

Accurate Classification of Brain Gliomas by Discriminate Dictionary Learning based on Projective Dictionary Pair Learning of Proton Magnetic Resonance Spectra

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ABSTRACT

Proton magnetic resonance spectroscopy is a powerful noninvasive technique that complements the structural images of conventional magnetic resonance imaging, which aids biomedical and clinical researches, by identifying and visualizing the compositions of various metabolites within the tissues of interest. However, accurate classification of proton magnetic resonance spectroscopy is still a challenging issue in clinics due to low signal-to-noise ratio, overlapping peaks of metabolites and the presence of background macromolecules. This paper evaluates the performance of a discriminate dictionary learning classifiers based on projective dictionary pair learning method for brain gliomas proton magnetic resonance spectroscopy spectra classification task and the result were compared to the sub-dictionary learning methods. The proton magnetic resonance spectroscopy data contains a total of 150 spectra (74 healthy, 23 grade II, 23 grade III, 30 grade IV) from two databases. The datasets

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from both databases were first coupled together, followed by column normalization. The Kennard-Stone algorithm were used to split the datasets into its training and test sets. Performance comparison based on the overall accuracy, sensitivity, specificity and precision were conducted. Based on the overall accuracy of our classification scheme, the dictionary pair learning method were found to outperform the sub-dictionary learning methods 97.78% compared to 68.89% respectively.

Keywords: Proton magnetic resonance spectroscopy, Brain gliomas, dictionary pair learning, sub-dictionary learning

I. INTRODUCTION

Proton magnetic resonance spectroscopy ($^1\text{H-MRS}$) is a powerful noninvasive technique that complements the structural images of conventional magnetic resonance imaging (cMRI) which aids biomedical and clinical applications by identifying and visualizing the compositions of various metabolites within the tissues of interest (brain, heart, etc.)^[1,2]. An observed $^1\text{H-MRS}$ spectra of the brain is made up of complicated signals corresponding to several overlapping peaks of different metabolites, as well as baseline coming from various macromolecules and lipids coupled with noise and distortions^[1,3], an accurate classification of $^1\text{H-MRS}$ brain spectra signals is needed for efficient and effective diagnosis of diseases.

With a decision support system for classification^[4,5], the $^1\text{H-MRS}$ spectra which is a multivariate data can achieve a higher reliability by developing a good statistical model to classify various tumorous $^1\text{H-MRS}$ data^[6,7]. Several classification methods for $^1\text{H-MRS}$ data has been proposed^[8-11], but the sparse representation technique is a recent method for classification^[12-14].

Sparse representation (SR) is a parsimonious principle that shows the representation of a signal as a linear combination of basis vectors which are chosen from a dictionary^[15,16]. The SR method has been found to be robust to noise while its basis vector are non-orthogonal which are sometimes found to be interpretable due to its sparseness property. The SR has achieved a remarkable success in various signal processing, image processing and computer vision applications^[17-19].

Dictionary learning (DL) which is a subclass of SR is obtained by finding a desired dictionary that can effectively represent the signal of interest^[20,21]. Analysis and synthesis types of dictionaries has been widely studied in literatures and are found to play active roles in signal representation^[22]. Synthesis based sparse representation method has been found to allow easy learning of a desired dictionary from a training set and can model complexity better of the local signal structures. However, the synthesis representation coefficient of signals are usually obtained via an lp-norm ($p < 1$) sparse coding process which is computationally more expensive than analysis dictionary representation.

The success of DL has been centered mostly on the discrimination capability of the learned dictionary. This simple property has found its applications in most signal restoration problems, and it has also been the bedrock of signal classification task where the main goal of classification problems is to assign correct class label to the test sample.

In literatures, several supervised dictionary learning (SDL) method which promotes the discriminative power of learned dictionary have been proposed. The SDL method works by encoding the test sample over the learned dictionary, where both the coefficients and the residuals of the learned dictionary can be used for classification depending on the DL model employed^[23,24].

