



A New Approach to Image Segmentation for Brain Tumor detection using Pillar K-means Algorithm

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Abstract : This paper presents a new approach to image segmentation using Pillar K-means algorithm. This segmentation method includes a new mechanism for grouping the elements of high resolution images in order to improve accuracy and reduce the computation time. The system uses K-means for image segmentation optimized by the algorithm after Pillar. The Pillar algorithm considers the placement of pillars should be located as far from each other to resist the pressure distribution of a roof, as same as the number of centroids between the data distribution. This algorithm is able to optimize the K-means clustering for image segmentation in the aspects of accuracy and computation time. This algorithm distributes all initial centroids according to the maximum cumulative distance metric.

This paper evaluates the proposed approach for image segmentation by comparing with K-means clustering algorithm and Gaussian mixture model and the participation of RGB, HSV, HSL and CIELAB color spaces. Experimental results clarify the effectiveness of our approach to improve the segmentation quality and accuracy aspects of computing time.

Key Words: Segmentation, Detection, Centroids, Clustering and computing.

INTRODUCTION

In image segmentation, one challenge is how to deal with the nonlinearity of real data distribution, which often makes segmentation methods need more human interactions and make unsatisfied segmentation results. Medical image segmentation plays an instrumental role in clinical diagnosis. An ideal medical image segmentation scheme should possess some preferred properties such as minimum user interaction, fast computation, and accurate and robust segmentation results.

Image segmentation is an image analysis process that aims at partitioning an image into several regions according to a homogeneity criterion. Image segmentation is a very complex task, which benefits from computer assistance, and yet no general algorithm exists. It has been a research field in computer science for more than 40 years now, and the early hope to find general algorithms that would achieve perfect segmentations independently from the type of input data has been replaced by the active development of a wide range of very specialized techniques. Most of the existing segmentation algorithms are highly specific to a certain type of data, and some

research is pursued to develop generic frameworks integrating these techniques.

Segmentation can be a fully automatic process, but it achieves its best results with semi-automatic algorithms, i.e. algorithms that are guided by a human operator. This concept of semi-automatic process naturally involves an environment in which the human operator will interact with the algorithms and the data in order to produce optimal segmentations. The simplest example of the need of a human intervention during the task of segmentation results from the specificity of the existing algorithms. Depending on the type of input data, the operator will have to carefully pick the best adapted algorithm, which most of the time cannot be done in an automatic way. The subjective point of view of the human is required.

In this paper we try to develop a segmentation algorithm for abnormal MRI images using Fuzzy C-means clustering technique and also to compare the results with the earlier techniques like Region growing method, K-means clustering algorithms. Abnormal brain images from



four classes metastases, meningioma, glioma and astrocytoma are being used in this work.

BRAIN TUMOR

A brain tumor is an abnormal growth of cells in the brain, which can be cancerous (malignant) or noncancerous (benign). It is defined as any intracranial tumor created by abnormal and uncontrolled cell division, normally in the brain itself (neurons, glial cells (astrocytes, oligodendrocytes, ependymal cells, myelin-producing Schwann cells), lymphatic tissue, blood vessels (blood) in the cranial nerves, in the brain envelopes (meninges), skull, pituitary and pineal gland, or spread from cancers primarily located in other organs (metastases).

Brain tumors (true) are usually located in the posterior fossa in children and in the anterior two thirds of the cerebral hemispheres in adults, although it can affect any part of the brain.

In the United States in 2005, there were approximately 43,800 new cases of brain tumors (Central Brain Tumor Registry of the United States, primary brain tumors in the United States, Statistical Report, 2005-2006), which represented 14 percent of all cancers, 2.4 percent of all cancer deaths, and 20-25 percent of pediatric cancers. Ultimately, there are about 13,000 deaths per year in the U.S. alone due to brain tumors.

