかった。

結論：VBM に基づく Alzheimer 病患者と健常者の判別には、灰白質体積による解析よりも灰白質濃度による解析が適していると考えられた。