One of the most popular strategy of discriminative DL model employed in literatures is to learn a shared dictionary of all classes while enforcing the coding coefficients to be discriminative and a classifier based on the coding coefficients can be trained simultaneously to perform the classification task^[25,26]. The label consistent KSVD (LC-KSVD) method which was proposed by Jiang et al introduced a binary class label sparse code matrix to encourage samples from the same class to have similar sparse codes^[27]. However, Mairal et.al also proposed a task driven dictionary learning (TDDL) framework which minimizes different risk function of the coding coefficients for different tasks where a learned dictionary with their corresponding linear classifier in the coding vector space^[28].

The structured DL model is another popular line of research interest which learns a structured dictionary that can promote discrimination between classes while atoms in the structured dictionary have class labels and the class-specific representation residuals that are computed for classification^[29,30].

Another exciting discriminative DL model was proposed by Ramirez et al which introduces an incoherence term to encourage the sub-dictionary of different class to be independent^[31]. Yang et al proposes a Fisher discrimination dictionary learning (FDDL) method which applies the Fisher criterion to both the representation residual and

representation coefficient^[32]. A max-margin dictionary learning (MMDL) algorithm was proposed from the large margin perspective to solve a classification problem^[33,34].

Shuhang et.al were the first researchers to propose the projective dictionary pair learning (DPL) which extends the conventional discriminative synthesis DL to discriminative synthesis and analysis DPL, the projective DPL utilizes a coding mechanism that largely improves the efficiency of both the training and testing phase and also achieve a good accuracy^[35]. The novelty of this work centers on learning the training dataset with DL which discriminates between classes of the gliomas.

The organization of this paper is as follows: Section II describes materials and methods of ¹H-MRS signal with detailed report on discriminate dictionary learning. Section III presents the model evaluation while section IV evaluates the results and discussion of our methods. Section V discusses the conclusions.

II. MATERIALS AND METHODS

¹H-MRS samples were collected from 1.5T dataset from INTERPRET EU project^[36-38]. This data set consisted of patients with glial tumors and consisted of three classes, defined according to the laid down rules of the World Health Organization (WHO): grade II (15 cases), grade III (18 cases) and high grade gliomas (32 cases). The spectra were validated by an expert panel of spectroscopists, and the histopathological diagnosis of these cases were also available. The datasets were obtained using ¹H-MRS scanners of manufacturers (Philips, General Electric and Siemens) from 10 international centers. The acquisition protocols includes Point-Resolved Spectroscopy (PRESS) or Stimulated Echo Acquisition Mode (STEAM) with spectral parameters: TR of 1600-2020 ms, TE of 30-32 ms, spectral width of 1000-2500 Hz and 512 data-points.

The second part is a collection of 51 patients over the range of cancer groups analyzed^[39]. This dataset consisted of grade II (11 cases), grade III (6 cases) and high grade gliomas (9 cases). Data related to healthy tissue were acquired from the contralateral brain regions of 25 healthy volunteers. ¹H-MRS data of these samples were acquired from patients with glial brain tumors and people with normal brain, according to the medical ethics regulations of Imam Khomeini Hospital, Tehran, Iran. These multi-voxel proton MRS data were acquired on a 3T scanner (Trim Trio, Siemens, Germany), STEM or PRESS pulse sequence on TE of

30 msec, TR=1500ms, spectral width of 500-2500Hz, 1024 data-points and the thickness 10-15 mm for the tissue.

The data from both databases were coupled to create a dataset with 150 spectra. With Kennard-stone algorithm, the spectra data were divided into training and test sets. Therefore, 111 spectra were selected for the training set, and 39 spectra were as an independent test set. The class members for the data analysis were labeled from class I to class IV which shows that the class were from health to grade IV gliomas respectively.

Discriminate Dictionary Learning

Denoting $X = [X_1, \dots, X_k, \dots, X_K]$ as a set of p -dimensional training samples from K classes, where $X_k \in \mathfrak{R}^{p \times n}$ is the training sample set of class, k and n is the number of samples of each class. Discriminative DL methods aim to learn an effective data representation model from X for the classification task by exploiting the class label information of training data. Most of the state-of-the-art discriminative DL methods can be formulated under the following framework:

$$\min_{D,A} \|X - DA\|_F^2 + \lambda \|A\|_p + \Psi(D, A, Y) \quad (1)$$

Where $\lambda \geq 0$ is a scalar constant, Y represents the class label matrix of samples in X , D is the synthesis dictionary to be learned, and A is the coding coefficient matrix of X over D .