CAUSES

Apart from exposure to vinyl chloride or ionizing radiation, there are no known environmental factors associated with brain tumors. Mutations and deletions of tumor suppressor genes known are considered responsible for some forms of brain tumors. Patients with various inherited diseases, such as von Hippel-Lindau syndrome, multiple endocrine neoplasia, neurofibromatosis type 2 are at high risk of developing brain tumors. He argues that mobile phones / cell phones could cause brain tumors, according to a report. (See radiation from mobile phones and health) An association of brain tumor incidence and malaria, suggesting that the Anopheles mosquito, the carrier of malaria, can transmit a virus or other agent that can cause brain tumors. Malignant brain tumor incidence and prevalence of Alzheimer's disease are associated in 19 states. The two diseases may share a common cause, perhaps inflammation.

TYPES OF BRAIN TUMORS

- [Glioblastoma multiforme](#)
- [Medulloblastoma](#)
- [Astrocytoma](#)
- [Brainstem glioma](#)
- [Germinoma](#)
- [Meningioma](#)
- [Oligodendroglioma](#)

[Schwannoma](#)

[Craniopharyngioma](#)

[Ependymoma](#)

Brain Metastasis

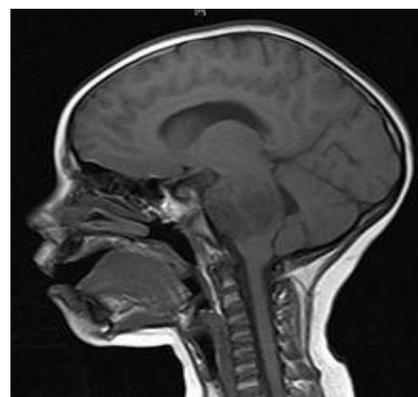
DIAGNOSIS

Imaging plays a central role in the diagnosis of brain tumors. Imaging early invasive and sometimes dangerous, as pneumonic paleography and cerebral angiography have been abandoned in recent times in favor of non-invasive high-resolution modalities, such as computed tomography (CT) and especially magnetic resonance imaging (MRI). Benign tumors are often presented as mass lesions hypodense (darker than brain tissue) on cranial CT-scans. On MRI, they appear either hypo-(darker than brain tissue) or (same intensity as brain tissue) or isointense on T1 hyper intense analysis (brighter than brain tissue) on T2 MRI, although appearance is variable. Perifocal edema also appears hyper intense on T2 MRI. Contrast agent uptake, sometimes in characteristic patterns, can be demonstrated in each CT or MRI in most malignant primary brain tumors and metastatic. This is because these tumors disrupt the normal functioning of the blood-brain barrier and lead to increased permeability.

In 2008 a study published by the University of Texas M. D. Anderson Cancer Center indicated that cancer patients who receive stereotactic radiosurgery (SRS) and whole brain radiation therapy (WBRT) for the treatment of metastatic brain tumors have more than twice the risk of developing learning and memory problems than those treated with SRS alone.^{[5][6]}

A [shunt](#) operation is used not as a cure but to relieve the symptoms. The [hydrocephalus](#) caused by the blocking [drainage](#) of the [cerebrospinal fluid](#) can be removed with this operation.

BRAIN TUMORS IN INFANTS AND CHILDREN



In the US, about 2000 children and adolescents younger than 20 years of age are diagnosed with malignant brain tumors each year. Higher incidence rates were reported in 1975-83 than in 1985-94. One theory is



that the trend is the result of improved diagnosis and reporting, since the jump occurred at the same time that MRIs became available widely, and there was no coincident jump in mortality. The CNS cancer survival rate in children is approximately 60%. The rate varies with the type of cancer and the age of onset: younger patients have higher mortality.

In children under 2, about 70% of brain tumors are [medulloblastoma](#), [ependymoma](#), and low-grade [glioma](#). Less commonly, and seen usually in infants, are [teratoma](#) and a typical teratoid rhabdoid tumor. [Germ cell tumors](#), including teratoma, make up just 3% of pediatric primary brain tumors, but the worldwide incidence varies significantly.

SEGMENTATION ALGORITHMS

REGION GROWING

Region growing is a technique for extracting an image region that is connected based on some predefined criteria. These criteria can be based on intensity information and/or edges in the image. In its simplest form, region growing requires a seed point that is manually selected by an operator and extracts all pixels connected to the initial seed based on some predefined criteria. For example, one possible criterion might be to grow the region until an edge in the image is met. Like thresholding, region growing is seldom used alone but usually within a set of image-processing operations, particularly for the delineation of small, simple structures such as tumors and lesions.

