Abnormality Detection from Multispectral Brain MRI using Multiresolution Independent Component Analysis

S. Sindhumol[1], Anilkumar[2] and Kannan Balakrishnan[1]

[1]*Artificial Intelligence Lab, Department of Computer Applications, Cochin University of Science and Technology, Kochi, Kerala, India*
[2]*Institute of Radiology and Imaging Sciences, Indira Gandhi Co-operative Hospital, Kochi, Kerala, India*

sindhumol09@gmail.com, anil.k@medall.in, mullayilkannan@gmail.com

Abstract

Multispectral approach to brain MRI analysis has shown great advance recently in pathology and tissue analysis. However, poor performance of the feature extraction and classification techniques involved in it discourages radiologists to use it in clinical applications. Transform based feature extraction methods like Independent Component Analysis (ICA) and its variants have contributed a lot in this research field. But these global transforms often fails in extraction of local features like small lesions from clinical cases and noisy data. Feature extraction part of the recently introduced Multiresolution Independent Component Analysis (MICA) algorithm in microarray classification is proposed in this work to resolve this issue. Effectiveness of the algorithm in MRI analysis is demonstrated by training and classification with Support Vector Machines (SVM). Both synthetic and real abnormal data from T1-weighted, T2-weighted, proton density, fluid-attenuated inversion recovery and diffusion weighted MRI sequences are considered for detailed evaluation of the method. Tanimoto index, sensitivity, specificity and accuracy of the classified results are measured and analyzed for brain abnormalities, affected white matter and gray matter tissues in all cases including noisy environment. A detailed comparative study of classification using MICA and ICA is also carried out to confirm the positive effect of the proposed method. MICA based SVM is found to yield very good results in anomaly detection, around 2.5 times improvement in classification accuracy is observed for abnormal data analysis.

Keywords: *MRI, Independent Component Analysis, Wavelet Transforms, SVM*

1. Introduction

Magnetic Resonance Images (MRI) acquisition provides different sequences like T1-Weighted Images (T1WI), T2-Weighted (T2WI), Proton Density Images (PDI), Fluid-Attenuated Inversion Recovery (FLAIR) etc. Massive information on tissue structure and pathology can be extracted from these sequences, but each sequence differs in available information content [1]. Slice by slice examination and extraction of small details and abnormalities from these large numbers of sequences is a tedious job in clinical applications. Multispectral data analysis combines the slices of the same brain portion from each sequence to form a single suite so that it helps to analyze the corresponding pixel information as a pixel signature [1]. For example, see the sample slices of T1WI, T2WI and Diffusion Weighted Image (DWI) shown in Figure 1. It is observed that details present in an image vary from slice to slice. In Figure 1, T1WI shows White Matter (WM) information clearly, whereas

T2WI contains Gray Matter (GM) and Cerebro Spinal Fluid (CSF) information. DWI fails to distinguish the brain tissues, but pathological information is clearly visible in it.

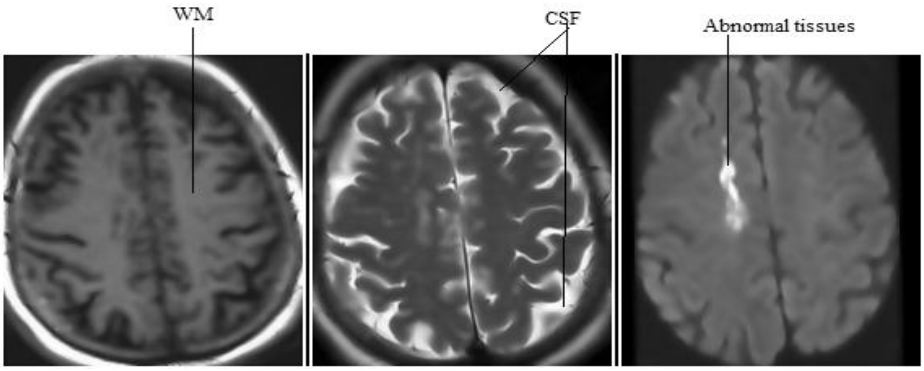

Figure 1. Input Slices of T1WI, T2WI and DWI (from left to right)

Researchers in MRI analysis have been intensively working for last few decades to improve the performance of existing data mining techniques using multispectral approaches. But it remains as a challenge because classification accuracy highly depends upon the input data characteristics and feature analysis methods. Pre-processing, feature extraction and classification are the main steps involved in a typical multispectral analysis system [1]. Pre-processing techniques like image registration, denoising and contrast improvement can contribute much to select the best features for further analysis. Classification methods in multispectral analysis can be effectively classified into two categories, unsupervised and supervised learning [2]. Unsupervised methods like k-means [3], Fuzzy C-Means (FCM) [4] and Expectation Maximization (EM) [5] can give satisfactory results for MR image analysis. But radiologists often rely on feedback from previous data and diagnosis to reach at a correct opinion for each case. Supervised learning techniques follow similar strategy, and widely used in computer aided categorization of MRI data. Artificial Neural Networks (ANN) [5] and Support Vector Machines (SVM) [6] are the two widely accepted techniques in supervised MRI classification [2, 7]. A detailed review of some supervised and unsupervised classification methods in MS lesion segmentation is described in [8].

