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Automatic classification of segmented MRI data combining Independent Component Analysis and Support Vector Machines

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Abstract. This paper proposes a novel method for automatic classification of magnetic resonance images (MRI) based on independent component analysis (ICA). Our methodology consists of three processing steps. First, all the MRI scans are normalized and segmented into gray matter, white matter and cerebrospinal fluid. Then, ICA is applied to the preprocessed images for extracting relevant features which will be used as inputs to a support vector machine (SVM) classifier in order to reduce the feature space dimensionality. The system discriminates between Alzheimer's disease (AD) patients, mild cognitive impairment (MCI), and normal control (NC) subjects. All MRI data used in this work were obtained from the Alzheimers Disease Neuroimaging Initiative (ADNI). The experimental results showed that our methodology can successfully discriminate AD and MCI patients from NC subjects.

Keywords. Alzheimer's disease, mild cognitive impairment, magnetic resonance imaging, independent component analysis, support vector machine

Introduction

Alzheimer's disease (AD) is a progressive and neurodegenerative disease that affects brain cells. It is by far the major common cause of dementia associated with aging. Currently, AD affects approximately 30 million individuals worldwide and with the growth of the older population in developing nations, the incidence of dementia is expected to triple during the next 50 years[1]. To clinically diagnose the progression of the disease, structural magnetic resonance imaging (sMRI) [2], one of biomedical imaging techniques, has been used. Structural MRI [3] has been widely used for early diagnosis of AD [4,5]. This imaging technique produces high quality images of the anatomical structures of the brain, and provides rich information for clinical diagnosis and biomedical research [6]. The early changes in the brain are reliable with the underlying pathology of AD. However, it has been challenging to use fully automated MRI analytic methods to identify potential AD neuroimaging biomarkers [7], and further to diagnose AD or MCI patients.

Several approaches have been proposed for providing an automatic tool that guides the clinician in the AD diagnosis process [8,9]. These approaches can be classified into two categories: univariate and multivariate approaches. Statistical parametric mapping(SPM) [10,11] software tool is a univariate statistical testing methodology which analyzes and compares each voxel value of the image under study to the mean values of the group of normal images. On the other hand, multivariate approaches analyze all the voxels together in a single scan and requires a higher number of available samples than the one of the features used in the training step. This fact reports the well-known small sample size problem. In this context, with the goal to solve the dimensionality problem, independent component analysis (ICA) technique was used to perform the feature reduction space.

ICA is a multivariate analysis method [12]that enables an exploratory analysis of MRI datasets to provide useful information about the relationships among voxels in local substructures of the brain. In this work, a new ICA-based approach is used in combination with supervised learning methods, which the main goal is to solve the dimensionality problem. Firstly, the presented work focuses separately on GM and WM brain tissues to delimit the most discriminant brain tissue for examining AD from MRI and secondly, information extracted from the different brain tissues are combined together in order to improve the classification accuracy for distinguishing AD and MCI subjects from NC. In addition, for the diagnosis or classification of AD and MCI patients, support vector machine (SVM) is used.

This paper is organized as follows. Section 2 shows a description of the database used for validation and details the ICA-based feature extraction method proposed. Section 3 describes the experiments carried out, shows the results and discussion; and conclusions are drawn in section 4.

1. Materials and methods

1.1. ADNI database

Data contained in this database, and used in the preparation of this article were obtained from the Alzheimers Disease Neuroimaging Initiative (ADNI) database (`www.loni.ucla.edu/ADNI`). The characteristics of the data set are shown in table 1.

Table 1. Demographic data of patients in the database (ADNI 1075-T1).

Diagnosis	Number	Age	Gender (M/F)	MMSE
NC	229	75.97±5.0	119/110	29.00±1.0
MCI	401	74.85±7.4	258/143	27.01±1.8
AD	188	75.36±7.5	99/89	23.28±2.0

MMSE: mini-mental state examination[13]

1.2. MRI data pre-processing

MRI images from the ADNI database were preprocessed and segmented using the Statistical Parametric Mapping (SPM) software [14]. SPM was initially designed for func-

tional images, but it also provides routines for realignment, smoothing and spatial normalization into a standard space of T1-weighted images. Moreover, the template from the VBM package [15] was used for this purpose. It is worth mentioning that normalization routines preserve the amount of tissues and not the intensities [14]. Thus, images from the ADNI database were resized to $121\times145\times121$ voxels with voxel sizes of 1.5 mm (sagital) x 1.5 mm (coronal) x 1.5 mm (axial).

The whole brain MRI data was automatically segmented and normalized using the voxel-based morphometry (VBM) toolbox under SPM8 software. This process partitions brain into gray matter (GM), white matter (WM) and cerebrospinal fluid (CSF) regions.