Region growing is a simple region-based image segmentation method. It is also classified as a pixel-based image segmentation method since it involves the selection of initial seed points.

This approach to segmentation examines neighboring pixels of initial "seed points" and determines whether the pixel neighbors should be added to the region. The process is iterated on, in the same manner as general data clustering algorithms. A general discussion of the region growing algorithm is described below.

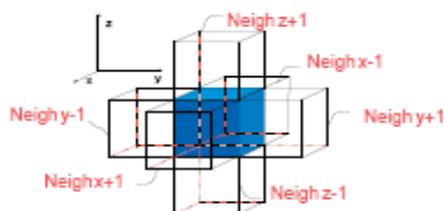


Figure 1. 6-connectedness

Figure. 1: connected region growing

Growth Algorithm

An auxiliary FIFO (First In First Out) structure is used when the seeds are first located, and where neighbors belonging to the area to visit are spooled. In Algorithm 1, we can see the growth Voxel pseudo-code algorithm in detail. The algorithm takes successively the elements of the queue. Each of these elements is a voxel volume already accepted. For each of them should go to their neighbors and decide if it belongs to the neighboring region in accordance with the selection criteria. To compare the 6-neighbor connection is used.^[2]

One of the strengths of this technique is that it always grows by neighbors, thus maintaining connectivity between elements that are included in the segmented region.

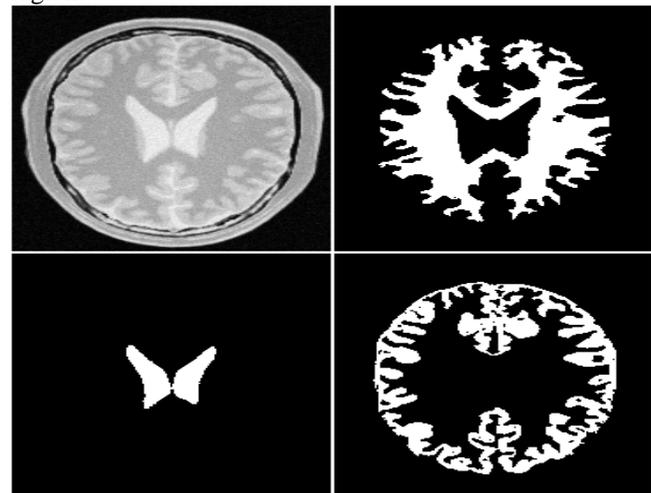


Figure. 2: Region growing method with different initial seeds. Top-left: Original Image, Top-Right: the white matter, bottom-Left: a ventricle bottom right: The grey matter.

HISTOGRAM BASED METHODS:

Histogram-based methods are very efficient in comparison with other methods of image segmentation, and which generally require a single pass through the pixels. In this technique, a histogram is calculated from the set of pixels of the image, and peaks and valleys of the histogram is used to identify clusters in the image. A refinement of this technique is applied recursively searching the histogram method in the image groups divided into small groups. This is repeated with the poles of smaller groups and smaller until it is formed.^[4]

A disadvantage of the method is that research histogram can be difficult to identify significant peaks and valleys in the image. In this technique of image classification distance metric matching and integrated region are familiar.

CLUSTERING METHOD

Clustering can be viewed as the problem of unsupervised learning is important because it provides information about the "right" answer to any of the objects.



Here's a priori information about the classes is not compulsory, it is not the number of groups and the distribution rules in groups are known. They are to be found only in the data set without any reference to a training set. Cluster analysis allows many options on the nature of the algorithm to combine the groups. [8]

There are two basic approaches to clustering, which we call supervised and unsupervised. In the case of clustering the group, do not have labels. If we know the labels of our input data, the problem is considered supervised or unsupervised otherwise known.

