Comparison of Moving Object Segmentation Techniques

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Abstract. Moving object segmentation is the extraction of meaningful features from series of images. In this paper, different types of moving object segmentation techniques such as Principal Component Analysis (PCA), K-Means clustering (KM), Genetic Algorithm (GA) and Genetic Algorithm Initialized K-means clustering (GAIK) have been compared. From our analysis we have observed that PCA reduces dimension or size of data for further processing, which in return reduces the computational time. However, the segmentation quality sometimes becomes unacceptable. On the other hand, due to random initialization of its centroids, KM clustering sometimes converges to local minimum which results in bad segmentation. Another algorithm which has been considered in this study is GA, which searches all the feature space and results in a global optimum clustering. Although the segmentation quality is good, it is computationally expensive. To mitigate these problems, KM and GA are merged to form GAIK, where GA helps to initialize the centroids of the clustering. From our study, it has been found out that GAIK is superior to GA in both the quality of segmentation and computational time. Therefore, in general, the analyses of the four algorithms shows that GAIK is optimal for segmenting a moving object.

Keywords: Clustering · Segmentation · PCA · KM · GA · GAIK

1 Introduction

Segmentation is the process of extracting meaningful features from an image or series of images (frames) in time domain. It is widely used in object detection, surveillance, tracking, content based image retrieval, medical imaging such as locating tumors, machine vision, locating objects in satellite imagery, pattern recognition etc.

There are several types of image segmentation techniques, some of which are thresholding, Edge-based, Region-based, Hybrid and Clustering. Thresholding delineates peaks, valleys, and shapes in its corresponding intensity histogram to segment an image, whereas edge-based segmentation is a set of linked pixels lying on the boundary

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between different regions, where there are intense discontinuities such as gray change, color distinctness, variation in texture and other similar features. Moreover, edge-based segmentation uses abrupt changes in intensity, color, and texture for segmenting an object [1]. By detecting the discontinuities, a moving object can be segmented. There are two types of Edge-based segmentations - Gray-histogram method and Gradient-based method [2].

Region-based segmentation divides an image into sections that are alike on some predefined criteria. Pixels within the same region need to have similar values of intensity, color or texture [3]. Hybrid techniques may use both region based and edge detection technique. The other segmentation technique is clustering. It is the process of grouping data into clusters in a certain metric, where objects within each cluster have high similarity, but are dissimilar to the objects in other clusters [4]. Each of these groups is called a cluster [5, 6]. Most of the time, the similarity is measured with distance, namely two or more objects belong to the same cluster if they are close enough according to a given distance limit. Patterns within a cluster are more similar to each other than patterns fit into different clusters [7].

Another method of segmentation is the fuzzy set theory. This method can be used in clustering and it allows fuzzy or soft boundaries to exist between different clusters. The main drawback of this algorithm is that it is difficult to confirm the attribute of fuzzy members [8]. There is also neural network based segmentation, in which every pixel is mapped to every neuron when the algorithm is applied to image processing. To segment a moving object using neural network, series of images are mapped into a neural network architecture. By using dynamic equations to optimize every neuron's energy image edges are extracted [9].

Table 1 summarizes some of the techniques that are used in image segmentation. This paper makes further comparison on PCA, KM, GA and GAIK using python libraries Numpy and OpenCV.

Table 1. Types of segmentation techniques [10].

Main categories	Techniques		Interpretation
Edge-based segmentation	Gray-histogram technique		Partition an image through detecting edge among different regions
	Gradient-based method	Differential coefficient techniques	
		Laplacian of a Gaussian (LoG)	
		Canny technique	
Region-based segmentation	Thresholding	Otsu	Extract the objects from the background by setting reasonable gray threshold for image pixels
		Optimal thresholding	

(*continued*)

Table 1. (*continued*)

Main categories	Techniques		Interpretation
		Thresholding image	
	Region operating	Region growing	Partition an image into regions that are similar according to a given criteria, such as gray character, color character or texture character
		Region splitting and merging	
		Image matching	
Segmentation based on Clustering, Hybrid and other methods	Fuzzy clustering segmentation		Introduce fuzzy set theory into image segmentation
	PCA Based		Segmentation based on PCA
	KM Clustering Segmentation		Segmentation based on KM clustering
	Neural networks based segmentation		It is a learning algorithm imitating the working pattern of neural networks
	GA based segmentation		Utilizes GA for segmentation
	GAIK Based segmentation		Uses hybrid of GA and KM clustering

The rest of the paper is organized as follows. PCA based moving object segmentation is discussed in Sect. 2. Section 3 expresses how KM can be used in image segmentation. Section 4 presents GA and its application in image processing. The hybrid of GA and KM is discussed in Sect. 5. Section 6 discusses the result & analysis, and Sect. 7 provides the conclusion of the study.