In the training model (1), the data fidelity term $\|X - DA\|_F^2$ ensures the representation ability of D ; $\|A\|_p$ is the l_p -norm regularizer on A ; and $\Psi(D, A, Y)$ stands for some discrimination promotion function which ensures the discrimination power of D and A .

Dictionary Pair Learning Model

The DPL model introduced by Shuhang et.al, the model extends the conventional DL model in (1) which learns a discriminative synthesis dictionary, to a novel DPL model, which learns a pair synthesis and analysis dictionaries. The proposed DPL model does not required l_0 or l_1 -norm sparsity regularizer, and the coding coefficients can be explicitly obtained by linear projections. However, DPL does not sacrifice the classification accuracy while achieving significance improvement in the efficiency. The formulation of DPL can be expressed as follows:

$$\{P^*, D^*\} = \arg \min_{P, D} \|X - DPX\|_F^2 + \Psi(D, P, X, Y) \quad (2)$$

Where $\Psi(D, P, X, Y)$ is the discrimination functions, D and P form the synthesis and analysis dictionaries respectively, and both are referred to as the dictionary pair. The analysis of P is used in coding X, and the synthesis dictionary D is used in reconstructing X. However, the optimization of (2) above while ensuring a column normalization of the dictionary with respect to the classes can be expressed as follows:

$$\{P^*, D^*\} = \arg \min_{P, D} \sum_{k=1}^K \|X_k - D_k P_k X_k\|_F^2 + \lambda \|P_k X_k\|_F^2 \text{ s.t. } \|d_i\|_2 \leq 1 \quad (3)$$

III. Model evaluation

The most widely used statistics for evaluating a diagnostic test were sensitivity and specificity. These tests are based on the following definitions: true positive (TP)-Sick people correctly diagnosed as sick, false positive (FP) - Healthy people incorrectly identified as sick, true negative (TN) - Healthy people correctly identified as healthy, false negative (FN)-Sick people incorrectly identified as healthy. To evaluate the performance of our method, we report the standard performance measures which includes the sensitivity, specificity, precision and overall accuracy (OA). These measures are defined as follows:

$$\text{Sensitivity} = \frac{TP}{TP + FN} \quad (4)$$

$$\text{Specificity} = \frac{TN}{FP + TN} \quad (5)$$

$$\text{Precision} = \frac{TP}{TP + FP} \quad (6)$$

$$\text{OA} = \frac{TP + TN}{TP + FN + FP + TN} \quad (7)$$

IV. RESULTS AND DISCUSSION

Patient Populations

The group consisted of 26 patient (11 men and 15 women), with ages ranging from 13 to 64 years. We investigated 11 grade II (42.31%), 6 grade III (23.08%) and 9 grade IV gliomas (34.61%).

Conventional MR imaging (cMRI) is a useful tool that provides an excellent information regarding the anatomic imaging of gliomas, contrast material enhancement, distant tumor foci, hemorrhage, necrosis, mass effect, and lots more parameters, which are all important in characterizing tumor grades. However, with good state of the art protocols and sequence optimization techniques, the classification and grading of gliomas with cMRI is sometimes unreliable because contrast material enhancement alone is not always accurate in predicting tumor grade^[40–42]. The proton MR spectroscopy as an advanced MR imaging technique is a powerful tool that supports tumor grading. Tumor grading of ¹H-MRS gliomas are expressed with metabolites ratios, this ratio has been found to be a reliable indicator of tumor detection.

Before the implementation of DPL and sDL methods on the dataset, Figure.1 shows the class plot of the MR spectra which shows the class of each individual MR spectra. The plot of average scaled dataset of the different profile, classes and MR spectra used in this study against the variance of the spectra distribution are shown in Figure.2 and Figure.3 respectively.

Several pre-processing steps like water suppression to enhance the intrinsic signal of interest, phase correction, zero filling and truncation were performed respectively to enhance the visibility of the signal. This ¹H-MRS signal were arranged into a matrix form and Kennard-Stone algorithm were used in splitting the data into its training and testing sets. Both the training and testing set were l2-norm column normalized.