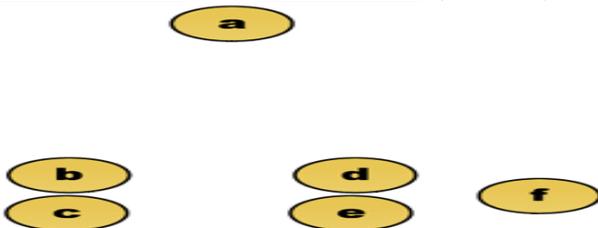
Definition of Clustering: Clustering is a set of data with similar characteristics. In dividing the data into groups of similar objects are used, here the distance functions are used to determine the similarity of the two objects in the data set. [7]

CLUSTER ANALYSIS

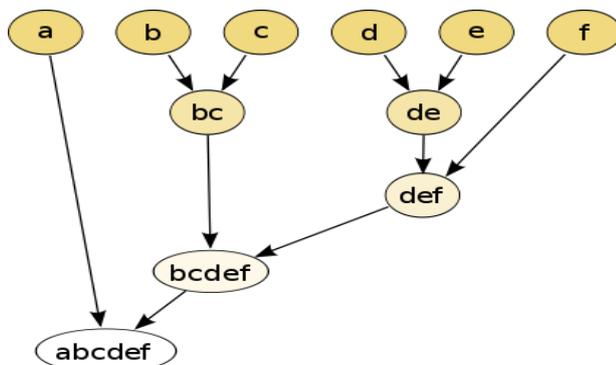
Cluster analysis or clustering is the assignment of a set of observations into subsets (called clusters) so that observations in the same cluster are similar in some sense. Clustering is a method of unsupervised learning, and a common technique for statistical data analysis used in many fields, including machine learning, data mining, pattern recognition, image analysis and bioinformatics.

AGGLOMERATIVE HIERARCHIAL CLUSTERING

For example, suppose this data is to be clustered, and the euclidean distance is the distance metric. (Raw data)



The hierarchical clustering [dendrogram](#) would be as such:



Traditional representation

This method builds the hierarchy of elements of particular groups of progressive melting. In our example,

we have six elements {a} {b} {c} {d} {e} and {f}. The first step is to determine which elements to merge in a cluster. Usually we take the two closest elements, according to the selected distance. [1]

Optionally, we can also create a distance matrix at this stage, where the number of the i-th row j-th column is the distance between the i-th and j-th elements. Then, as the group progresses, groups of rows and columns merged and the distances updated. This is a common way to implement this type of grouping, and has the advantage of caching distances between groups.

Suppose we have merged the two closest elements b and c, we now have the following clusters {a}, {b, c}, {d}, {e} and {f}, and want to merge them further. To do that, we need to take the distance between {a} and {b, c}, and therefore define the distance between two clusters. Usually the distance between two clusters **A** and **B** is one of the following:

The maximum distance between elements of each cluster (also called complete linkage clustering):

$$\max\{d(x, y) : x \in A, y \in B\}.$$

The minimum distance between elements of each cluster (also called single-linkage clustering):

$$\min\{d(x, y) : x \in A, y \in B\}.$$

The mean distance between elements of each cluster (also called average linkage clustering, used e.g. in UPGMA):

$$\frac{1}{|A| \cdot |B|} \sum_{x \in A} \sum_{y \in B} d(x, y).$$

The sum of all intra-cluster variance. The probability that candidate clusters spawn from the same distribution function (V-linkage).

Each agglomeration occurs at a greater distance between clusters than the previous agglomeration, and one can decide to stop clustering either when the clusters are too far apart to be merged (distance criterion) or when there is a sufficiently small number of clusters (number criterion).

K-MEANS CLUSTERING

One of the most popular and widely studied clustering algorithms to separate the input data in the Euclidian space is the K-Means clustering. It is a nonhierarchical technique that follows a simple and easy way to classify a given dataset through a certain number of clusters (we need to make an assumption for parameter k) that are known a priori. The K-Means algorithm is built using an iterative framework where the elements of the data are exchanged between clusters in order to satisfy the criteria of minimizing the variation within each cluster and maximizing the variation between clusters. When no elements are exchanged between clusters, the process is halted. The four steps of this algorithm are briefly described below. [3]

K-means Clustering performs pixel-based segmentation of multi-band images. An image stack is



interpreted as a set of bands corresponding to the same image. For instance, an RGB color images has three bands: red, green, and blue. Each pixels is represented by an n-valued vector , where n is a number of bands, for instance, a 3-value vector [r,g,b] in case of a color image.