2 PCA

PCA focuses on finding orthogonal projections of dataset that contain the highest variance possible in order to ‘find hidden linear correlations’ between variables of the dataset. Most of the time, features are correlated. So, PCA de-correlates data for feature extraction and reducing the size. Many features rely on each other or on an unknown variable. A single feature can embed/hide a lot of information with in it. Removing such a feature can remove sensitive information. Hence, before eliminating features or reducing the size, the data is transformed into feature space for the purpose of avoiding dependency among variables, i.e. the feature space becomes de-correlated. So, the data is projected onto the largest eigenvectors of its covariance matrix in the feature space which encodes the most information; covariance matrix uses a sequence of rotation and scaling operations on data, where the rotation matrix is the eigenvectors of this covariance matrix.

In information theory, the valuable information or largest entropy is found in the feature with the highest variance. The data is defined by the largest eigenvectors or principal components, whereas the smallest eigenvectors are neglected as noise [11].

PCA reduces linear M-dimensional subspace of the original N-dimensional data, where $M \leq N$. Furthermore, if the unknown, uncorrelated components are Gaussian distributed, then PCA actually acts as an independent component analysis since uncorrelated Gaussian variables are statistically independent. However, if the underlying components are not normally distributed, PCA merely generates decorrelated variables which are not necessarily statistically independent. Principal components' are obtained by the Eigen Decomposition of the covariance matrix of the data. The size is then reduced by projecting the data onto the largest eigenvectors. The covariance matrix in the x-direction is given as

$$\sigma_x^2 = \frac{1}{M}\sum_{i=1}^{M} (x_i - \mu)^T (x_i - \mu) \tag{1}$$

$$\begin{aligned} \sigma_x^2 &= \frac{1}{M}\sum_{j=1}^{M} (x_i - \mu)^2 \\ &= \mathrm{E}[(x - \mathrm{E}(x))(x - \mathrm{E}(x))] \\ &= \sigma(x, x) \end{aligned}$$

Where $x_i - \mu$ the zero is mean and x_i is the input data.

The variance $\sigma(x, x)$ shows spread of the data in the x-direction and the variance $\sigma(y, y)$ depicts the spread in the y-direction. However, there is no correlation between x and y. When one variable is dependent on the other one, we use covariance matrix.

$$\sigma(x, y) = \mathrm{E}[(x - \mathrm{E}(x))(y - \mathrm{E}(y))] \tag{2}$$

For two dimensional data, the covariance matrix can be stated as

$$\begin{bmatrix} \sigma(x, x) & \sigma(x, y) \\ \sigma(y, x) & \sigma(y, y) \end{bmatrix} \tag{3}$$

Similarly, we can generalize the covariance matrix for an $N \times N$ dimensional data.

Following the covariance matrix, the singular value decomposition (SVD) can be calculated as

$$\sigma_x^2 = O \Lambda O^T, \tag{4}$$

Where O is the eigenvector matrix and Λ is the diagonal matrix. The Eigen-decomposition extracts transformation matrices; the eigenvectors depict the direction and the eigenvalues represent the magnitude [11].

Steps Used in PCA

```
Step 1: Center the Data (frames)
    The data is centered in order to get zero average.
Step 2: Normalize the Data
    Divide each feature by its standard deviation.
Step 3: Calculate the Eigen Decomposition
    It is calculated using Singular Value Decomposition
    (SVD).
Step 4: Project the Data
    Data is projected onto the largest eigenvectors.
```

3 KM Algorithm

There are different methods for clustering data [5]. K-means clustering is widely used due to its good computational performance [12]. It optimizes the distance criterion, mostly Euclidian distance, either by minimizing the within cluster spread or by maximizing the distance among clusters. Clustering may be performed based on other criteria's like graph theoretical approach and hierarchical approach. Survey and comparative analysis of different clustering methods are presented in [13] and suggests that there is no general strategy which works equally in every domain. The Algorithm (Pseudo-code) for KM Clustering is presented in [14] as follows.

Step 1: Choose K initial cluster centers $z_1, z_2, \cdots, z_k$ randomly from the n points $\{x_1, x_2, \cdots, x_n\}$.