1.3. The framework of the proposed method

The framework of our proposed methodology is shown in Figure 1. First of all, we normalized the MRI images of each subject into a standard space defined by the template image supplied with the Statistical Parametric Mapping (SPM) software. Therefore, all MRI images were normalized into $121\times145\times121$= 2,122,945 voxels. Secondly, the whole brain MRI image was segmented by segment module in SPM into three tissue classes: gray matter (GM), white matter (WM), and cerebrospinal fluid (CSF). However, the presented work focuses only on GM and WM tissues to analyze the degree of significance for discriminating AD and MCI from NC; due the major change that affects these regions. Then, the segmented brain images are decomposed into MRI basis functions and the corresponding independent coefficients using the FastICA algorithm [21]. Finally, the separated coefficients are fed into a SVM-based classifier that determines if the feature vectors are more similar to subjects with AD, MCI or NC.

The validation of the proposed methodology was conducted using the *k*-fold cross-

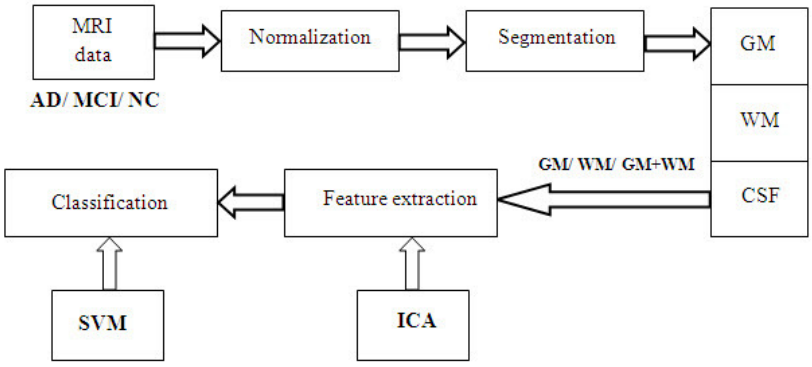

Figure 1. The methodology framework for the analysis of structural MRI data.

validation method with a number of folds equal to 10 (k=10). Then, the accuracy, sensitivity and specificity were computed to evaluate the performance of the classifier. Three performance metrics are defined as follows:

$$\begin{aligned} \text{Accuracy} &= \frac{TP+TN}{TP+TN+TN+FP} \\ \text{Sensitivity} &= \frac{TP}{TP+FN} \\ \text{Specificity} &= \frac{TN}{TN+FP} \end{aligned} \tag{1}$$

where *TP*, *TN*, *FP* and *FN* are the number of true positives, true negatives, false positives and false negatives, respectively.

1.4. Independent Component Analysis

Independent Component Analysis (ICA) [17] is a probabilistic and multivariate method for learning a linear transform of random vectors. The basic goal of ICA is to search for the components which are maximally as independent and non-Gaussian as possible. It has proved to be a powerful method for analyzing neuroimage data [18,19]. It is one of the multivariate techniques that enables an exploratory analysis of MRI datasets to extract useful information in local brain substructures and, it has been widely used in the segmentation of medical images [20]. In this paper, ICA has been successfully applied to dimension reduction problems by expanding the data into its independent components, performing that way the reduction. The MRI images have been processed by the FastICA

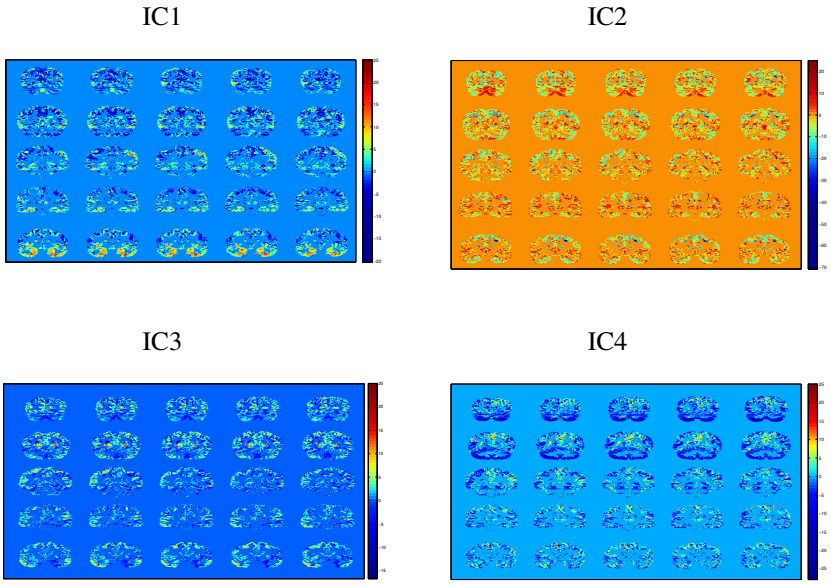

Figure 2. Representation of the first four components obtained by ICA in the ADNI database.

algorithm [21] in order to solve the computational cost in the standard ICA algorithms.