Each cluster is defined by its centroid in n-dimensional space. Pixels are grouped by their proximity to cluster's centroids. Cluster centroids are determined using a heuristics: initially centroids are randomly initialized and then their location is interactively optimized.

Steps of the K-Means clustering algorithm:

1. Initialization – define the number of clusters and randomly select the position of the centers for each cluster or directly generate k seed points as cluster centers.
2. Assign each data point to the nearest cluster center.
3. Calculate the new cluster centers for clusters receiving new data points and for clusters losing data points.
4. Repeat the steps 2 and 3 until a convergence criterion is met (when there is no exchange of data points between the k clusters). The aim of the K-Means is the minimization of an objective Function:

$$J = \sum_{j=1}^k \sum_{i=1}^n \|x_i^{(j)} - c_j\|^2$$

is the distance measure (usually Euclidian metric) between a data point $x_i^{(j)}$ and the cluster center c_j (this is an indicator of the distance of the n data points from the cluster centers). There are situations when the K-Means algorithm doesn't find the optimal solution corresponding to the global objective function J and in addition is sensitive to the initialization process that selects the initial cluster centers that are usually randomly picked from input data. The main advantages of this algorithm are its simplicity and low computational cost, which allows it to run efficiently on large datasets. The main drawback is the fact that it does not systematically yield the same result each time the algorithm is executed and the resulting clusters depend on the initial assignments. The K-Means algorithm maximizes inter-cluster (or minimizes intra-cluster) variance, but does not ensure that the algorithm will not converge to local minima due to an improper starting condition (initialization of the cluster centers).

K-means is a widely used clustering algorithm to partition data into k clusters. Clustering this the process for grouping data points with similar feature vectors into a single cluster and for grouping data points with dissimilar feature vectors into different clusters. Let the feature vectors derived from l clustered data be $X = \{X_i | i=1, 2, \dots, l\}$. The generalized algorithm initiates k cluster centroids $C = \{C_j | j=1, 2, \dots, k\}$ by randomly selecting k feature vectors from X. Later the feature vectors are grouped are

grouped into k clusters using a selected distance measure such Euclidean distance so that $d = \text{mod}(X_i - C_j)$.

Fuzzy c-means clustering:

In fuzzy clustering, each point has a degree of belonging to clusters, as in fuzzy logic, rather than belonging completely to just one cluster. Thus, points on the edge of a cluster, may be in the cluster to a lesser degree than points in the center of cluster. For each point x we have a coefficient giving the degree of being in the kth cluster $u_k(x)$. Usually, the sum of those coefficients for any given x is defined to be 1:

$$\forall x \left(\sum_{k=1}^{\text{num. clusters}} u_k(x) = 1 \right).$$

With fuzzy c-means, the centroid of a cluster is the mean of all points, weighted by their degree of belonging to the cluster:

$$\text{center}_k = \frac{\sum_x u_k(x)^m x}{\sum_x u_k(x)^m}.$$

The degree of belonging is related to the inverse of the distance to the cluster center:

$$u_k(x) = \frac{1}{d(\text{center}_k, x)^m},$$

then the coefficients are normalized and fuzzyfied with a real parameter $m > 1$ so that their sum is 1. So

$$u_k(x) = \frac{1}{\sum_j \left(\frac{d(\text{center}_k, x)}{d(\text{center}_j, x)} \right)^{2/(m-1)}}.$$

For m equal to 2, this is equivalent to normalizing the coefficient linearly to make their sum 1. When m is close to 1, then cluster center closest to the point is given much more weight than the others, and the algorithm is similar to k-means. The fuzzy c-means algorithm is very similar to the k-means algorithm.^[4]

EXPERIMENTAL RESULTS

The practical results for **K-Means, c-Means & Pillar K-Means** for a particular image is shown below:

ENTER 1 FOR K-Means
 ENETR 2 FOR c-Means
 ENTER 3 for Pillar K-Means
 Please enter ur choice 3
 SI = 0.6203
 OF = 0.4613
 EF = 0.0261
 Tm = 0.2031