Step 2: Assign point x_i, $i = 1, 2, \ldots, n$ to cluster $C_j = j \in \{1, 2. \cdots K\}$ iff

$$\|x_i - z_j\| < \|x_i - z_p\|, p = 1, 2, \ldots, K, \ and j \neq p. \tag{5}$$

Step 3: Compute new cluster centers $z_1^*, z_2^*, \cdots, z_k^*$ as follows

$$z_i^* = \frac{1}{n_i} \sum_{x_j \in C_i} x_{j,} \ i = 1, 2, \ldots, K, \tag{6}$$

Where n_i is the number of elements belonging to cluster C_j.

Step 4: If $z_i^* = z_i$, $i = 1, 2, \ldots, K$ then terminate.

Otherwise, continue from step 2.

KM may sometimes converge to a local minimum which is undesired process. This depends on the random initialization of the centroids. Simply put, different runs of KM on the same input data might produce different results.

4 GA Algorithm

Evolutionary algorithms such as simulated annealing, evolution strategies, evolutionary programming, ant colony, genetic algorithms and swarming (honey bee) are stochastic optimization algorithms based on the theory of survival of the fittest for an optimum solution to a given problem, [15]. By using evolutionary or genetic operators such as selection, recombination, crossover, mutation, migration, locality and neighborhood at each generation and iterating those leads to a natural adaptation, strong population which adapts to its environment in genetics sense [16].

Many researchers have proposed genetic algorithms for clustering data [13]. The basic idea is to simulate the evolution process of nature and evolve solutions from one generation to the next. In contrast to KM, which might converge to a local optimum, genetic algorithm is insensitive to the initialization process and always converges to the global optimum. However, these algorithms are usually computationally expensive. In all iterations of the GA, the individuals in the populations whose fitness score was in the top half were chosen to directly join the next generation population without mutation. In all the tests, the probability of mutation considered was 0.001, and the population size was 20.

Goldberg's Pseudo-code of GA

```
      Begin
Step 1: t = 0
Step 2: Initialize population P(t)
Step 3: Compute fitness P(t)
Step 4: t=t+1
Step 5: If termination criterion achieved go to step 10
Step 6: Elect P(t) from P(t-1)
Step 7: Crossover P(t)
Step 8: Mutate P(t)
Step 9: Go to step 3
Step 10: Output best and stop

      End
```

Genetic algorithms enhance the searching capability of cluster centers for the purpose of optimization in the feature space. Chromosomes encode the centroids. GA-clustering is superior to KM for it always converges globally [14]. Genetic Algorithm encodes its parameters as chromosome*s*. Initially, a random population is created from the data at hand, which represents different points in the search space. An objective and fitness function is associated with each string that represents the degree of goodness of the string. Based on the principle of survival of the fittest, a few of the strings are selected and each is assigned a number of copies that go into the mating pool. Operators like crossover and mutation yield a new generation of strings.

53^{rd} frame 54^{th} frame Segmented

Fig. 1. Segmentation using PCA

The process of selection, crossover and mutation continues for a fixed number of generations or till a termination condition is satisfied as can be seen in Fig. 1.

5 GAIK Algorithm

It is a combination of KM and GA. It takes the best quality of each algorithm and combines them. KM is simple and computationally faster. It works for large number of variables, and GA is insensitive to the initialization process and its output converges optimally because it searches all the feature space of the input data. So, GAIK applies genetic algorithm as an initialization method for the KM clustering technique to enhance the segmentation of a moving object [17].

```
Input:
      Mutation Probability, $P_m$;
      Population size, N;
      Maximum Number of Generation, MAX_GEN;
Output: Solution string, s*;
{Initialize the population, $P$;
    Geno = MAX_GEN;
    s* = $P_1$; ($P_i$ is the $i^{th}$ string in $P$)
    while (geno > 0)
    {Calculate Fitness values of strings in $P$;
      $P^*$ = Selection ($P$);
      for i = 1 to N, $P_i$ = Mutation (P*);
      for i = 1 to N, k-means ($P_i$);
         s = string in $P$ such that the corresponding
         weight matrix $W_s$ has the minimum SE measure;
      if ($S(W_{s^*}) > S(W_s)$), s* = s;
      geno = geno-1;
    }
    Output s*;
}
```

In all the tests, the probability of mutation considered was 0.001, and the population size was 20.