For sDL, the l₁-nnls sparse coding method, knn predictor and the linear choice of kernel parameters were used, while the DPL method used the following; the dictionary size is set to 30, tau=0.5, lambda=0.03 and gamma=0.001.

Table 1 describes the DPL and sDL classification parameters based on the diagnostic test clinical criterion. The overall accuracy of the sDL model was 68.89% with 40.26% error rate and 59.74% non-error rate. After the evaluation of the model, the sensitivity of the model from healthy to GBM was 81.82%, 14.29%, 42.86% and 100% respectively. This result shows that the sDL is able to extract the correct direction of the grade IV patient, which also shows lower sensitivity and precision value in grade II and grade III respectively. The sDL method of classification denotes inconsistency in model prediction power and unreliable validation results. With the poor prediction power of sDL, the projective DPL method was applied instead of the conventional sDL.

The overall accuracy of projective DPL was 97.78% with 3.57% error rate and 96.43% non-error rate. Table 1 shows the performance values for the projective DPL method, after the evaluation of the model by this set, the sensitivity of the model from health to GBM was 100%, 100%, 85.71% and 100% respectively. The DPL method was able to extract the correct direction of the healthy patient, grade II and grade IV respectively.

In literature, the metabolites of healthy normal tissue is characterized with a higher value of N-acetylaspartate (NAA) peak, higher total creatine (tCr) peak, and a lower peaks for total choline (tCho), Glx, Gly and myo-inositol (Myo) when compared with abnormal spectra. Precisely, the increase in Cho with a decrease in NAA is a good indicator of tumor. There is extensive literature substantiating the metabolite ratios of Cho/ Cr, NAA/Cr, and Myo/Cr and the presence of lipids and lactate to be useful in grading tumors and predicting tumor malignancy^[40,43-45].

This study of brain gliomas (grade II-IV) is characterized by a lower value of NAA, and tCr, and a higher value of lactate when compared with healthy tissue. There are compelling evidence from literature that MR spectroscopy provides important supplemental information to that of cMRI^[46-49]. The general characteristics of the ¹H-MR brain spectra is having a low signal-to-noise ratio (SNR), baseline distortions, large width and asymmetric line shapes as a result of poor shimming. Both sDL and DPL methods are robust to noise, since their formulation is subjected to the difference between the observed and the reconstructed spectra. However, DPL shows better denoising result because of the optimization in the learning methods that involve both the construction of synthesis and analysis dictionaries. As a result, DPL method is a good choice to discriminate between the grades of gliomas class irrespective of the presence of noise in the spectra.

V. CONCLUSION

The application of discriminate dictionary learning for classifying ¹H MR Spectra of brain gliomas tumor was investigated. The *in vivo* spectra were known to be noisy with low level of SNR. In this paper, we have compared the performance of discriminate sub-dictionary learning method and projective dictionary pair learning on the classification of brain gliomas. The figure of merits shows that projective DPL performs consistently better than the sub-dictionary learning methods, while both methods were robust to noise.

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Table 1. The figure of merit table showing the performances of each methods based on the widely used statistics for evaluating diagnostic test

| Figure of Merit | DPL Method | | | | sDL Method | | | |
|-----------------|------------|----------|-----------|----------|------------|----------|-----------|----------|
| | Healthy | Grade II | Grade III | Grade IV | Healthy | Grade II | Grade III | Grade IV |
| Sensitivity | 100 | 100 | 85.71 | 100 | 81.82 | 14.29 | 42.86 | 100 |
| Specificity | 95.65 | 100 | 100 | 100 | 95.65 | 92.11 | 84.21 | 88.89 |
| Precision | 95.65 | 100 | 100 | 100 | 94.74 | 25.00 | 33.33 | 69.23 |