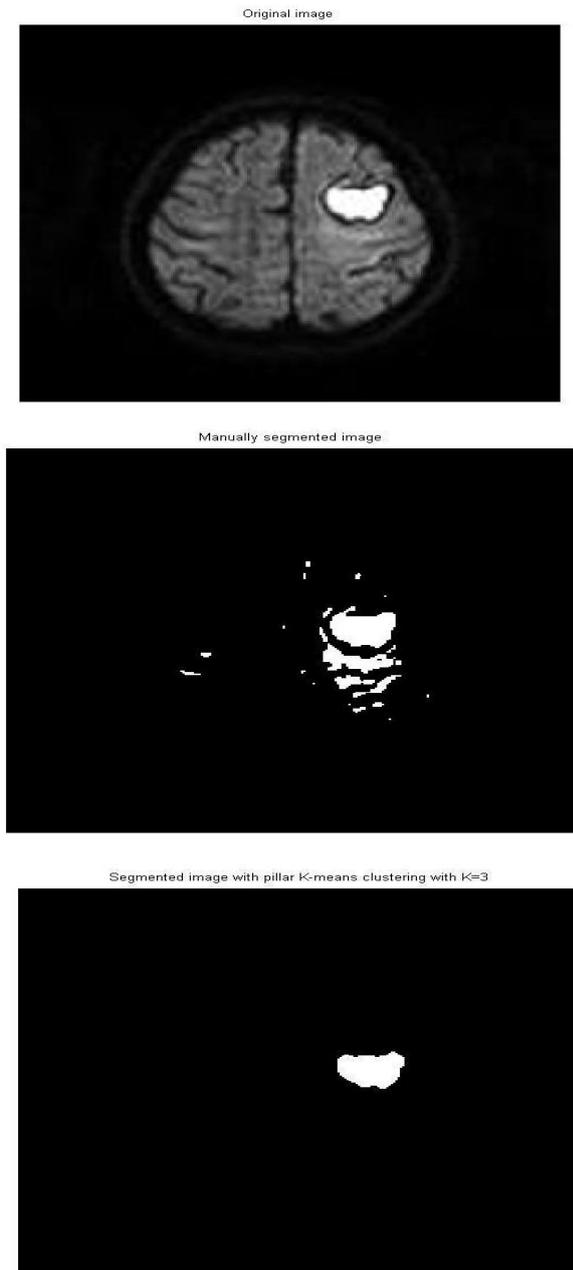


Figure. 3 Original image, Manual image & Pillar K-means image

To perform practical applicability of our proposed approach for image segmentation, we made a series of experiments and tested its performance using variance. Variance constraint can express the density of the clusters with the variance within cluster and the variance between clusters. The ideal cluster has minimum variance within cluster to express internal homogeneity and maximum variance between clusters to express external homogeneity [14]. Let $X = \{x_i \mid i=1, \dots, N\}$ be data set, $S = \{s_i \mid i=1, \dots, k\}$ be clustered X where $M \in X$ $M_i = \{m_{ij} \mid j=1, \dots, n(s_i)\}$ as members of s_i , variance within cluster can be defined as follows

$$v_w = \frac{1}{N-k} \sum_{i=1}^k (n(s_i) - 1) v_i^2$$

where N is number of data points, k is number of clusters, and n_i is number of members in i -th cluster, while v_i is given as:

$$v_i^2 = \frac{1}{n(s_i) - 1} \sum_{j=1}^{n(s_i)} (m_{ij} - \bar{s}_i)^2$$

where m_j is members of i -th clusters. Variance between clusters then can be

$$v_b = \frac{1}{k-1} \sum_{i=1}^k n(s_i) (\bar{s}_i - \bar{x})^2$$

defined as follows:

For our experimental study, we use the well known simplicity dataset of Wang et al. These images are manually divided into 10 categories which are people, beaches, historical buildings, buses, dinosaurs, elephants, roses, horses, mountains, and foods. We conducted the performance comparison between our approach for image segmentation and two comparing algorithms which are K-means algorithm and Gaussian Mixture Model (GMM) algorithm. For performing the K-means algorithm, we run 10 times of K-means and noticed its average results. For GMM algorithm, we use the spherical model with 50 numbers of iteration. [9]

