Genetic Algorithm Framework for Image Block Clustering

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ABSTRACT--- *Principal Component Analysis (PCA) for image coding suffers the difficulties of computation complexity and projection errors. A typical method to solve this problem is the usage of clustering which partitions the image blocks into groups of smaller sizes. Moreover, the individuals belonging to the same group should exhibit the same visual properties such as edges and textures. In this paper, the genetic algorithm (GA) is adopted as a framework in the clustering process with visual properties imposed in the fitness function. Under such mechanism, the proposed method can effectively increase the retrieved quality and preserve the visual effects.*

Keyword--- Genetic algorithm; K-means clustering; Principal component analysis

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1. INTRODUCTION

Cluster analysis [1, 2] is a generic technique for a wide range of numerical methods. Clustering is a form of unsupervised learning whereby a set of observations (or data points) is partitioned into natural groupings or clusters of patterns in such a way that the measure of similarity between any pair of observations assigned to each cluster minimizes a specified cost function. It is to divide the collected information into various clusters and can effectively show the behavior patterns of the system. That is, it discovers groups of observations that are homogeneous and separates from others.

A common problem in statistical pattern recognition is feature selection, or feature extraction [3, 4]. Feature selection refers to a process in which a data space is transformed into a feature space that theoretically has exactly the same dimension as the original data space. However, the transformation is designed in such a way that the data set may be represented by a reduced number of effective features, yet retaining most of the intrinsic information content of the original data. In other words, the data set undergoes a dimensionality reduction. PCA, also known as the Karhunen-Loeve transformation, maximizes the decrease rate of variance and is therefore a right choice [5, 6].

In the paper, we separately implement PCA for each cluster, which consists of some specified block images, to reconstruct the original (or input) image. Unfortunately, the pre-specified error thresholds are empirical values and therefore GA is employed to solve the optimal problem for these thresholds. The genetic algorithm (GA) [7, 8], originally developed by Holland over the course of the 1960s and 1970s, is a biological analogy. In the proposed method, we group the dataset into numerous clusters, in which the numbers of principal components using PCA are adaptive. Here, we use GA as a framework with three stages, namely, GA operation, repartition clustering, and clustering PCA for image coding. We repeat the partition for the remaining individuals in the data set until the specified number of clusters is met.

In the study, the multi-stage clustering method will be proposed to improve the image quality and visual effect. The proposed method indicates some important observations. Under the condition that the total numbers of variables to store are roughly the same, the proposed algorithm removes redundant variables in the clusters where the structures are simple. On the other hand, the algorithm increases the number of principal components to improve the reconstructed quality for the clusters where the structures are complex. In addition, due to the homogeneity in each cluster, the details of retrieved image have better visual effects.

2. PCA IMAGE CODING

Given an image, we scan all of the non-overlapping blocks of size $p \times p$ as the dataset. For convenience, we regard these blocks as n-dimensional vectors, where $n = p \times p$, that is, $S = \{x_i\}_{i=1}^{l}$, $x_i \in R^n$. For the dataset, we consider an m-dimensional projection subspace, where $m < n$. The optimal linear projection, y_i for $i = 1, 2, \cdots, l$, is defined by the m eigenvectors, a_j for $j = 1, 2, \cdots, m$, computed from the covariance matrix of the dataset corresponding to the first m largest eigenvalues. Figure 1. (a) and (b) represent the computation network.

For the image coding, PCA would be used as a efficient method. For example, an image block of size $n = 8 \times 8$ can be viewed as a 64-dimensional vector where $m = 16$.01. In the encoding process, the inner product of the 64-dimensional vector and the eigenvectors is referred to as the compression code for that image block. Moreover, the codebook consists of eigenvectors. On the other hand, the summation of vectors calculated by multiplying the compression codes and the code words from the codebook is called the predicted vector which retrieves the image in the decoding process.
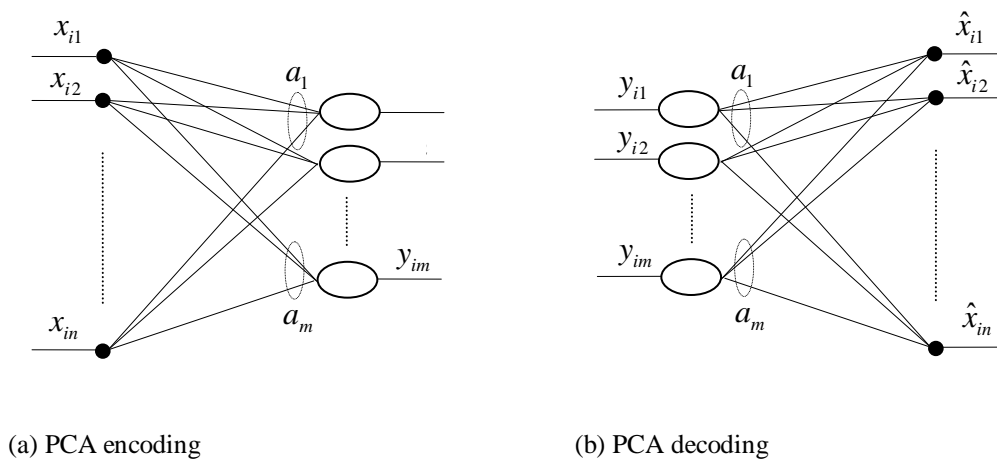

(a) PCA encoding   (b) PCA decoding

Figure 1. The encoder and decoder corresponding to (a) and (b), respectively

3. PROPOSED PCA METHOD WITH MULTI-STAGE CLUSTERING

3.1 Genetic Algorithm
The GA is an optimization method inspired by the process of evolution for living organisms. GA starts by an initial population generated mostly at random and proceeds in quite the same manner as nature in evolving ever better solutions. Chromosomes with higher fitness are crossed over, producing progeny that replaces chromosomes with lower fitness. A low rate of mutation, a small random modification of a chromosome, is applied to prevent a premature convergence to a local optimum. After the genetic operations of crossover and mutation, a new generation of candidate solutions is formed. This process will be repeated until some stopping criterion is met.

3.2 Multi-stage Clustering
To reduce the difficulty of examining every possible partition, we use a multi-stage method which partitions progressively the original data only if all individual MSE values in each cluster satisfy the clustering criterion. In the proposed clustering process, we will partition the data set according to the initial error thresholds. In the last partition, we perform separate PCA in each cluster. Note that the number of principal components in each cluster is decided using a progressive operator.

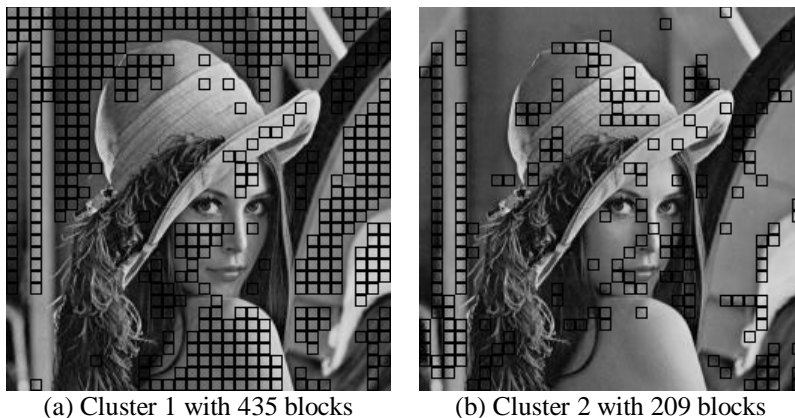The essential steps of the proposed method are as follows:
1. Initialize the error thresholds in GA and pre-specify the allowed minimal size in each cluster. The initial data is the original data.
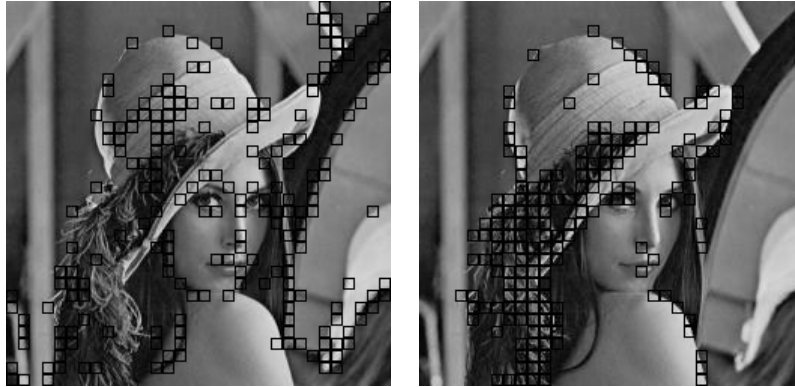2. Compute the whole eigenvectors for the current.

3. Choose the first eigenvector to calculate individual MSE value for every data point and increase progressively the number of eigenvectors in order.
4. Assign the data point to the proper cluster if the individual MSE is not larger than the corresponding error threshold.
5. Repeat Step 3 to 4 until the allowed size of this cluster is achieved. It is necessary to record the final eigenvectors.
6. Repeat Step 2 to 5 for the remaining points until the specified number of clusters is met.
7. Stop the process if GA converges.

4. EXPERIMENTAL RESULTS

In this study, coefficients of eigenvectors and PCA projections (or scores) are used to represent the compression ratio of different k clusters for $k = 1, 2, \cdots, K$. For given m_k eigenvectors, the summation of coefficients (or variables) of the kth cluster are equal to $m_k \times l_k + n \times m_k$. The term $n \times m_k$ corresponds to the amount of coefficients of the eigenvectors, and $m_k \times l_k$ is the number of components of PCA projection. Therefore, the total amount of stored variables are calculated as $\sum_{k=1}^{K} (l_k + n) \cdot m_k$. Here, Lena is the input image of size 256×256 pixels. The dataset are non-overlapping 8×8 image blocks, i.e., $n = 64$ and $l = 1024$. In the proposed multi-stage method, we group the dataset into four clusters, i.e., $K = 4$. For the GA framework, each chromosome is a 3-dimensional vector and the population size is 40. The lower and upper bound are set as 30 and 100, respectively. The uniform crossover and mutation probability are 0.8 and 0.2, respectively. The minimal allowed cluster size is 200 which is empirically selected. The optimal error thresholds obtained by GA are of 31.25, 60.38 and 82.87, i.e., $E = (31.25, 60.38, 82.87)$.

The final cluster sizes are 435, 209, 202, and 178, i.e., $C = (C_1, C_2, C_3, C_4)$ which are illustrated in Figures 2(a) to 2(d). The final number of principal components of each of the 4 clusters are 4, 7, 18 and 36, respectively, i.e, $M = (4, 7, 18, 36)$. As observed, the blocks inside each group exhibits homogeneous property on the edge features. If the blocks in a cluster are smoother, the number of principal components required to reconstruct blocks are smaller than the other clusters, e.g., Figures 2(a) and 2(b). In contrast, clusters 2(c) and 2(d) consist of edged and textured blocks of different degrees. We can see that for a cluster of smoother blocks, only fewer principal components are required. Table 1 explains these results, e.g., for the Lena image, the first cluster consists of 435 smooth blocks, and we only need four principal components to retrieve the qualities of 38.30 dB in PSNR. In Table 1, we also compare the overall results between the proposed method ("proposed" row) and the traditional PCA method ("Trad. PCA" row). The number of stored variables of them are 17407 and 17408, respectively, under the rough same compression ratios. The reconstructed qualities, PSNR, are of 34.58 and 31.10 dB. In the experiment, the proposed method has the significantl great improvement than the traditional PCA method.

(a) Cluster 1 with 435 blocks   (b) Cluster 2 with 209 blocks

(c) Cluster 3 with 202 blocks   (d) Cluster 4 with 178 blocks

Figure 2. Block images of each cluster using the proposed method

Table 1. Comparison between traditional PCA (Trad. PCA) and multi-stage PCA (Proposed) methods

Lena							
Cluster No.	# Blocks	m	MSE	PSNR (dB)	#Coefficients		#Variables
					Eigenvectors	Projections	
1	435	4	9.61	38.30	256	1740	1996
2	209	7	26.34	33.92	448	1463	1911
3	202	18	33.98	32.82	1152	3636	4788
4	178	36	37.09	32.44	2304	6408	8712
Proposed	1024	65	22.67	34.58	4160	13247	17407
Trad. PCA	1024	16	50.48	31.10	1024	16384	17408

5. ACKNOWLEDGMENT

6. REFERENCES

[1] B. S. Everitt, S. Landaus, and M. Leese, *Cluster Analysis*, London, UK: Arnold, 4th edition, 2001.

[2] P. De Lit, E. Falkenauer, and A. Delchambre, "Grouping genetic algorithms: an efficient method to solve the cell formation problem," *Math. Comput. Simulat.* 51, pp. 257-271, 2000.

[3] J. Gertler and J. Cao, "PCA-based fault diagnosis in the presence of control and dynamic," *AIChE J.* 50, pp. 388–402, 2004.

[4] J. Gertler and J. Cao, "Design of optimal residuals from partial principal component models for fault diagnosis in linear system," *J. Process Control 15*, pp. 585–603, 2005.

[5] S. Costa "Fiori, Image compression using principal component neural networks," *Image Vis. Comput. 19*, pp. 649-668, 2001.

[6] J. Gertler, W. Li, Y. Huang, and T. McAvoy, "Isolation enhanced principal component analysis," *AIChE J. 45*, pp. 323–334, 1999.

[7] D. E. Goldberg, *Genetic Algorithms in Search, Optimization, and Machine Learning*. Addison Wesley, Massachusetts, 1989.

[8] J. G. Hsieh, "A simple guide to machine learning and soft computing," (tutorial session speech). *Proceeding of 14th International Conference on Intelligent System Applications to Power System,* pp. 1-10, 2007.