In this way, the segmented brain images were decomposed into independent components (ICs) as shown in figure 2. In this plot, the first four ICs obtained using this algorithm applied to the MRI database when AD and NC subjects are shown. These components have been spatially represented by assigning the brain coordinate of each voxel to each of the values in these IC. We can observe that each component highlights different zones that are usually related to Alzheimer's disease.

1.5. Classification using support vector machine (SVM)

SVM [22] is one of the machine learning methods based on statistical learning theory. It has been recently used to distinguish AD and MCI subjects from NC subjects using anatomical MRI images [23]. SVM conceptually implements a linearly or nonlinearly mapping to a very high dimensional feature space. In this feature space, a linear separation surface is created using training data by minimizing the margin between the vectors of the two classes. The training ends with the definition of a decision hyperplane that divides the space into two subspaces. Each subspace corresponds to one class of the training data. Once the training is completed, the test data are mapped to the feature space. A class is then assigned to those data depending on which subspace they are mapped to. In this work, we used the Linear SVM and RBF as classifiers to diagnose AD or MCI subjects from normal controls.

2. Experimental results and discussion

In this work, different brain tissues are used from the MRI database in order to verify the performance of our proposed methodology for discriminating AD and MCI from NC. On the other side, the segmented data is used to distinguish the most important brain tissue which yields the best classification accuracy. In addition, we applied the FastICA algorithm to extract features from segmented MRI images. Promising classification accuracy obtained by the SVM-based classifier has proven that the proposed method is very useful for the analysis of the structure of MRI images. The database used in our methodology were arranged into three different groups.

The following groups were designed:

- **Group 1** Only AD and NC images are considered. In this group, we test our method with all the database (229 NC and 188 AD).
- **Group 2** Only 185 MCI and 185 NC images are considered.
- **Group 3** Only AD and MCI images are considered. Also, in this group we have used the same number of images as group 2 (185 AD images and 185 MCI images).

The classification results are summarized in table 2 with different experiments (GM images, WM images and the combination of feature extracted from GM and WM segmentation), using ICA feature extraction method and different SVM classifiers.

It can be noted from this table that the highest accuracy value obtained for the group 1 and it is decreased in group 2 and 3 when MCI images are included; this diminution of their performance metrics can be explained by the high variability of the MCI pattern of each image. Second, it can be concluded from the measures of performance metrics

Brain tissues	Kernel	Group 1 Acc/Sens/Spec(%)	Group 2 Acc/Sens/Spec(%)	Group 3 Acc/Sens/Spec(%)
GM	Linear	**84.65/86.46/82.45**	**69.46/69.03/69.96**	**69.19/70.27/68.11**
	RBF	82.97/83.41/82.45	68.38/68.65/68.11	64.05/61.62/66.49
WM	Linear	**70.26/72.93/67.02**	**63.51/63.24/63.78**	**59.46/62.16/56.76**
	RBF	68.82/68.56/69.15	61.08/56.22/65.95	53.51/51.89/55.14
GM+WM	Linear	**86.37/88.34/83.98**	**70.19/72.89/67.49**	**69.83/73.43/66.24**
	RBF	78.66/75.11/82.98	65.13/61.08/69.19	64.32/51.89/76.76

Table 2. Statistical measures of performance of ICA feature selection method with different SVM classifiers, for the three sample groups, and using eight components.

that the linear SVM classifier yields a higher accuracy rate with ICA feature extraction method than SVM-RBF (see figure 3). Thus, the linear SVM might be the best technique to distinguish AD and MCI patients from NC. Third, it is remarkable that when using the combination of feature extracted from GM and WM as input features and afterwards transformed them with ICA coupled with linear SVM increase the accuracy of the classifier, thus, adds a valuable robustness to our system for distinguishing AD and MCI from NC subjects.

As a conclusion, combining features extracted from both GM and WM tissue distributions increase the classification and accuracy of the classifier. Furthermore, our methodology can produce a valid approach to perform a CAD system for early diagnosis of AD.