In order to perform comparisons in several color spaces, we used 4 different color spaces which are RGB, HSV, HSL and CIELAB. We set the comparison parameters up with 4 and 5 numbers of clusters, and with respectively different data normalization algorithms: Z-Score and Softmax ($\lambda=10$). Fig. 4 shows the performance comparison of variance within cluster (V_w) which expresses the internal homogeneity of image segmentation results. The comparison came from average results of 10 image experiments with 4 and 5 clusters in different color spaces. Fig. 4 shows that our approach for image segmentation using Pillar-Kmeans algorithm reached the lowest V_w in all color spaces and outperformed the two comparing algorithms in all color spaces. Fig.5 shows the performance comparison of variance between clusters (V_b) which expresses the external homogeneity.

The good clusters have high external homogeneity that defines the degree of separation between clusters. In Fig.5, our approach also reached the highest V_b and outperformed the others. These two figures which represent the precision of segmentation result show the advantage of adequate segmentations by our proposed approach Pillar-Kmeans algorithm. Our approach is able to enhance the quality of the image segmentation.

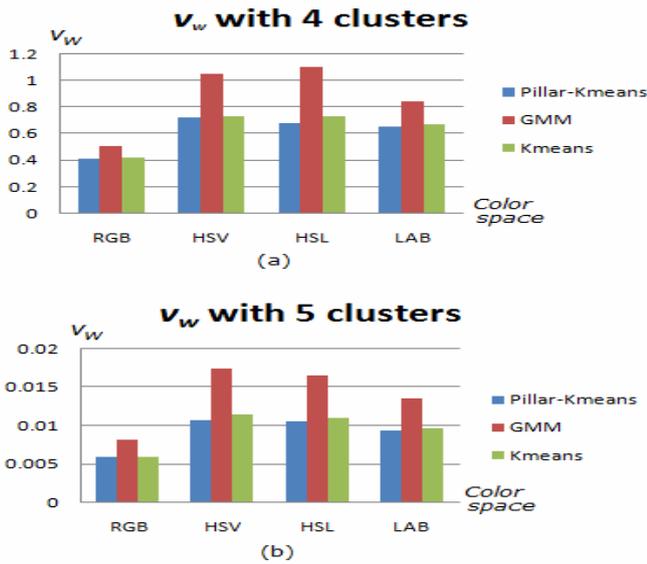


Figure. 4 Performance comparison of V_w

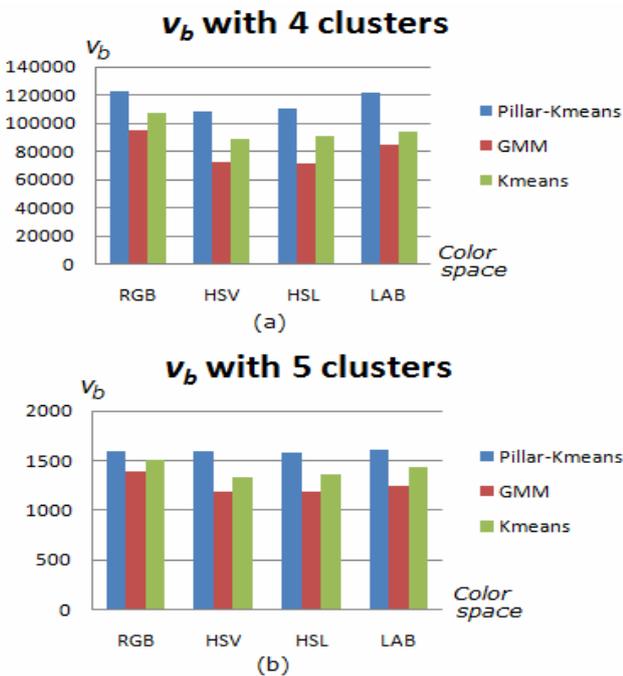


Figure. 5 Performance comparison of V_b

This figure shows one of visual comparisons of image segmentation between K-means algorithm, GMM, and our proposed Pillar-Kmeans algorithm. The Pillar-Kmeans performed the high quality of image segmentation rather than the two comparing algorithms. Moreover, in the view point of execution time, our approach is able to reach the computational time as fast as Kmeans clustering in all color spaces, as shown in Fig. 7. It means that our proposed approach is able to make the image segmentation as fast as K-means and reach high quality of the segmented results.

