Biomedical Signal Processing and Control 40 (2018) 41–48

Contents lists available at ScienceDirect

Biomedical Signal Processing and Control

journal homepage: www.elsevier.com/locate/bspc

Research paper

A novel method based on independent component analysis for brain MR image tissue classification into CSF, WM and GM for atrophy detection in Alzheimer's disease

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ARTICLE INFO

Article history:
Received 4 April 2017
Received in revised form 26 July 2017
Accepted 5 September 2017

Keywords:
Independent component analysis
Band expansion process
Brain MRI
Support vector machines
Alzheimer's disease

ABSTRACT

Brain Magnetic Resonance Image (MRI) plays a vital role in diagnosis of diseases like Brain Tumor, Alzheimer, Multiple Sclerosis, Schizophrenia and other White Matter Lesions. In most of the cases accurate segmentation of Brain MRI into tissue types like Cerebro-Spinal Fluid (CSF), White Matter (WM) and Grey Matter (GM) is of interest. The diagnostic accuracy of expert and non-expert Radiologists can be improved with accurate and automated tissue segmentation and classification system. Such system can also be used for trainees to understand the individual tissue distribution in MRI scans. In this paper, we propose a novel automated tissue segmentation and classification method based on Independent Component Analysis (ICA) with Band Expansion Process (BEP) and Support Vector Machine (SVM) classifier which with input as T1, T2 and Proton Density (PD) scans of patient, provides output as CSF, WM and GM indicating the possible atrophy in brain which can help in diagnosis of Alzheimer's disease (AD). The objective of this work is to test the effectiveness of ICA with different input images generated using BEP for accurate brain tissue segmentation by validating results with different quality metrics. The novel method for generating input images for ICA has been implemented and segmented tissues are used for atrophy detection. The BEP + ICA + Thresholding + 'SVM trained with Grey Level Co-occurrence Matrix (GLCM) based texture features' is giving 100% tissue classification accuracy for test samples under consideration.

1. Introduction

Structural MRI is one of the important neuroimaging modality with high-resolution imaging and high brain tissue contrast capabilities. It is particularly used to look for brain tumors, stokes, blood clots, or other abnormalities that might account for Multiple Sclerosis (MS) or Alzheimer's.

MRI scans are acquired by different pulse sequences specified by three MR tissue parameters: spin–lattice (T1), spin–spin (T2) relaxation times, and Proton Density (PD) [5]. These are labeled as T1 weighted, T2 weighted, and PD weighted (Fig. 1).

The constituents of brain, such as Gray Matter (GM), Cerebrospinal Fluid (CSF),White Matter (WM), Glial Matter, Fat, Muscle/Skin, etc. show unique characteristics under a magnetic field. However, the major tissue types of brain are CSF, GM and WM; which have been distributed in T1, T2 and PD. As a result, spatial as well as tissue characteristics based features can be extracted from these MRI scans [6]. Reader based classification methods for these tissues are non-reproducible, and are practically difficult for the large amounts of data. Thus, development of fully automatic and accurate brain tissue classification from MRI in case of various disease symptoms like Tumors, MS, AD and other White Matter Lesions (WML) is of great interest [13,17] and is a challenging task.

AD, the most common type of dementia is a major cause of disability worldwide. It can be detected at an early stage with the help of MRI so as to avoid irreversible damage of the brain with proper treatment plan. MRI can depict 'atrophy' – a decrease or shrinkage in the size of different areas of the brain caused due to wasting away of brain tissues in response to a disease process [10] like AD. Fig. 2 shows the various stages of Alzheimer's disease.

As can be seen in Fig. 2, MRI shows increasing atrophy as the disease progresses from MCI to AD (with no atrophy for healthy/normal controls). Measuring atrophy based on tissue volume distribution is important to diagnose, to monitor the disease

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http://dx.doi.org/10.1016/j.bspc.2017.09.005
1746-8094/

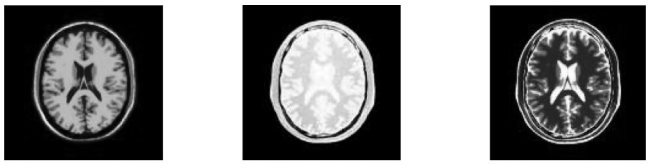

Fig. 1. MRI Axial Scans.

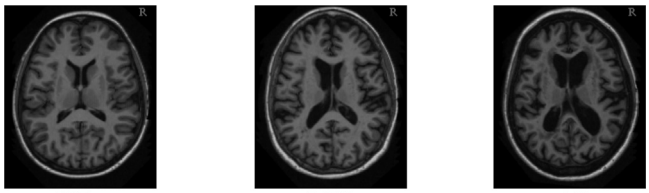

Fig. 2. Normal Control (NC), Mild Cognitive impairment (MCI) and AD (T1 Weighted Axial Brain MR Images).

progression and in turn helps in the planning of treatment. Most of the segmentation methods are sensitive to the tissue intensity overlaps caused by limitations of MR image acquisition process (partial volume effect).

