iJRASET
International Journal For Research in Applied Science and Engineering Technology

INTERNATIONAL JOURNAL FOR RESEARCH

IN APPLIED SCIENCE & ENGINEERING TECHNOLOGY

Volume: 6 **Issue:** III **Month of publication:** March 2018

DOI: http://doi.org/10.22214/ijraset.2018.3123

www.ijraset.com

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International Journal for Research in Applied Science & Engineering Technology (IJRASET)
ISSN: 2321-9653; IC Value: 45.98; SJ Impact Factor: 6.887
Volume 6 Issue III, March 2018- Available at www.ijraset.com

A Review on Medical Image Classification Algorithms

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Abstract: ***This paper focuses on different algorithms and techniques that can be used for processing the medical images digitally. The algorithms starting from the pre-processing phase to the final result phase have been listed and explained here. Newer algorithms are more powerful and proficient. The advancement in the devices such as microscopes and digital cameras has led to a high-quality input dataset. This progress has contributed to the increased efficiency of the algorithms. The advantages and disadvantages of each method are described. Each algorithm is explained separately with its ability and features for the analysis of grey-level images. The following study helps an individual to choose a best fit algorithm that suits his requirements.***
Keywords: Image processing, algorithms, segmentation, classification.

I. INTRODUCTION

In mathematics and computer science, an algorithm is an unambiguous specification of how to solve a class of problems. Algorithms can perform calculation, data processing and automated reasoning tasks. An algorithm is an effective method that can be expressed within a finite amount of space and time and in a well-defined formal language for calculating a function. [1]

Medical images have made a great impact on medicine, diagnosis, and treatment. These images play an important role in medical applications for the purpose of diagnosing various medical conditions by doctors, who otherwise use traditional means of detecting them. Diagnosis by a human is more prone to errors and is less accurate when compared to that of a computer which uses generalized algorithms.

Over the course of years, contributions by medical image processing are of great amount in medical applications; for example, the use of image segmentation, and image guided surgery is common in medical surgery. The oldest is X-ray, which has been applied by the doctors for over hundred years. In this method, electromagnetic radiation with shorter wavelength and higher energy has been used. CT is yet another technique in medical imaging that uses X-ray in capturing the images of internal body organs. It produces many slices of each organ that are parallel to each other, by passing X-ray pulses through the body [4-7]. The other imaging technique is Magnetic Resonance Imaging (MRI). This medical imaging technique works based on the characteristics of magnetism and provides a great deal of information about internal organs. It is commonly used in medical applications due to the fact that this technique has various benefits compared to other techniques. It also provides a number of parallel slices for each organ in three dimensions with high contrast between tissues. One of the biggest hurdles in MRI application is that the data volume is too huge for manual analysis [3, 8, 9]. The other disadvantages are noise, intensity in homogeneities, low contrast between certain tissues, and partial volume effects in the segmentation task. The most important step of image processing in medical field is image segmentation which is a process for extracting the region of interest (ROI) through an automatic or semi-automatic procedure.

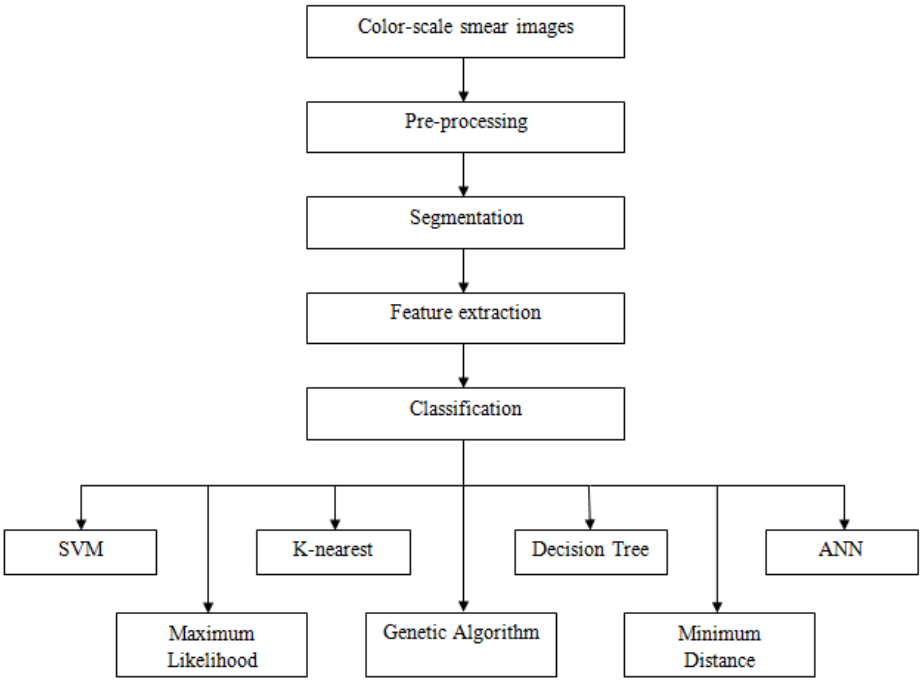
Many image segmentation methods are available in medical applications to segment tissues and body organs. Some of the applications consist of border detection in angiograms of coronary, surgical planning, simulation of surgeries, tumor detection and segmentation, brain development study, functional mapping, blood cells automated classification, mass detection in mammograms, image registration, heart segmentation and analysis of cardiac images, etc. [10-18]. In medical research, segmentation can be used in isolating different tissues from each other, through the extraction and classification of features. Classifying image pixels into anatomical regions may be useful in extracting muscles, bones, and blood vessels. For example, the aim of some brain research works is to partition the image into different region colors such as white and different grey spectra which can be useful in identifying the cerebrospinal fluid in brain images, white matter, and grey matter [19]. This process can also prove useful in extracting the specific structure of breast tumors from MRI images [20].