Methods like Principal Component Analysis (PCA) [9], ICA [10], its nonlinear version kernel ICA [11] and Wavelets [12] are very useful in dimensionality reduction and feature analysis. In recent years, SVM classification coupled with ICA has proved to be very efficient in clinical application of MRI [13]. However, studies in gene array classification [14] revealed that ICA, as a global transform, failed to project the small abnormalities present in high dimensional data. In an attempt to retain the local information in multidimensional gene data, Han and Li [14] introduced a new Multi-resolution ICA (MICA) method for feature analysis in microarray classification. The new method is observed to generate better results for gene data analysis compared to other conventional methods. Multiresolution part of this MICA algorithm is adopted in this work to analyze MRI images for abnormality detection in the context of multispectral analysis.

In this work, each 2-D MRI slice is reshaped to a 1-D data and used as a component signal in the multisignal form of multispectral data. Multisignal wavelet analysis is applied on these signals to extract approximation coefficients and detail coefficients. Detail coefficients are processed with PCA to retain the local information. ICA is applied on the reconstructed signals to get relevant features. Feature selection and subspace decomposition explained in

MICA algorithm is excluded from this work, since it is not practical with MRI data. Feature vectors for further analysis are selected under the supervision of experienced radiologists.

This study uses both synthetic and real brain MRI images to evaluate the proposed algorithm. Simulated samples of Multiple Sclerosis (MS) lesions (combination of registered T1-weighted, T2-weighted and PD) obtained from BrainWeb database are given as input in synthetic image analysis. T1, T2, FLAIR and diffusion weighted images for total 55 cases collected from Siemens' whole body 3T MRI machine are used in clinical data analysis. The proposed method is compared with ICA based SVM (ICA+SVM) to evaluate the performance improvement in classification of brain matters like GM, WM and abnormality presence. Visual and quantitative results confirm that MICA based SVM (MICA+SVM) is a promising and effective method for abnormal tissue analysis.

This paper is organized in the following manner. An overview of the materials and methods used in this work is given in Section 2. Section 3 discusses the experimental results from visual and quantitative analysis. Section 4 concludes the paper.

2. Materials and Methods

2.1. Database

The input database in this study consists of three sets of abnormal MRI data. The first set contains synthetic brain MR images obtained from BrainWeb, Simulated Brain Database at the McConnell Brain Imaging Centre of the Montreal Neurological Institute (MNI), McGill University (http://www.bic.mni.mcgill.ca/brainweb). Axial T1WI, T2WI, and PD slices representing Multiple Sclerosis details are combined to generate the multispectral image sets. Slices with 1-mm thickness and 181x217 size are collected from each sequence for noise levels 0%, 1% and 3%.

T1WI, T2WI and FLAIR images of 20 abnormal clinical cases are included in the second set and third set is a collection of T1WI, T2WI and Diffusion Weighted Image (DWI) slices from 35 abnormal clinical cases. These images were sampled by Siemens' whole body 3T MR system (Siemens, AG Medical Solutions, Erlangen, Germany) and collected from Institute of Radiology and Imaging Sciences (IRIS) Pvt. Ltd, Kochi, India as per the data use agreement approved by Institutional review board. The clinical brain MR images were acquired by axial spin echo T1WI with repetition time (TR) = 1600 ms, echo time (TE) = 8.9 ms and T2WI with TR/TE = 4000ms/95 ms, FLAIR images with TR/TE = 6000 ms/ 94 ms and inversion time (TI) = 2026.5 ms. Additional parameters were, slice gap 6.5 mm, thickness 5mm and size 209x244. Echo-planar diffusion weighted images in the third set were collected with thickness 4mm, TR/TE = 6500ms/ 95ms, slice gap 6mm and size 184x216 as parameter settings.

2.2. Multisignal Wavelet Analysis

Each image in multispectral MRI is reshaped as a 1-D signal to form multisignals in wavelet analysis of MRI [12, 15]. Wavelet transform of the multisignal is computed from projection of the signal onto the scaled and shifted version of the basic function, mother wavelet. Multiresolution wavelet transform provides a time-scale domain representation of the signal under consideration where time and scaling information can be studied simultaneously. Multiresolution analysis (MRA) of input signals using Mallat algorithm [15] is shown in Figure 2. Input multisignal is passed through a low pass filter (H_{low}) and its corresponding high pass filter (H_{high}) simultaneously. A dyadic decimation that halves the resolution removes extra elements of the signals. These steps are applied recursively to the

result of low pass filter subbands from input signals and increasingly smoother versions of the original signals are generated. Decomposed spectral signatures from one-dimensional multisignal wavelet analysis are expanded by inserting zeros in the upsampling process [12] to reconstruct the original spectral bands.