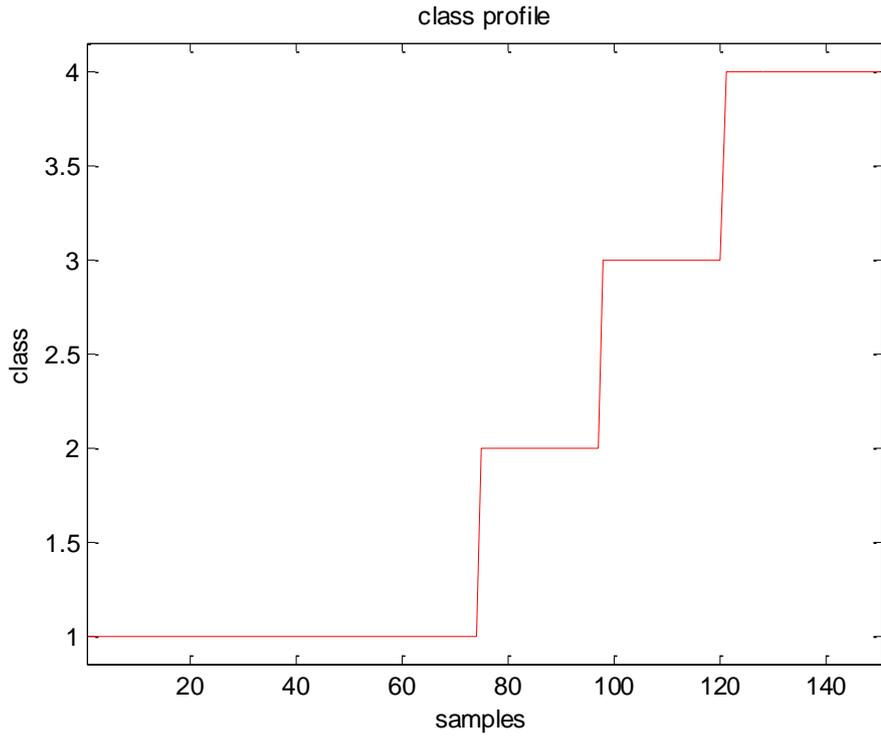


Figure 1: Class distribution of sample used. The figure shows that four classes data were

used.

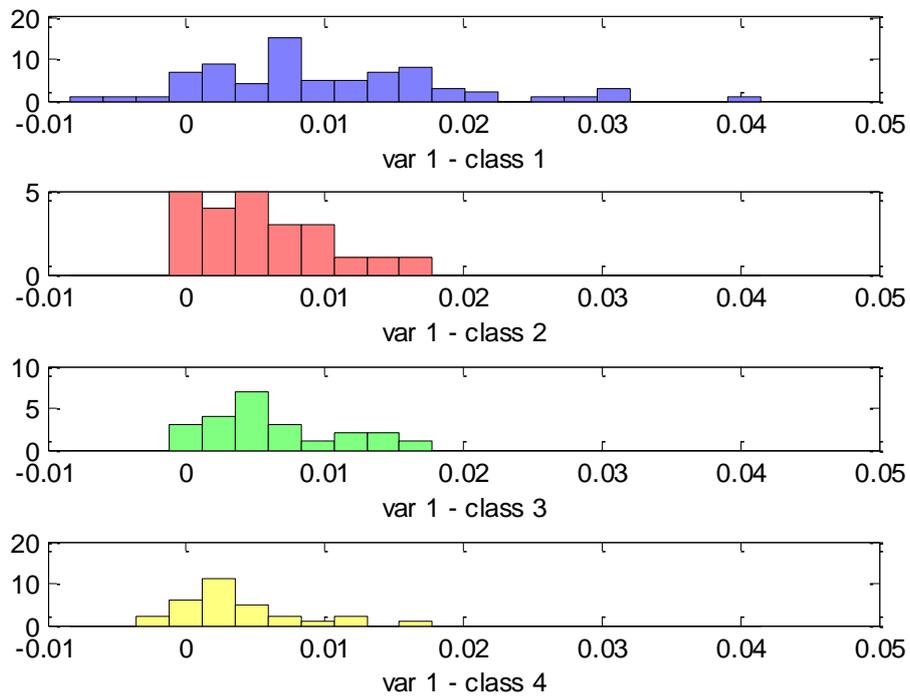


Figure 2: Shows the variance plot of each classes. Class 1=Healthy patient, Class 2= Grade II glioma, Class 3= Grade III glioma, Class 4= Grade IV glioma.