6 Result and Analysis

The different test frames that have been simulated are Hall frames [18] in an Intel corei3, 4 GB RAM with CPU 1.9 GHZ. Python libraries OpenCV and Numpy were used to implement all the algorithms. As can be seen in the results, PCA and KM need less computational time. However, they are not accurate; Figs. 1 and 2 are good examples. On the other hand, GA and GAIK are accurate. GAIK is preferable to GA because it is fast and has good quality output. Figures 3 and 4 and Tables 2, 3 and 4 clearly show all the differences among PCA, KA, GA and GAIK. There is a trade-off between accuracy and computational time. Furthermore, there is an additional requirement for KM, GA and GAIK, the background frame is needed as a reference. But, in some situations we may not have the background image in advance. So, optical flow, PCA or similar method of moving object segmentation seems preferable at the cost of computational time (for optical flow) and accuracy (for PCA). In this paper, we have used only two consecutive frames and a background (background, Hall 53rd & 54th [18]). But, the whole video test frames are tested for completeness, for instance all the 249 Hall frames are tested. Furthermore, there was no iteration in PCA. However, in KM we have used different iterations from 1 to 100 to get good segmentation result. GA and GAIK were iterated only twice by varying the population generation from 1 to 100. The different simulated results and their computational performances are shown from tables and figures. The metrics that are used for measuring the quality of the segmentations are objective (computational time) and subjective (accuracy, i.e. visual) methods. In other words, the results shown in the table are measured using objective method. The reason is that we have used the same standard, ‘computational time’ for all the algorithms, see the tables. But, the figures show subjective way of evaluation, by looking into the segmented images we can comment whether the quality is good or bad. For example, in Fig. 1, the segmented object is hard to identify, this is one simple instance of bad segmentation using PCA. We may sometimes get acceptable segmented quality using PCA if the data size is relatively small. KM clustering for moving object segmentation is demonstrated in Fig. 2. As can be observed, the segmentation is not really good. Figure 3 is segmented by using GA. It is better than PCA and KM, but still it has some noises around the segmented object which is undesired. GAIK based


Background image 53rd frame 54th frame Segmented Object

Fig. 2. Segmentation using KM (5 iterations)

segmented object is shown in Fig. 4, and it can be observed that it is accurate, neat and computationally acceptable when it is compared with the other three methods.


Background image 53rd frame 54th frame Segmented Object

Fig. 3. Segmentation based on GA (5 generations)

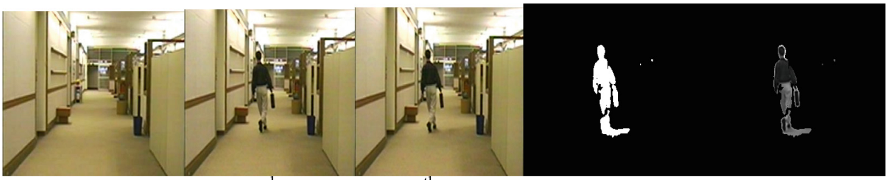
Background image 53rd frame 54th frame Segmented Object

Fig. 4. Segmentation based on GAIK (5 generations)

Table 2. Computational time and accuracy for a 'Hall' test frame for 1 generation.

	Accuracy (visual)	Computational t(sec)	Comment
PCA	Less accurate	0.0326185483252	Not applicable
KM	Less accurate	0.213585236708	1 iteration
GA	Accurate	1.25684074966	1 generation
GKA	Accurate	0.998757	1 generation

Table 3. Computational time and accuracy for a 'Hall' test frame for 5 generations.

	Accuracy (visual)	Computational t(sec)	Comment
PCA	Less accurate	0.0326185483252	Not applicable
KM	Less accurate	0.215545061382	5 iterations
GA	Accurate	4.05593981372	5 generations
GKA	Accurate	4.01345731871	5 generations

Table 4. Computational time and accuracy for a ‘Hall’ test frame for 50 generations.

	Accuracy (visual)	Computational t(sec)	Comment
PCA	Less accurate	0.0326185483252	Not applicable
KM	Not always accurate	0.216087956580	50 iterations
GA	Accurate	38.038828081	50 generations
GKA	More accurate	37.51	50 generations

7 Conclusion

In this research, comparison of four image segmentation algorithms (PCA, KM, Genetic Algorithm (GA), and GAIK) has been made using different test frames of a Hall. The objective of the research was to distinguish which algorithm is optimal in both accuracy and computational cost. The metrics that are used for measuring the quality of the segmentation methods are objective (for computational time) and subjective (for accuracy, i.e. visual). From the results, it has been observed that PCA and KM need less computational time at the expense of segmentation accuracy. On the other hand, GA and GAIK are accurate but not computationally as fast as PCA or KM. Furthermore, it has been observed that GAIK is faster and has better segmented image output than GA. Therefore, GAIK based segmentation has been found to be accurate and computationally acceptable (optimal) when compared with the other three methods.

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