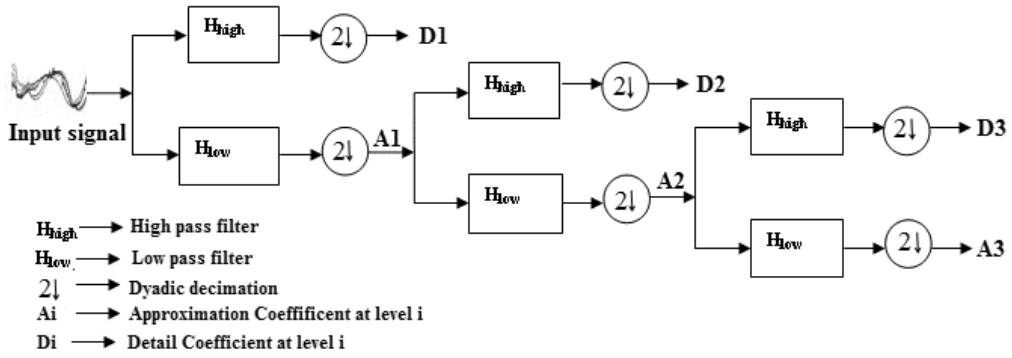

Figure 2. Concept of Multiresolution Analysis

2.3. Proposed Multi-resolution Independent Component Analysis in MRI

As a global transform, conventional ICA fails to project the significant and precise information from input multispectral data. MICA algorithm solves this issue by suppressing redundant global information, but retaining the local features with more priority [14]. The proposed steps from MICA for MRI analysis are shown in Figure 3 and explained through the following steps.

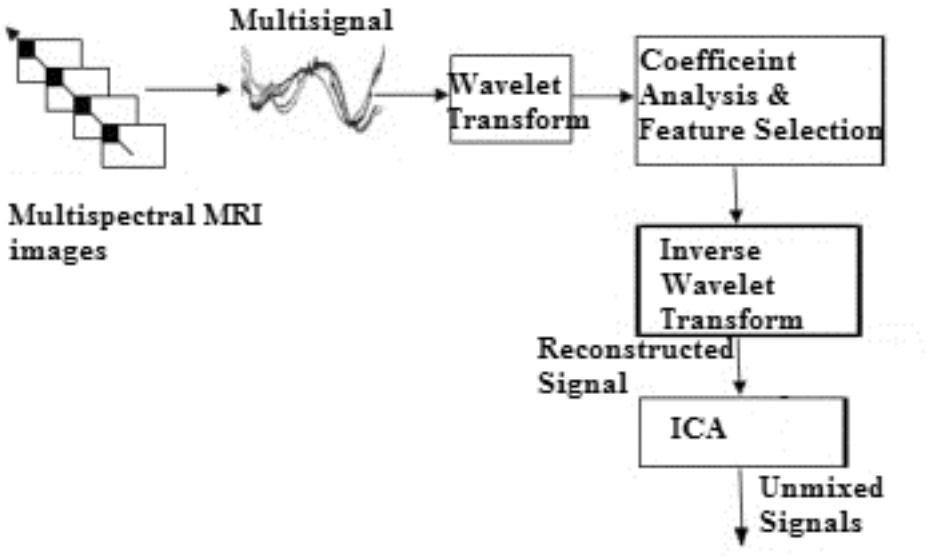

Figure 3. Proposed MICA for MRI

1. Pre-processing and Multisignals formation.

MRI sequences for clinical trials are usually acquired with different size and orientation. Registration of the images [16] to form a co-registered multispectral suite is the preliminary step in analysis process. Each pixel vector in a multispectral image forms the spectral signature corresponding to that pixel and a collection of these spectral signatures generate multisignals as shown in Figure 3.

2. Wavelet Transform and Analysis of detailed coefficients

1-D wavelet analysis of multisignals generates approximation coefficients and detail coefficients for different resolutions. Let $\mathbf{X}= [x_1, x_2,\ldots, x_p]^T$ be the spectral signature of a pixel as shown in Figure 3, where 'p' is the number of bands in multispectral image. L-level discrete wavelet decomposition of **X** forms a set $\{D_1, D_2...D_L, A_L\}$, where D_i's are the detail coefficient at level 'i' and A_L is the approximation coefficient. Detail coefficients contain global features. So global feature selection is done by thresholding and recalculation of D_i's using a level threshold μ, where $1\leq\mu\leq$ L-1. Wavelet coefficient analysis and principal component calculations for different threshold values proposed in MICA algorithm [14] is summarized here.

if $1\leq j\leq \mu$,

Conduct principal component analysis of D_i's to get PC matrix $\mathbf{U} = [U_1, U_2 \ldots U_p]$ and corresponding score matrix $\mathbf{S}= [S_1, S_2,\ldots S_p]$.

Reconstruct the original D_j by $D_j = (1/n_j)D_jIn_j+S_1xU_1^T$

if $j>\mu$,

Reconstruct and update each detail coefficients matrix D_j by using loading vectors $U_1, U_2...U_k$ consisting of 100% explained variance [14] percentage and their corresponding vectors in the score matrix such that

$D_j=(1/n_j)D_jIn_jIn_j^T+[S_1,S_2,\ldots,S_k]x[U_1,U_2,\ldots U_k]^T$,

where n_j is the number of rows in D_j and In_j is a unit vector of size n_jx1.

3. Reconstruction of Multisignal

The new wavelet decomposed data at level 'L' can be represented as $\mathbf{T^*} = \{D_1, D_2...D_L, A_L\}$. Inverse discrete wavelet transform, IDWT (**T***), gives the reconstructed signal **X*** for further analysis.

4. Independent Component Analysis

Independent component analysis (ICA) is a generic model which helps to find a linear representation of non-gaussian and mutually independent data [10]. Let $\mathbf{x} = [x_1, x_2, ..., x_n]^T$ be a random vector where x_i's are mixtures, and '**s**' be another random column vector representing independent components $s_1, ..., s_n$.

Let '**A**' be the matrix with elements $a_{ij,\ i=1\ldots n,\ j=1\ldots n}$ such that

$$\mathbf{x} = \mathbf{As} \qquad (1)$$

W, inverse of the matrix **A** can be computed from an estimation of '**A**' and is used to obtain the independent component simply by,

$$\mathbf{s} = \mathbf{Wx} \qquad (2)$$

Steps to calculate independent components using FASTICA [10] can be summarized as follows:

Step 1. Centering, it is the most basic and necessary preprocessing step in ICA computation. Mixed vector '**x**' is centered by subtracting mean vector '**m**' from it. *i.e.*, $\mathbf{x_c = x-m}$.

Step 2. Whitening process, it transforms the data so that it has an identity covariance matrix. *i.e.*, $E(\mathbf{x_c x_c}^T)=\mathbf{I}$. It makes components of $\mathbf{x_c}$ uncorrelated. Eigen value decomposition of the covariance matrix of $\mathbf{x_c}$ can be used to reduce the complexity of the problem. *i.e.*, Whitening can be done by decomposition, $\mathbf{x_c}= \mathbf{E}\mathbf{D}^{-1/2}\mathbf{E}^T\mathbf{x}$, where **E** is the orthogonal matrix of eigenvectors of input covariance matrix $\mathbf{C_X}$ and **D** is the diagonal matrix of its eigen values. Whitening matrix **P** is calculated as $\mathbf{P}=\mathbf{D}^{-1/2}\mathbf{E}^T$ and it is used to compute the whitened data, $\mathbf{z}=\mathbf{P}\mathbf{x}$. Subsequent ICA estimation is done with **z**.

*Step 3. Iteration for **W***, it is a process of finding orthogonal unmixing matrix **W** for whitened data using an appropriate learning rule. **W** is computed such that projection $\mathbf{W}^T\mathbf{x}$ maximizes the measures of nongaussianity. Optimization of objective functions or contrast functions is used to measure the nongaussianity [10]. Unmixed signal vector '**s**' is calculated from **W** using eq. (2).

In this work, FastICA learning algorithm [10] is applied on reconstructed signal **X*** to get **W** and unmixed signals.

2.4. Classification Using SVM

It has been proved in latest studies that Support Vector Machines (SVM) is a better option for MRI analysis [7] compared to other methods in supervised classification. Originally, Vapnik [6] develops it in statistical machine learning theory as a linear binary classifier based on the class of hyper-planes,

$$(\mathbf{W}.\mathbf{x}) + \boldsymbol{b}=0,\ \mathbf{W}\in \boldsymbol{R}^N,\ \boldsymbol{b}\in \boldsymbol{R} \qquad (3)$$

and decision functions

$$f(\mathbf{x}) = \text{sign}((\mathbf{W}.\mathbf{x}) + \boldsymbol{b}) \qquad (4)$$

where '**W**' is a weight vector and '***b***' is the threshold or bias. SVM searches for an optimal hyper-plane having maximal margin of separation between two classes for a particular training dataset. Therefore, the classification task is only a function of the *support vectors*, the training data that lie on the margin.

In dual form [6] the problem reduces to

$$\text{Maximize} \quad \sum_{i=1}^{n}\alpha_i - \frac{1}{2}\sum_{i,j}\alpha_i\alpha_j y_i y_j K(x_i, x_j) \qquad (5)$$

$$\text{Subject to } \alpha_i \geq 0 \text{ and } \sum_{i=1}^{n}\alpha_i y_i = 0$$

and solve for α_i. $K(x_i, x_j)$ can be a linear or non-linear kernel [5, 6].

A detailed explanation of MRI analysis using SVM is present in [7, 13]. SVM with Radial Basis Function (RBF) non-linear kernel is used in this work for brain tissues analysis.

2.5. Quantitative Measures

Performance evaluation of the proposed method is done with two types of measurements. First criterion is Tanimoto Index, the most commonly used measurement in medical imaging [13]. It is used to measure the similarity of the obtained result with ground truth as follows,

$\mathbf{T} = \frac{|A \cap B|}{|A \cup B|}$, where A and B are two datasets involved in the classification comparison.

Other set of measurements contains statistical measures like Sensitivity, Specificity and Accuracy [8]. Sensitivity is the proportion of actual positives correctly classified and specificity is the proportion of negatives correctly identified. Specificity, sensitivity and accuracy can be calculated as follows:

Sensitivity = (TP/ (TP+FN)) *100%

Specificity = (TN/ (TN+FP)) *100%

Accuracy = ((TP+TN)/ (TP+TN+FP+FN))*100 %, where TP, TN, FP and FN can be defined in the context of MRI analysis as,

True Positive (TP) - Tumor pixels correctly identified as tumor,

False positive (FP) - Other tissues incorrectly identified as tumor,

True Negative (TN) - Other tissues correctly identified,

False Negatives (FN) - Tumor pixels incorrectly identified as others.

3. Experimental Results and Discussions

Feature extraction and classification are the major steps involved in this analysis. Proposed MICA and classical ICA method are implemented for feature extraction process. These techniques are applied on synthetic and clinical datasets described in Section 2.1 to generate independent components. No image registration was required in the case of synthetic images, but image registration using Matlab functions is applied on clinical dataset as a preprocessing step. Implementation of step 2 in proposed algorithm is done with a 4-level wavelet decomposition of input multisignals using Daubechies-8 (db8) wavelet. An optimal value for threshold ‘μ’ is set as 2 by trial and error. Training and testing datasets for abnormalities and affected tissues were selected from generated MICA results. For each brain matter class, a feature vector is formed by a 3x3 window of nine samples selected under the guidance of an experienced radiologist.