The above discussed techniques used for diagnosis requires complex and huge machines. Therefore, the recent advancement uses a simple digital camera having high-definition color. The digital images of blood smears are taken with certain magnification factor. These microscopic images along with appropriate algorithms help to interpret the disease.

II. RELATED WORK

A. Pre-processing Algorithms

The acquired image should be pre-processed in order to obtain accurate results. The following are the techniques required to be performed before the image is being processed.



B. Clustering Algorithms

In image processing and machine learning applications, image segmentation presents division of areas having similar properties. Through image segmentation, a given image can be converted into a meaningful form for further analysis.

1) Standard K-Means: K-means (MacQueen, 1967) is one of the simplest unsupervised learning algorithms that solve the well-known clustering problem. The main idea of the learning process is based on the center-based clustering method. The method is divided into 2 phases: first phase is defining the k-centroids, one for each cluster which contribute to the initial steps for the whole process. Then each point from data set will be mapped to the nearest centroids until all points are assigned based on minimum Euclidean Distance. Second phase observed the updates each of the points. The k-centroids need to be recalculate as new k-centroids and new mapping need to be done between the points and the new k-centroids. This process will give changes in k-centroids location step by step until the k-centroids do not move anymore.

According to D. Malyszko [26], the general steps of the center-based clustering are:

a) Initialize step with initial k-centroids value randomly.
b) For each data point x_j, compute its minimum distance with each center μ_i.
c) For each center μ_i, recomputed the new center from all data points x_j belong to this cluster.
d) Repeat steps 2 and 3 until convergence.

Algorithm [33]: Input (k, data)

i. Choose k random positions in the input space
ii. Assign the cluster centres μ_j to those positions
iii. For each $x_i \epsilon$ data
  a) Compute the distance $\mathbf{Dist}(x_i, \mu_j)$ for each μ_j
  b) Assign x_i to the cluster with the minimum distance

iv. For each μ_j:

Move the position of $\mu_j$to the mean of the points in that cluster:

$$\mu_j = \frac{1}{N_j}\sum_{i=1}^{N_j} x_i$$

The algorithm is based on the following objective function:

$$W(C) = \sum_{i=1}^{N}\sum_{X_j \in Si} \|X_j - \mu_i\|^2 \quad (1)$$

where μ_i is the mean of point Si for i^{th} cluster based on the assignment C. The interest is to minimize the sum of square distance within the cluster and such assignments have to map each point to its nearest centroids.

2) Fuzzy C-Means: Fuzzy C-Means is a clustering method which allows single data belong to more than one clusters. This method (Dunn, 1973) is a pattern recognition based on minimization of the following objective function given as Equation (2) below:

$$I_m = \sum_{i=1}^{N}\sum_{j=1}^{C} u_{ij}^m \|X_i - c_j\|^2$$

where m is any real number greater than 1, u_{ij} is the degree of membership of xi in the cluster j, x_i is the i^{th} of d-dimensional measured data, c_j is the d-dimension center of the cluster, and ||*|| is any norm expressing the similarity between any measured data and the center. Fuzzy clustering approach is carried out through an iterative optimization of the objective function shown in (2) with the update of membership u_{ij} and cluster center c_j of:

Algorithm [33]:

(1) