An enforced block diagonal low-rank representation method for the classification of medical image patterns

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Received: 30 September 2021 / Accepted: 18 November 2021 / Published online: 20 January 2022
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Abstract Low-rank representation based methods have been used on a variety of medical imaging databases for the segmentation and classification of biomedical images. The subspace segmentation of the data is performed by generating the block diagonal coefficient matrix. Whereas, the data is classified by performing the partitioning of the low-rank representation matrix. There exist several such methods for analysing medical images. The major difference between them lies in the construction of the data dictionary. Most of the time, the input data pattern is used as the dictionary for learning the representation matrix. The direct use of the input data for learning the representation degrades the performance of the model because medical images are subjected to outliers of multiple types, which include environmental lighting, image appearance and varying illumination. These types of errors induce noise in the data. It has been observed that the representation-based model is robust when the training data is clean. If the training data contains corrupted subsamples, the performance of the model drops down. We have addressed the mentioned problem by adopting a class-wise dictionary learning approach. In which the pattern of each class is learnt as the set of tuples in the dictionary. The model has been evaluated on several medical imaging datasets, which includes the Break-his dataset, ALL-IDB, biomedical images, covid CT and chest X-ray. The classification performance of the model is best for the biomedical database (99.16%) followed by the Covid dataset (94%), ALL-IDB database (93.47%) and Break-his dataset (93%).

Keywords Block diagonal representation · Class-wise dictionary learning · Medical image classification and Subspace segmentation

1 Introduction

The medical staff generates a large volume of the data in the form of medical images, deoxyribonucleic acid (DNA) microarray and ribonucleic acid sequencing (RNA). The manual procedure of analyzing this volume of information relies on the knowledge of the medical expert. The approach is time-consuming and prone to errors. Due to the complexity in the structure of data, a large portion of the information is underutilized. Which leads to inaccurate diagnosing of the disease and the improper selection of the treatment methods. It has been observed in cancer patients about the harmful effects of the following cancer treatment methods, which include molecular therapies, bone marrow transplantation and chemotherapy [1, 2]. The problems have been observed in the form of premature greying of hair and hair loss. The factors that are responsible for the mentioned problems, include inefficient utilization of the patient's data and the improper treatment plan. Thus, there arises the need for the development of the automatic solution, which will process the required volume of data efficiently and without complexity overheads.

Nowadays, there exist different types of computer-aided methods for processing medical imaging data. The method that we have adopted in our work is based on representation-based learning. The objective of the model is to exploit the self-expressive power of data. Given a set of data points that exist in the input data pattern of the observation matrix. These data points belong to different subspaces. The model finds the subclass-label for each of

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the individual data points by performing the linear decomposition of the input observation into the dictionary and the coefficient matrix. The segmentation and the classification, of the input observation, is performed by generating the global grouping patterns for different subspace segments. The problem is non-convex. It is converged to the convex-one by the nuclear-norm based strategy. Whereas its optimization is performed by the alternating direction method.

Low-rank representation has been widely used for subspace segmentation and classification of biomedical image data. Cao et al. [3] has utilized a hybrid LRR based segmentation model for the smooth extraction of leucocytic cells. The experimental results indicate the discriminative power of LRR was very high, in comparison to the k-means and fuzzy c-means algorithm. We have utilized the representation-based method on four different types of medical imaging databases, which include cell images (leukaemia and non-leukaemia), biomedical images (CT, chest X-ray and brain MRI), breast cancer (malignant and non-malignant) and the covid dataset (chest X-ray and CT-images). The objective was to differentiate the data pattern of infected and non-infected medical images. Which is obtained by performing the subspace segmentation and clustering of the different image patterns. The general procedure of training is to perform the linear decomposition of the input data matrix X , into the dictionary D and the coefficient matrix Z . The representation matrix encompasses the block diagonal structure. In which each block represents the different data pattern of the input observation.