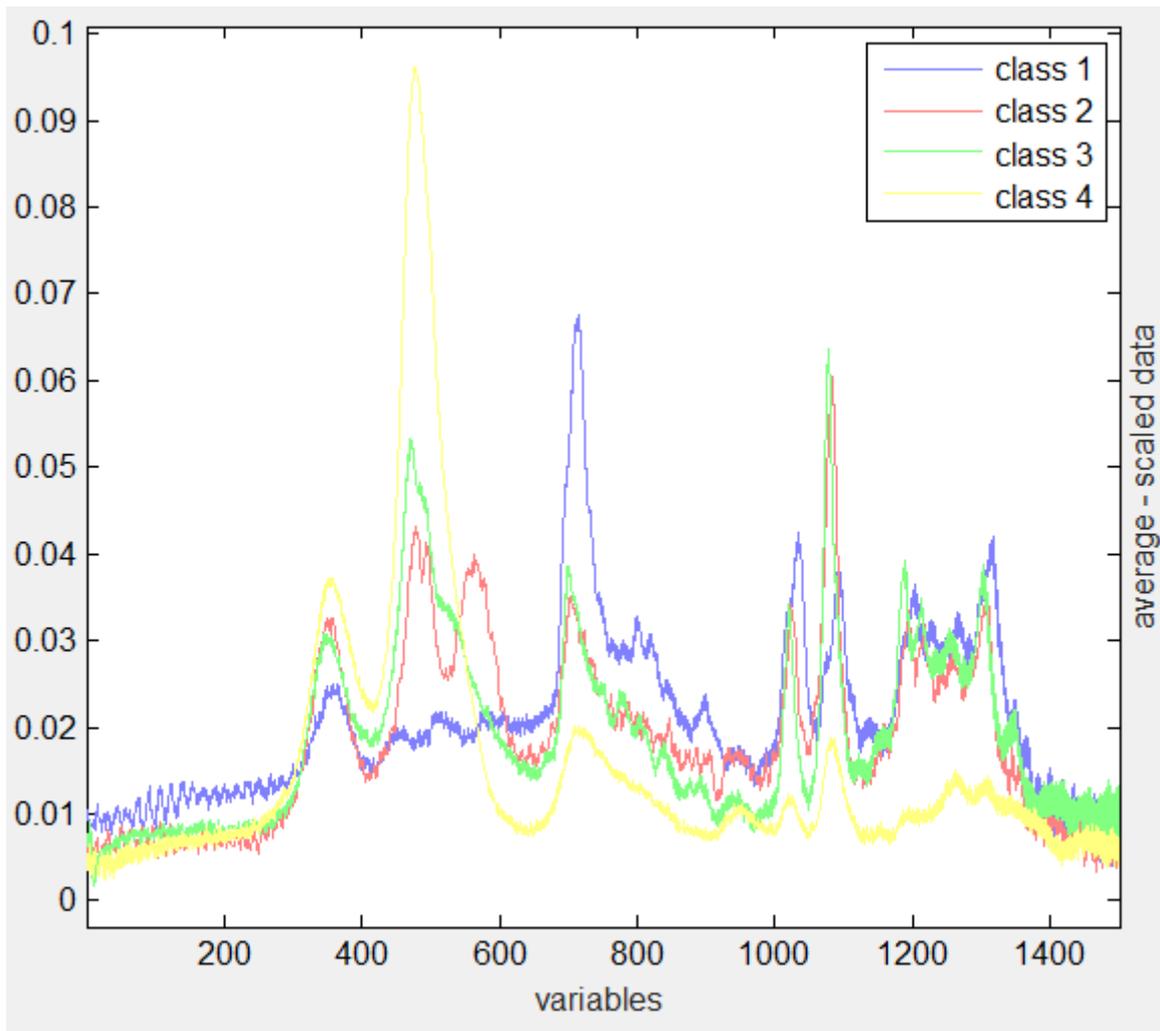


Figure 3: Shows the average-scale of the MR spectra data based on the classes. Class 1=Healthy patient, Class 2= Grade II glioma, Class 3= Grade III glioma, Class 4= Grade IV glioma.