3. Conclusions

In this paper, we have shown a novel method for segmented MRI image based on the ICA feature extraction method. This proposed method makes use of a preprocessing step, in which the images are spatially normalized, segmented and a binary mask applied to these images to select the high intensity voxels. Furthermore, our method was developed by combining the different segmented brain tissues in order to improve the classification accuracy of the Alzheimer's disease system. Then, the voxels of the segmented MRI brain images are modeled in terms of independent component analysis (ICA) to extract a low number of Independent Components (IC) which work as feature vectors for each image. In addition, features extracted using ICA method allow us to extract highly representative features, which relate to typical AD patterns, and yielding on a high-accuracy classification. Finally, different SVM classifiers; linear and nonlinear, are trained to distinguish AD and MCI patterns from NC patterns. The resulting of our system was trained using 818 segmented MRI images from the ADNI database (188 AD,401 MCI and 229 NC) and the statistical performance of our method was estimated using a k-fold cross-validation methodology. The proposed system shows excellent accuracy, sensitivity and specificity values in the classification task when we combine the feature extracted from GM and WM brain tissues together.

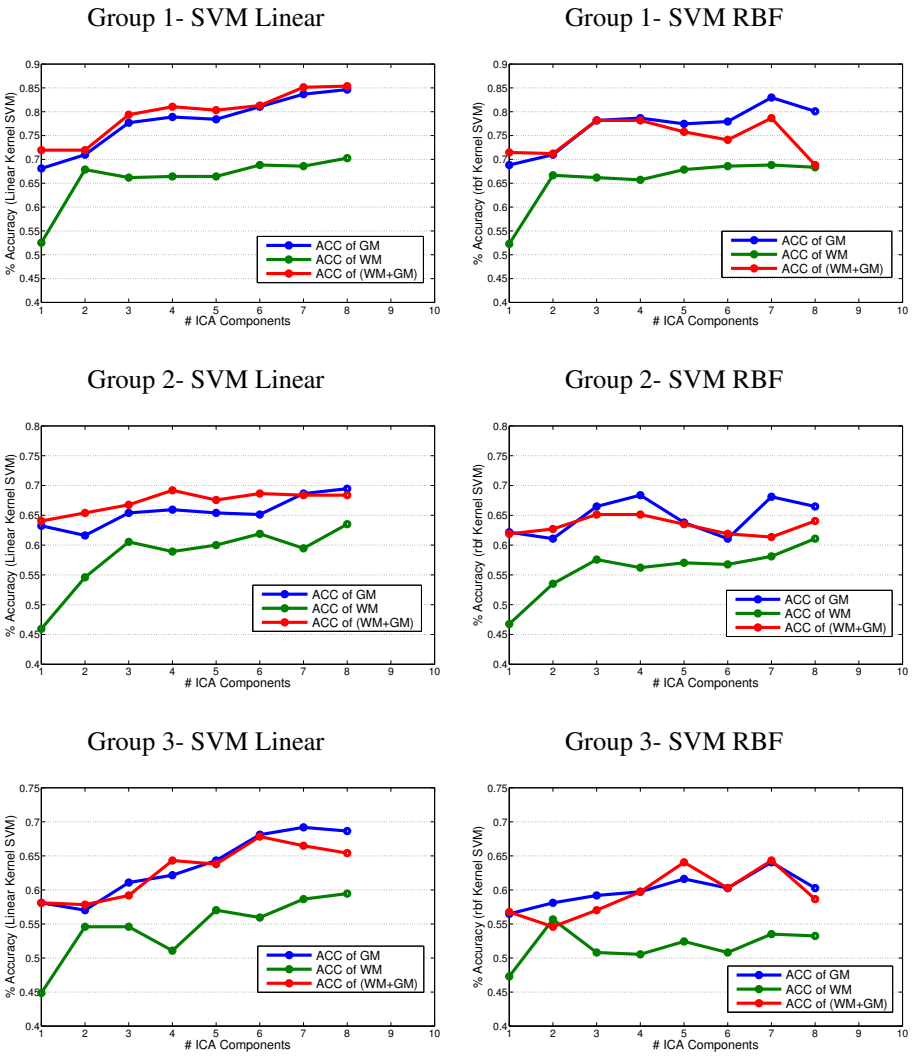

Figure 3. SVM classification: Values of Accuracy (%) computed for ADNI database in function of number of component with ICA feature extraction:(Above) the classification accuracy of group1 (NOR versus AD), in (the middle) the classification accuracy of group2 (NOR versus MCI) and (below) the results of group3 (MCI versus AD).

To sum up, the selection of the classifier has the highest impact in the classification performance, being the linear SVM classifier coupled with the ICA method in combination with feature extracted from segmented GM and WM brain images. Thus, the resultant system demonstrates its ability and robustness in AD and MCI patterns detection from NC pattern.

Acknowledgments

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