Mathworks Matlab 7.0 (R2009a) implementation on a PC with Pentium Dual CPU of 2.0GHz and 2GB RAM running Microsoft Windows 7 was executed for the complete system evaluation. Pattern recognition Toolbox in Matlab served the purpose of non-linear (RBF kernel) SVM training and classification with its default parameter settings. Leave one out cross validation is used in performance analysis to evaluate the improvement in classification accuracy. The same environment and feature selection method is repeated to generate the classified results using conventional ICA. A detailed comparative study of MICA and ICA is conducted and obtained results are summarized below.

3.1. Synthetic Image Analysis

Synthetic MRI data analysis contains images with noise levels 0%, 1% and 3%, each set consisting of seven multispectral slice sets of T2WI, T1WI and PD images (total 21x3 slices)

collected from Brainweb database. The 0% noise sample images (slices of MS lesions) are shown in Figure 4A and unmixed results are given in Figure 4B. Top row in Figure 4B is the extracted components by ICA and bottom row gives MICA results.

It is observed from Figure 4B that abnormalities (circled portion) are so clear in MICA results that radiologists can visually analyze the points directly from the components before classification. Brain abnormalities (lesions) and affected tissues (WM and GM) are studied to analyze the improvement in anomaly detection on applying MICA instead of ICA with SVM classification. Figure 4C shows GM in 1st column, WM in 2nd column and lesions in 3rd column. It is easily seen that tumor information from classified result using MICA (last row last column) exceeds that from ICA+SVM (first row last column). Figure 4C 2nd column comparison shows that affected portions in WM can be seen as black holes in the MICA +SVM results. However, unaffected portion of WM and GM are better classified by ICA+SVM. A performance evaluation using the measures specified in Section 2.5 confirm these observations with quantitative results summarized in Table 1.

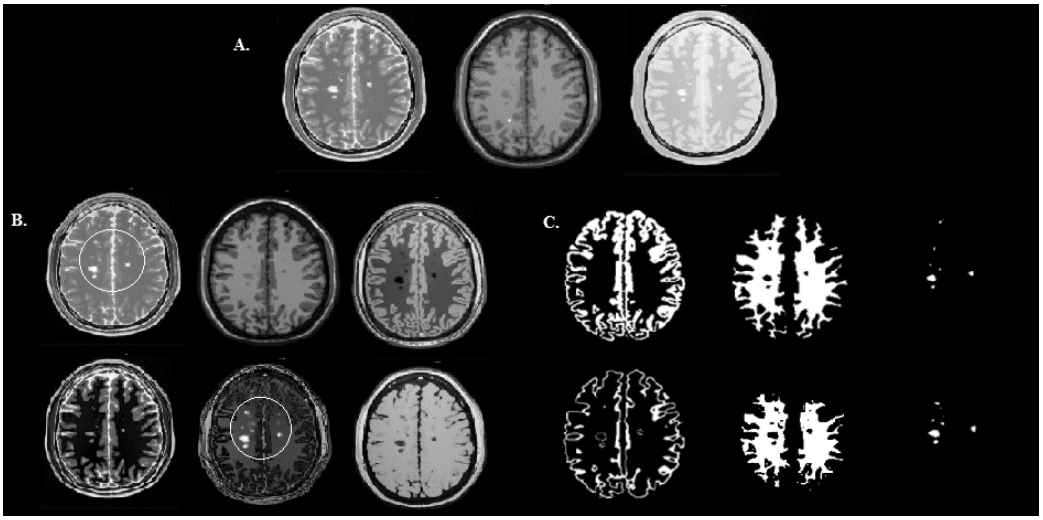

Figure 4. Feature Extraction and Classification Results: A) Input Slices T2WI, T1WI and PDI (from left to right); B) Feature Extraction Results, top row- ICA results, bottom row-MICA Results; C) Classified GM, WM and MS lesion (from left to right): top row- ICA results, bottom row-MICA Results

Table 1. Tanimoto Indices and Accuracy Estimates of MS Lesions in Noisy Environment

Noise		Tanimoto Index	Specificity	Sensitivity	Accuracy
0%	ICA+SVM	0.7279	99.9030	73.7931	99.8067
	MICA+SVM	0.8211	99.9310	81.3793	99.8625
1%	ICA+SVM	0.6552	99.8724	65.5172	99.7457
	MICA+SVM	0.7213	99.8978	72.4138	99.7964
3%	ICA+SVM	0.3517	99.7604	35.1724	99.5225
	MICA+SVM	0.4898	99.8138	49.6552	99.6290

Positive changes in Tanimoto index values for different noise levels support improvement in image quality on applying MICA. For 0% noise, it is observed as 0.0932, for 1% noise it is 0.0661 and it is highest for 3% noise, 0.1381. Average of the sensitivity, specificity and accuracy of the obtained classification results is also added to Table 1. Sensitivity and accuracy values support the positive impact of MICA in tumor extraction, especially in noisy environment. Values in Table 1 indicate the efficiency of multiresolution analysis in noisy data classification. To evaluate MICA in real environment, a detailed analysis of clinical data is performed as discussed in the next section.

3.2. Clinical Image Analysis

Two sets of clinical data are used in visual and quantitative analysis. The first dataset contains T1WI, T2WI and FLAIR images with specifications as described in Section 2.1. Total 70 multispectral slice sets were selected for analysis from 20 abnormal cases. Figure 5 top row shows slices in a sample multispectral image set. T2WI and FLAIR images show

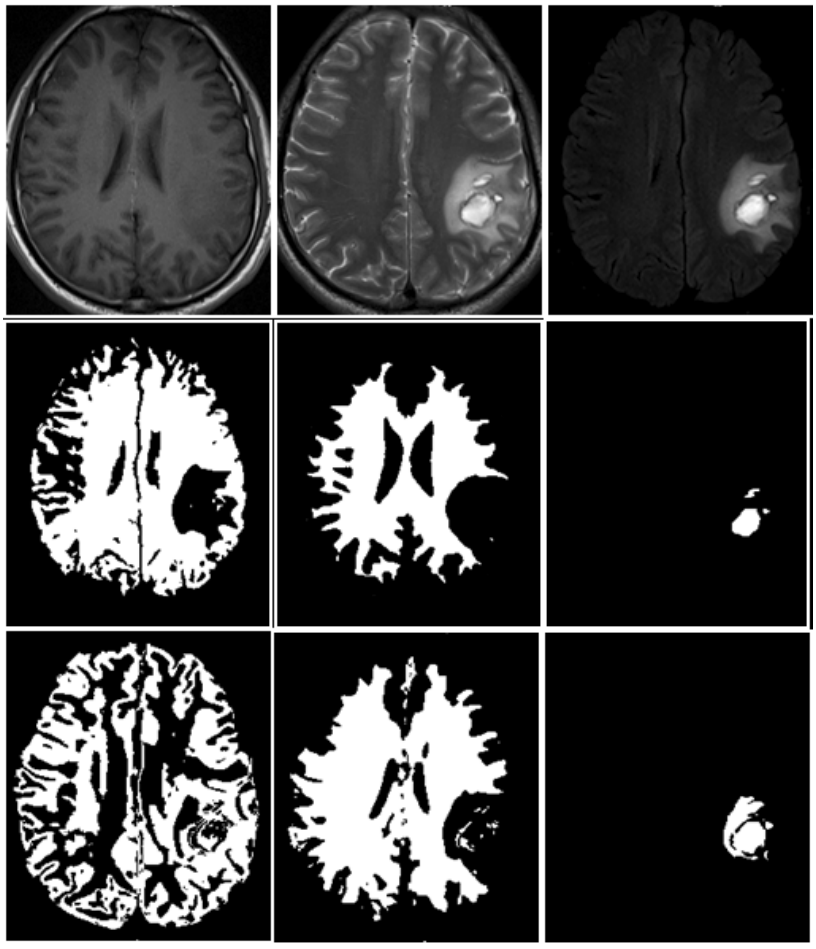

Figure 5. Classification Results using Dataset 1: (from left to right) top row - Input Slices T1WI, T2WI and FLAIR image, middle row- ICA Results, GM, WM and Abnormal Tissue, bottom row-MICA Results GM, WM and Abnormal Tissue

lesion surrounded by edema, but that information is not visible in T1WI. Classified results from ICA+SVM and MICA+SVM are given in Figure 5 middle row and last row respectively with GM in the 1st column, WM in the 2nd column and abnormality in the 3rd column. MICA+SVM results show the lesion and the surrounding edema (Figure 5 last row last column) with a clear description of the separation between lesion and edema in the original image. On observing the affected portion of WM (Figure 5 2nd column), MICA+SVM results looks better than ICA+SVM results. However, MICA cannot reach the performance of ICA in classification of WM.

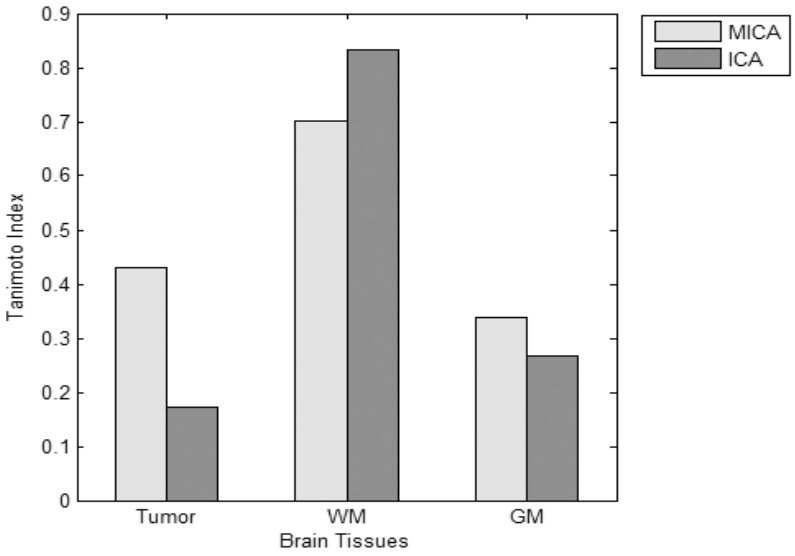

Figure 6. Bar Chart Showing Tanimoto Index of Tumor, WM and GM for Clinical Dataset 1