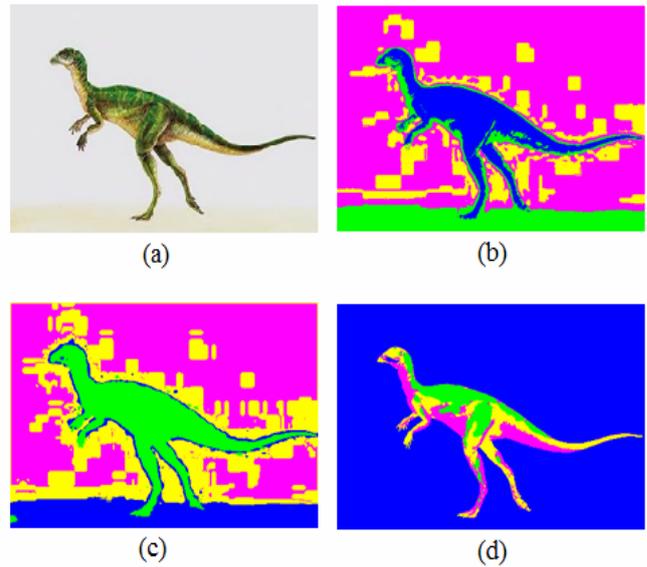


Figure. 6 Visual comparison of image segmentation (a) Image source. (b) K-means clustering. (c) GMM (d) Pillar-Kmeans algorithm

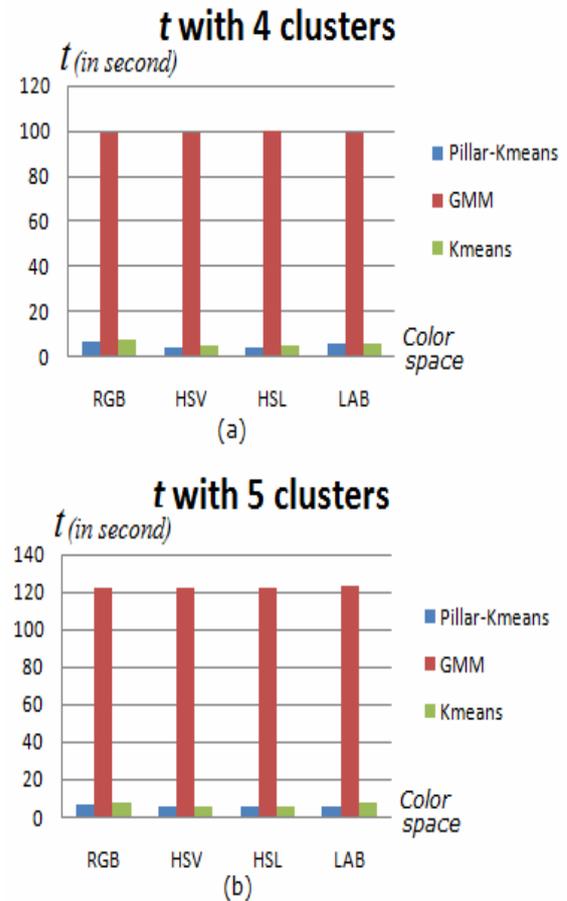


Figure7:Performance comparison of computational time



CONCLUSION

In this Paper, we proposed a new approach to image segmentation using Pillar K-means algorithm. The system applies the k-means algorithm optimized after Pillar. Pillar algorithm considers the placement of pillars should be located as far from each other to resist the pressure distribution of a roof, as same as the number of centroids between the data distribution. This algorithm is able to optimize the K-means clustering for image segmentation in the aspects of accuracy and computation time. A series of experiments with four different color spaces with restricted variance and execution conducted. The experimental results show that our proposed approach for image segmentation using Pillar-KMeans algorithm is able to improve the accuracy and enhance the quality of image segmentation in all color spaces. We also made the computation time faster than K-means and maintaining the quality of results.

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