Most of the recent methods utilize the input data matrix X as the dictionary. The direct use of the input data for learning the representation degrades the performance of the model because the medical image is subjected to errors of multiple types (environmental lighting condition, image appearance, varying illumination, and the quality of microscope). These types of errors induce noise in the training of the model. It has been observed in [4], that representation-based models are robust when the training data is clean, if the training data contains corrupted subsamples, the performance of the model degrades considerably. We have addressed the problem by inducing the dictionary and the enforced block diagonal regularizer. This approach reduces the impact of noise in the training by learning a class-level dictionary learning and minimizing the cross-block diagonal entries.

2 Literature review

There exist different machine learning algorithms that can be used to analyze the structure of several medical imaging databases. Anilkumar et al. [5] have classified the medical image segmentation methods into the following three categories, which include the filter-based method, pattern-based clustering algorithms and the representation-learning methods.

Filipnovoselnik et al. [6] have segmented the microscopic blood sample images for the smooth extraction of the cell nucleus. We have observed that the approach does not work on the different types of leucocytic cell images. Consider the case of granulocytes, the machine learning method has shown the multiple counts for the divided nucleus segments. This problem can be addressed by utilizing low rank representation (LRR) which obtains the global representation of the different blood cell components. Reta et al. [7] have differentiated between acute lymphoblastic leukaemia (ALL) and acute myeloid leukaemia (AML) medical images. The authors have used different types of pattern-based classifiers for classification, which include K-nearest neighbor (KNN) and support vector machine (SVM). The model has not differentiated some of the cell images which are affected by outliers of different types (sample-specific and random corruptions). The problem can be solved by incorporating the regularization strategies which minimize the impact of noise in the training. Firdosi et al. [8] have extracted leucocytes by utilized $L \times a \times b$ colour model. They have applied the K-Means clustering approach to the cell image components. Some of the non-leucocytic cell components were also included in the cell identification process. This induces false positiveness in the results. It can be avoided by incorporating the class-wise dictionary learning approach that minimizes the misclass labelling of data.

Fayez et al. [9] have performed clustering of medical images by using two different methods, which include gray level co-occurrence matrix (GLCM) and the 2D wavelet transformation. For the case of the first method, the authors have extracted the textual features of an image by utilizing GLCM and Haralick's statistical measures. Whereas feature clustering was performed with the k-means algorithm. A similar procedure was repeated for the second method, in which 2D wavelet transformation is utilized for extraction of features and then clustering was performed with the k-means algorithm. The methodology was evaluated on 500 medical images of five different classes, which include

chest X-rays, neck X-rays, knee X-rays, brain CT-scan and spine CT-scan. The clustering performance of the 2D wavelet was very high in comparison to the GLCM method. Prakashas et al. [10] have used different clustering algorithms on the brain MRI images for the detection of brain tumours. The algorithms that they have used, include the fuzzy C-means clustering (FCM), spatial fuzzy C means (SFCM), K-means, particle swarm optimization incorporative fuzzy C means clustering (PSOFCM), Gustafson kessel (GK) clustering and density-based clustering of applications with noise (DBSCAN). It was concluded that the brain tumour detection of MRI images was performed efficiently by PSOFCM, GK and DBSCAN. The problem with these methods is that the results were computed on a smaller set of parameters. Their performance can be improved by incorporating a variety of parameters during the computation of the results.

Considering the drawbacks of the mentioned techniques, we have adopted a desirable solution that is based on the (LRR). Instead of directly dealing with the pattern of the several subspace components, the approach works by performing the indirect linear decomposition of the input observation. The idea of LRR comes from the concept of robust principal component analysis (RPCA), which decomposes the data observation into the low-rank normal part and the sparse noise part. The problem with RPCA is that it can only handle the data drawn from a single subspace of data. So, it cannot handle the outliers drawn from the union of multiple subspaces. To accommodate the data drawn from the union of multiple subspaces, Liu et al. [11] proposed the concept of LRR. Its general objective function is depicted in Eq. (1).

$$\min_{Z,E} \text{rank}(Z) + \lambda \|E\|_0 \text{ s.t. } X = DZ + E. \quad (1)$$

Based on the low-rank representation method, some of the new improvements that have been achieved so far are discussed as follows. Mia et al. [12] have integrated rank minimization into sparse representation for dictionary learning. The objective was to exploit the low rank and sparsity property of the input data patterns. The results have demonstrated the effectiveness of the combined approach for the classification of the image data. It has resulted in the performance development of the model. Zhang et al. [13] have performed image classification by proposing a discriminative low-rank subspace structured framework. The discrimination has been done by introducing a regularization strategy that focuses on the idealized structure of the data. Whereas all the samples that belongs to the particular class were regularized to be the same. Li et al. [14] have adopted discriminative dictionary learning with the low-rank regularization ($D^2L^2R^2$). To make the learned dictionary noise-free, they combine the Fishers discrimination function with a low-rank constraint. It has been used for image classification.

Most of the recent work has focused on the retention of structural information. In [13] some have observed the impact of training on the performance of the model. In the work, the authors have directly used the input data as a dictionary. Which has adversely affected the classification performance because of the presence of outliers in the data. To deal with the mentioned problem we are inducing a regularization strategy that enforces a block diagonal representation in the coefficient matrix. It exploits the structural information of high dimensional data by adopting class wise dictionary learning of data.

Jia et al. [15] has developed a registration network based on the LRR approach. The objective was to remove the noise from the cardiac and abdominal inter-modality images. The experimental results have shown the effectiveness of the concerned approach on the recovery of data samples that were affected by multiple corruptions. Li et al. [16] have diagnosed Alzheimer's disease by combining the features of LRR with the discriminant component analysis (DCA) method. The salient features of the data were obtained by the LRR approach. Whereas, the analysis on the observed features was performed by using DCA. Lou et al. [17] proposed a multimodal latent low-rank representation algorithm for the brain MRI (Magnetic resonance images) medical images. The authors have enhanced the quality of medical images (lesions) by solving fuzzy details. Chen et al. [18] proposed the model based on LRR and sparse representation. The experimental results indicate the performance improvement in the reconstruction of quality content on the cardiac cine imaging.

3 Methodology

To deal with the high dimensional biomedical imaging data. We have adopted a discriminative block diagonal low-rank representation model. In which the discrimination is performed by incorporating a regularization strategy that focuses on the idealized structure of the data. The training of the model is performed by inducing the class-wise dictionary learning of the data. Which reduces the impact of noise by retaining the noiseless data pattern from the input observations that are given to the model. The block-diagonal structure of the data during the training is preserved by the regularization term, $\|L \odot Z\|_F^2$. It minimizes the off-block-diagonal entries of the representation matrix. The values of matrix L are computed from Eq. (2). The general formulation of the objective function is depicted in Eq. (3).

$$L(i,j) = \begin{cases} 0, & \text{if } d_i \text{ and } x_i \text{ belong to the same class} \\ 1, & \text{otherwise} \end{cases} \quad (2)$$

$$\min_{Z,E} \|Z_i\|_* + \lambda \|E\|_1 + \frac{\alpha}{2} \|L \odot Z\|_F^2 + \beta \|Z\|_1, \quad (3)$$

$$s.t. X = DZ + E.$$

The variable (Z), represent the coefficient matrix, E handles the noise in the data and D , is the dictionary matrix. d_i and x_i , are the i th items in the dictionary and the input observation. The symbol $\|\cdot\|_*$, is the nuclear norm. It controls the low-rank parameter of the data. It is the sum of singular values. The parameters λ and β , induce the sparsity in the data. The symbol (α) constrains the values of the regularizer.

3.1 Class wise dictionary learning of data

Discriminative dictionary learning acts as the base in pattern classification when the training data contains corrupted sub-samples. The approach has shown promising performance on the classification of image data [12–14]. Since most of the time, biomedical data is affected by outliers of different types (sample-specific and random corruptions). To remove the impact of noise in the training of the model, we have incorporated the class-wise dictionary learning approach. Its objective function is depicted in Eq. (4). The block diagram of dictionary learning is depicted in Fig. 1.

$$\min_{Z,E,D} \|Z\|_* + \lambda \|E\|_1 + \frac{\alpha}{2} \|L \odot Z\|_F^2 + \beta \|Z\|_1 + \frac{\gamma}{2} \|D\|_F^2, \quad (4)$$

$$s.t. X = DZ + E.$$

The Eq. (4) is convex, it can be solved in polynomial time. Some of the well-known polynomial-time algorithms that can be used for optimization fall in the category of first-order methods. These methods are further divided into constrained and non-constrained algorithms. Since our objective function constrains the values of the representation matrix, we have followed the path of constrained algorithms. The most commonly used optimization algorithm in this category, include the alternating direction method (ADM). Which places penalties in the objective functions that constrain the values of the coefficient matrix. The objective is to minimize the mean square distance

Fig. 1 Construction of L by applying the regularization on the input observation (X) and the dictionary (D)

between the observed and the target values. If there exists, an increase in the value of the error function, we penalize the values of the coefficient matrix. The ADM provides the closest approximated result on the separable convex problems. This method of convergence is suitable for our objective function (4). Based on the unitary and non-unitary linear mappings of the representation matrices, multiple variants of the ADM have been proposed. To produce global convergence solutions on the non-unitary mappings, a variant of ADM termed LADM [19] (linearized alternating direction method) has been proposed. Both of the given methods work sufficiently on the two-block cases. The linear mappings between the coefficient and the input observation are obtained by the equation given in (5).

$$\min_{Z,J,L,E,D} \sum_{i=1}^n \|J\|_* + \lambda \|J\|_1 + \frac{\alpha}{2} \|L \odot Z\|_F^2 + \beta \|L\|_1 + \frac{\gamma}{2} \|D\|_F^2, s.t. X = DZ + E, Z = J, Z = L \quad (5)$$

The transformation of the objective function (5) to the augmented lagrange multiplier (ALM) is given in Eq. (6).

$$\Lambda(Z, J, L, E, D, Y1, Y2, Y3, \mu) = \|J\|_* + \lambda \|J\|_1 + \frac{\alpha}{2} \|L \odot Z\|_F^2 + \beta \|L\|_1 + \frac{\gamma}{2} \|D\|_F^2 + \langle Y1, X - DZ - E \rangle + \langle Y2, Z - J \rangle + \langle Y3, Z - L \rangle + \frac{\mu}{2} (\|X - DZ - E\|_F^2 + \|Z - J\|_F^2 + \|Z - L\|_F^2) \quad (6)$$

The variables Z, L, E, D and J are updated in each iteration by the equations from (7)–(11).

$$Z^{k+1} = \arg \min_Z \frac{\alpha}{2} \|A \odot Z\|_F^2 + \frac{\mu^k}{2} \|X - D^k Z - E^k + \frac{y_1^k}{\mu^k}\|_F^2 + \frac{\mu^k}{2} \|Z - J^{k+1} + \frac{y_2^k}{\mu^k}\|_F^2 + \frac{\mu^k}{2} \|Z - L^k + \frac{y_3^k}{\mu^k}\|_F^2 \quad (7)$$

$$L^{k+1} = S_{\frac{\beta}{\mu^k}} \left[\|Z^{k+1} + \frac{y_3^k}{\mu^k}\|_F^2 \right] \quad (8)$$

$$E^{k+1} = S_{\frac{\mu^k}{\mu^k}} \left[\|X - D^k Z^{k+1} + \frac{y_1^k}{\mu^k}\|_F^2 \right] \quad (9)$$

$$D^{k+1} = \left[\frac{y_1^k (Z^{k+1})^T}{\mu^k} - (E^{k+1} - X) (Z^{k+1})^T \right] \left(\frac{\gamma}{\mu^k} I + Z^{k+1} (Z^{k+1})^T \right)^{-1} \quad (10)$$

$$J^{k+1} = U S_{\frac{\lambda}{\mu^k}}(\Sigma) V^T \quad (11)$$

3.2 The output of the training phase

From the input observation (X_{input}) of training, we have obtained the dictionary D and the coefficient matrix M . The performance of the model is tested by generating the test matrix (Z_{test}) from the set of test observations (X_{test}). Where $\hat{z}_j$ is the representation vector for the j th test sample. The partitioning of data points is obtained by utilizing the linear classifier M^* . Its objective function is given in Eq. (12).

$$M^* = \arg \min_M \|V - MZ\|_F^2 + \eta \|M\|_F^2 \quad (12)$$

where the classifier M , is designed by using the representation Z , of the training data and the corresponding label matrix V . The symbol $\eta > 0$, is a parameter. Its closed-form solution is written in Eq. (13).

$$M^* = VZ^T (ZZ^T + \eta I)^{-1} \quad (13)$$

The test sample j is determined in (14).

$$i^* = \arg \max_i M^* \hat{z}_j \quad (14)$$

where i^* , is the best output from (14).

4 Result and discussion

The data on which we have evaluated the model constitutes the medical imaging data of four different categories, which include acute lymphoblastic leukaemia international database (ALL-IDB) [20], BreakHis (Breast Cancer Histopathology) [21], X-ray and CT images of severe-acute-respiratory-syndrome (SARS) [22] and biomedical images (chest X-ray, neck X-ray and brain MRI).

ALL-IDB is an international database. It contains microscopic blood images of leukaemia and non-leukaemia patients. The dataset is divided into two groups, segmented and non-segmented images. The segmented set contains around 260 blood images, where 130 belongs to leukaemia and the remaining 130 belongs to normal patients. This dataset requires only classification because it is already segmented. The non-segmented set contains around 108 blood images, among them 46 belongs to leukaemia, and the remaining 62 belongs to non-leukaemia patients. This subset needs, both the segmentation and classification of blood images. We have utilized a non-segmented ALL-IDB dataset for evaluation, in which we have performed subspace segmentation and classification. The blood images in a dataset are of non-uniform size. To make them in uniform size, we have resampled the size of each blood image to the dimension of $500 \times 500 \times 3$. Each of the

blood images is presented in a single column vector. The resultant data matrix hits the dimension of $250,000 \times 92$. It is then used as the input to the model.

The biomedical image dataset is obtained from a local hospital. It contains data from three different classes, which include chest X-ray images, neck X-ray images and Brain MRI images. We have collected a total of 180 images from the three classes. Next, we have resampled the size of the input data pattern to the dimension of $(225 \times 225 \times 1)$. Each of the biomedical images is represented in a joint matrix as a column vector, hitting the target dimension to $((225 \times 225) \times 180)$. Our objective was to classify each of the biomedical images, in their appropriate classes. It is performed by doing representation and partitioning of data using a subspace segmentation approach. That segments data patterns in their specified classes.

The Break-his (Breast Cancer Histopathology) is another public access dataset on which we have evaluated our model. This dataset contains benign and malignant cancer images of different magnifications ($40 \times$, $100 \times$, $200 \times$ and $400 \times$). We have evaluated our model on a $40 \times$ magnification set of 100 cancer cases (50 belongs to the adenosis and 50 to ductal carcinoma). The image samples were then resampled to the matrix dimension of $((300 \times 300 \times 3) \times 100)$. This matrix is then used as input to the representation model. The operations that we have applied to the former datasets, were also repeated for the concerned dataset.

One more dataset on which we have evaluated the model, include the covid dataset of CT and chest X-ray image. It is a public access dataset that is obtained from the Kaggle. We have randomly selected a total of 200 image samples. Among them, 100 samples are selected from the CT image class. whereas the remaining 100 images consist of chest X-rays. Further, the selected set is divided into covid and non-covid labels. These image samples are then resized to the target dimension of $((500 \times 500) \times 100)$ for each of the CT and X-ray classes. The objective is to identify the accurate subclass labels for each of the test images that are given as input to the model.

The image samples of the biomedical database are depicted in Fig. 2. The medical samples of the remaining databases, which include ALL-IDB, Covid and BreakHis, are depicted in Fig. 3.

4.1 Evaluation metrics

The overall classification performance of the model is measured in terms of accuracy, sensitivity and precision. These metrics compute the classification performance of the model. The general formulation of the metrics is depicted in Table 1. Where the parameters TP, TN, FP and

Fig. 2 Different types of biomedical images were **A** is the neck X-ray, **B** brain MRI and **C** chest X-ray

Fig. 3 Different types of medical image samples. were rows representing the type of database and the columns represent the medical image samples. Column **A** represents the samples of infected patients, which include Covid, Leukaemia and Malignant. Whereas, column **B** represents the samples of healthy patients from a similar database

Table 1 Formulation of performance measures

Metric	Formula
Accuracy	$\frac{TP+TN}{TP+TN+FP+FN}$
Sensitivity	$\frac{TP}{TP+FN}$
Precision	$\frac{TP}{TP+FP}$

FN, represent the true positive rate, true negative rate, false-positive rate and false-negative rate. The confusion metrics for the different medical datasets are depicted in Fig. 6.

4.2 Results

The objective of the adopted approach was to characterize the pattern of different subspace structures that are present in the medical samples. Which is obtained by performing the linear decomposition and classification of image samples. The performance of the model is improved by adopting two different strategies, which include the class-wise dictionary learning and the enforced block diagonality approach. In which the training performance is improved by the dictionary approach, which learns the noiseless data features for the construction of the coefficient matrix. Whereas, the enforced block diagonality regularizer improve the classification performance by minimizing the cross-block-diagonal entries. The classification performance of the model is depicted in Fig. 5. In which the mean best accuracy is high for the biomedical dataset, followed by the Covid dataset, ALL-IDB database and the BreakHis dataset. To test the performance of the model with the noise in the data, we have performed the manual induction of different levels of Gaussian noise. While increasing the level of noise in the data, we have observed a slight drop in the performance of the model. Its results are depicted in Fig. 6.

4.3 Future scope

We have utilized the enforced block diagonal approach for characterizing the pattern of different medical image components. The objective was to perform the subspace segmentation and clustering of the medical samples (infected and non-infected images). Multiple challenges have been addressed while solving the given objective, which includes the robust discrimination of the medical imaging patterns and the recovery of data from the corrupted samples. It has been achieved by incorporating the class-wise dictionary learning while training the model and the regularization strategies. The concerned technique has shown efficient performance on the mentioned medical imaging databases in comparison to the related methods. In addition, there is a lot that needs to be done for improving the discriminative power of the representation matrix. In the future, we will improve the framework of the model by incorporating the image fusion strategy which will enhance the quality content of the image components.

5 A comparison with other methods

The performance of the model is compared with some of the recent representation-based techniques. These methods include the low-rank representation (LRR) approach, block diagonal low-rank representation (BDLRR) [13] and sparse

Fig. 4 Confusion metrics for different types of medical image databases, in which the confusion metric **A** is for the Covid CT dataset, **B** represent the Covid chest X-ray, **C** is for the ALL-IDB

dataset, **D** is for the BreakHis dataset, **E** is for the chest and neck X-ray datasets, and confusion metric **F** represent is for the neck and brain MRI

Fig. 5 Performance of the model on the Covid, ALL-IDB and BreakHis database. In which the horizontal axis represents the type of database and the vertical axis represents the performance scores

low-rank representation (SLRR) [23]. The comparison was performed on the following four types of medical imaging datasets, which include ALL-IDB, Biomedical, BreakHis and Covid datasets. The experimental results of the mentioned techniques are depicted in the Fig. 7. In which the enforced block diagonal low-rank representation (EBDLRR) has outperformed all the related methods in terms of the classification accuracy on the medical data samples.

Fig. 6 Change in the values of classification accuracy based on the different levels of Gaussian noise. Where the horizontal axis represents the type of database and the level of noise, and the vertical axis represents the classification score

6 Conclusion

There exists a large volume of medical imaging data that are produced by different medical hospitals. The manual approach of data processing depends on the medical expert. The approach is complex and prone to errors. To perform the automatic analysis, representation-based methods have been proven to be very effective in terms of data

Fig. 7 Comparison of our proposed work with different machine learning algorithms on different medical image datasets. In which the horizontal axis represents the type of method and the desired database. Whereas, the vertical axis represents the classification score

decomposition and quality content reconstruction. Most of these methods directly use the input observations for training the coefficient matrix. These approaches induce noise in the training because the data is affected by outliers of different types. To minimize the impact of noise we have incorporated the class-wise dictionary learning approach. Which learns the noiseless data pattern for each of the subclasses that is present in the input observation. In addition we have induced enforced regularizations strategies that generate the robust block diagonal representation matrix by removing off-block entries. The approach has been tested on different types of medical imaging datasets. Although, the performance of the model is high. But there is a slight need to improve the efficiency of the model by incorporating the multilevel decomposition and reconstruction strategies in the adopted framework.

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