Table 2. Statistical Analysis of Clinical Dataset 1

Noise	Feature Extraction	Specificity	Sensitivity	Accuracy
Abnormality	ICA+SVM	50	17.3085	37.6814
	MICA+SVM	97.2599	43.3540	94.7727
GM	ICA+SVM	85.7690	57.6267	78.6936
	MICA+SVM	96.1801	83.7134	93.8117
WM	ICA+SVM	94.8525	85.6485	92.4228
	MICA+SVM	90.9110	82.7608	88.0974

The bar chart shown in Figure 6 clearly depicts the Tanimoto index difference between two methods. Significant improvement observed for tumor class is a vital point in this analysis. But here also WM classification looks good with ICA+SVM. Tanimoto differences between MICA+SVM and ICA+SVM are observed as 0.2566, 0.071 and -0.1316 for tumor, GM and WM respectively. Specificity, sensitivity and accuracy values obtained for GM, WM and abnormality by MICA+SVM and ICA+SVM are summarized in Table 2. Quantitative analysis results in Table 2 strongly support the visual results. Accuracy value increased from

37.6814 to 94.7727 in tumor classification, *i.e.*, around 2.5 times performance improvement is observed for MICA+SVM.

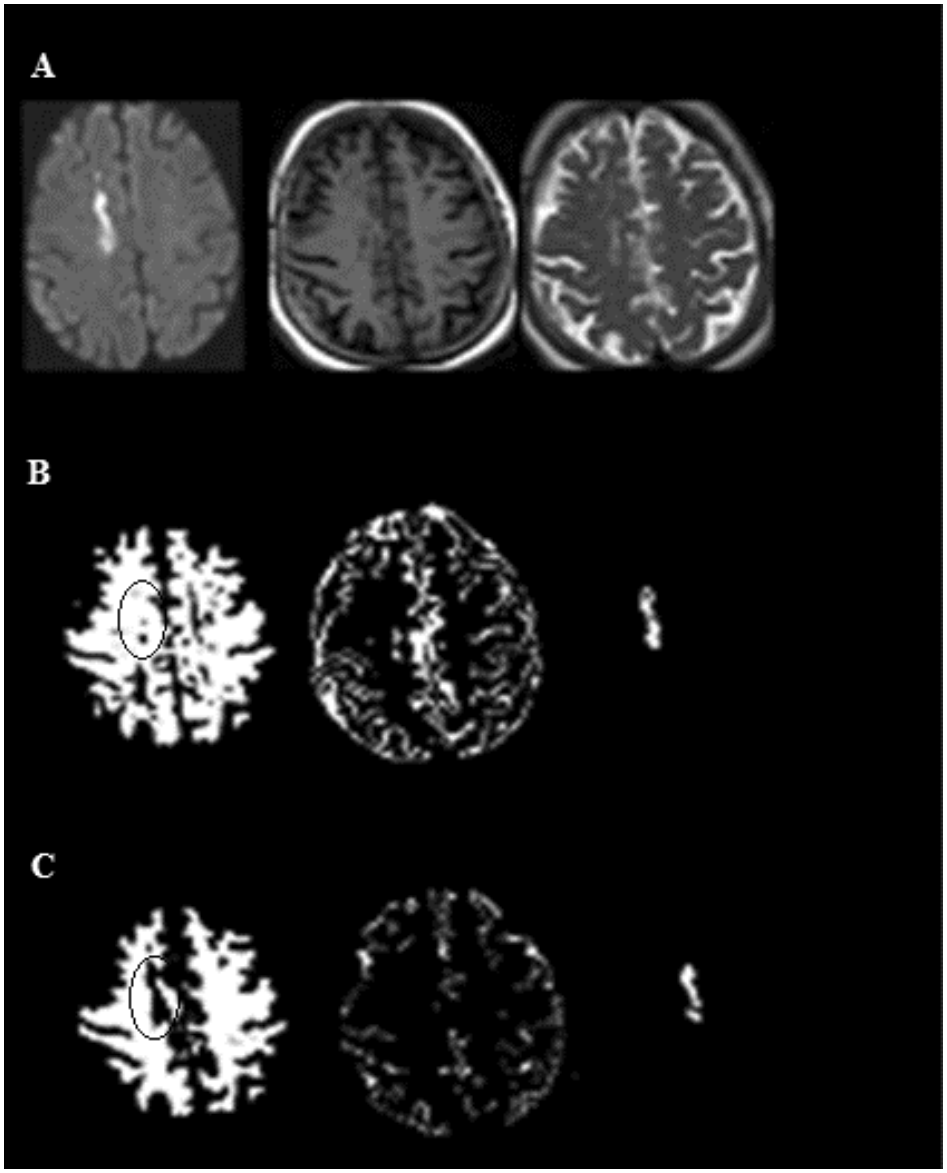

Figure 7. Classification Results using Dataset 2: (from left to right) A) Input Slices DWI, T1WI and T2WI; B) ICA Results, WM, GM and Abnormal Tissue; C) MICA Results WM, GM and Abnormal Tissue

Total 110 multispectral slice sets of T1WI, T2WI and DWI selected from 35 abnormal cases were included in the second set of clinical data analysis. Some input slices showing white matter abnormalities are given in Figure 7A (top row). Figure 7B gives ICA+SVM results and Figure 7C shows MICA+SVM results in the order of WM, GM and abnormality from left to right. Classification result for abnormality is similar to the previous results, abnormal tissue details in MICA+SVM results (Figure 7C last column) exceeds that in ICA+SVM (Figure 7B last column). The first column comparison of Figure 7B and 7C

shows that affected portion of WM (circled portion) is almost completely detected by MICA+SVM. But in the case of unaffected portion of GM (2nd column) ICA+SVM performs better than MICA+SVM.