There are three software packages widely used in neuroimaging community for structural and functional brain imaging study: FMRIB Software Library (FSL) [14], Statistical Parametric Mapping (SPM) [15] and BrainSuite [12]. FSL provides very effective tools like BET, FAST, FIRST, FLIRT etc. for structural MRI scans like T1-w or T2-w. FAST needs brain extracted images as input, which can be obtained using BET. SPM needs MATLAB and is based on a mixture model clustering algorithm. Kazmi K et al. in [18] presented detailed performance evaluation of these 3 methods. Chris et al. in [13] described and validated a completely automatic, non-parametric brain tissue classification system, based on a probabilistic anatomical atlas (model) for different tissue labels. Also, in [11] comparative study of different model based tissue classification methods is presented. Among other methods, ICA is also very popular [5,6,8,16]; often as a pre-processing step of SVM based classifier [6,16] and uses different types of structural MRI scans such as T1-w, T2-w and PD as an input.

An application of ICA to MR image (MRI) analysis was investigated by Nakai et al. in [8] for contrast enhancement of GM and WM, till then it was in wide use for functional MRI (fMRI) [4]. In paper [8], study revealed that the involvement of grey or white matter in brain tumor cases and demyelination in the case of MS were enhanced and visualized in IC images. Also, in the same study [8], the potential of ICA for further analysis of anatomical images by enhancing the contrast among normal tissue or between normal and pathologic tissues has been investigated.

In paper [6], Ouyang et al. pointed out two problems which were not addressed by Nakai et al.:i. Implementing Over Complete ICA (OC ICA) – number of image pulse sequences used for acquisition is generally smaller than the number of brain substances of interest and ii. ICA algorithm is initialized with initial random projection vectors to generate Independent Components (ICs). Because of this ICs generated are random and hence image evaluation cannot be performed until all ICs are generated. In [6], in order to mitigate this issue, the OC-ICA is used in conjunction with a feature extraction-based classifiers like- SVM and Fisher's linear discriminant analysis (FLDA) for tissue classification.

The performance of the method/algorithm for Tissue Segmentation can be validated by comparing the segmented tissue with Ground Truth image. For AD, for evaluating the disease progression, individual tissue volumes need to be measured and atrophy should be measured with some parameter/s. Sadek in [10] has suggested three measures – Atrophy Ratio (AT), Alzheimer disease factor (ADF) and Progressive AD rate; for this purpose.

In this paper, we present the automatic brain tissue classification based on ICA and SVM with novel method for generating input images (using BEP) for ICA to overcome limitations of ICA (mentioned in Section 2). The set of input images is selected with combination of original images (T1, T2 and PD) and band generated images (using different BEP); to generate independent Components (ICs). The approach is towards generating ICs which are as independent as possible with separate IC for each of the tissue of interest such as WM, GM and CSF. The idea for achieving accurate tissue classification is based on training of SVM with texture based spatial features evaluated on the most accurately segmented tissue samples (of WM, GM and CSF). Four different segmentation methods (Model I–IV) are proposed. The performance of all is tested and compared with different quality metrics like Mutual Information (MI), Tanimoto Index (TI) [16], Similarity Index (SI), Precision and Recall [20]. The paper also describes a case study for Alzheimer's disease. In this study, the segmented tissues for AD cases are used further for calculation of Atrophy Ratio (AT).

This paper is organized as follows: Section 2 introduces the ICA and its limitations. Section 3 is about BEP to create more inputs for ICA. Section 4 is about SVM classifier and GLCM Features. Section 5 describes the database used for experimentation. Section 6 gives the detailed methodology implemented in this work. Section 7 describes the various quality parameters used for quantitative analysis of methods implemented and results obtained. Section 8 is for results and discussions. Section 9 is about case study of AD followed by Conclusion in section 10.

2. Independent component analysis (ICA)

ICA [1–4] is a linear transformation method. If 'x' denotes an m-dimensional random variable; the problem is then to find a function 'f' so that the *n*-dimensional transform $s = (s1; s2; \ldots\ldots sn)^T$ defined by $s = f(x)$ has some desirable properties and can be represented $s = Wx$ where W is a matrix to be determined.

The problems associated with ICA, of ICA being an over-determined system with the number of samples (M) is usually greater than the sources to be separated (S) is pointed out in [6]. There were generally no solutions for such case. On the other hand, for $M < S$, ICA becomes an under-determined system. Nakai et al. [8] assumed that $M \geq S$, where M in an MR imaging system consists of T1, T2, PD images [6,8] and their unique combinations. In [6] S is considered as the number of brain tissue substances, which includes water, blood, fat, GM, WM, CSF, and muscle, as signal sources to be separated; thus $M < S$ and the ICA must deal with an over-complete representation of a mixed model, in which case many solutions are possible.

In this work, Fast ICA: efficient and popular algorithm for ICA invented by Aapo Hyvärinen at Helsinki University of Technology [3,4] has been used. The classical application of the ICA model is that of blind source separation [1,7]; that is, no prior information about distribution of different tissues of interest in input images is required to be known.

3. Band expansion process (BEP)

Ouyang et al. in [6] resolved the issue of having less number of input (band) images for ICA in MRI analysis by introducing the Band Expansion Process (BEP). The idea of BEP is to capture the correlation between original MR band images (T1, T2 and PD) and generate a set of second-order statistical band images [5]. The second-order statistics that can be used for BEP includes autocorrelation, cross-