Tanimoto index values obtained from similarity checking of classified results with ground truth are shown as a bar chart in Figure 8. Tanimoto differences between MICA+SVM and ICA+SVM were observed as +0.0973 and +0.0665 for tumor and WM respectively. Quantitative analysis with second set of measurements supports these results with noticeable increase in specificity, sensitivity and accuracy as summarized in Table 3.

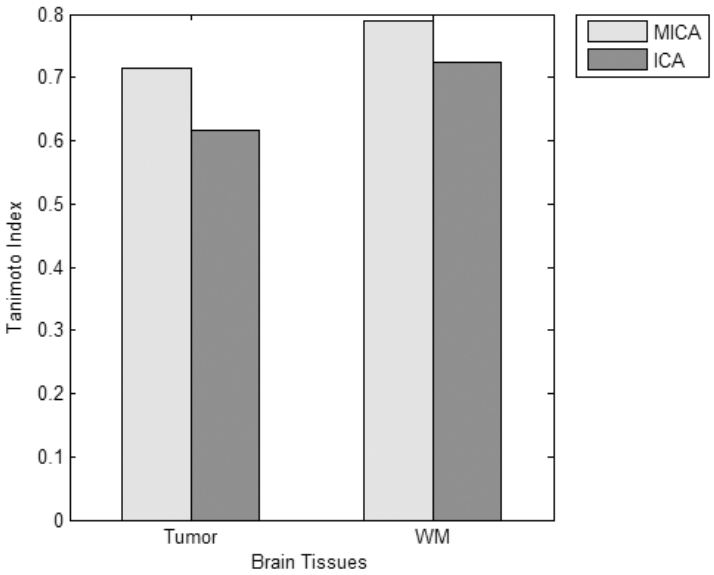

Figure 8. Bar Chart Showing Tanimoto Index of Tumor and WM for Clinical Dataset 2

Table 3. Performance Analysis of Clinical Dataset 2 for Abnormal Tissues (Abn.) and WM

	Feature Extraction	Specificity	Sensitivity	Accuracy
Abn.	ICA+SVM	99.7998	74.7604	99.6027
	MICA+SVM	99.8101	76.0383	99.6233
WM	ICA+SVM	93.4206	83.5774	90.6051
	MICA+SVM	95.3921	89.5794	93.6099

Experimental results demonstrate that multiresolution analysis avoids the loss of significant MRI details in feature extraction, and it provides a relatively good pre-processing step for high performance tissue classification and abnormality analysis. MICA is robust and reliable in noisy environment also. However, it suppresses the majority information before wavelet reconstruction. Sometimes this will affect normal brain matter extraction, as it is observed in the case of unaffected WM and GM tissue classification.

4. Conclusion

In recent years, multispectral approach helped MRI analysts a lot to improve the analysis time and accuracy of the clinical trials. However, extraction of very critical features like small lesions is a great challenge in pathology analysis due to lack of efficiency of the existing methods. The proposed multiresolution analysis coupled with ICA is demonstrated as a good choice to resolve this issue. SVM classification is used to investigate and evaluate the performance of the method in abnormality analysis. Experimental results using synthetic and clinical data confirm that the proposed method performs better than ICA based classifications in lesion/tumor detection. Experiments conducted for noisy synthetic images also support these findings with acceptable results in favor of MICA. Refinements of MICA are under consideration to give equal priority to normal and abnormal tissue classification in future works.

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Authors

Sindhumol S. received her M.Tech degree in Digital Image Processing from University of Kerala, Trivandrum, India in 2005 and is currently pursuing Ph.D. degree in medical imaging from Cochin University of Science and Technology, Cochin, India. She has been working with audio, video and image processing algorithms in IT industry for last 7 years. Her research interest includes multimedia and streaming, multispectral analysis, wavelets, medical imaging, pattern recognition and classification.

Dr. Anil Kumar is a Senior Consultant Radiologist at IRIS, Medall Centre in Cochin, Kerala. He is also working as Associate Professor in Department of Radio diagnosis and Nuclear medicine at Amrita institute of medical sciences, Kochi. He received his MBBS from Medical College, Trivandrum, University of Kerala, MD (Radio Diagnosis) from Army Hospital Research, New Delhi and DNB from National Board of Examination, New Delhi. He has over 17 years of experience in Radio Diagnosis, Operations and Teaching. He has published more than 10 publications in various national and international journals.

Dr. Kannan Balakrishnan received his M.Sc and M. Phil degrees in Mathematics from University of Kerala, India, M. Tech degree in Computer and Information Science from Cochin University of Science & Technology (CUSAT), Cochin, India and Ph. D in Futures Studies from University of Kerala, India in 1982, 1983, 1988 and 2006 respectively. He is currently working with CUSAT, Cochin, India, as Associate Professor (Reader), in the Department of Computer Applications. He has published several papers in International Journals and National and International conference proceedings. His present areas of interest are Graph Algorithms, Intelligent Systems, Image Processing, CBIR and Machine Translation. He is a reviewer of American Mathematical Reviews. He has served in many academic bodies of various universities in Kerala, India.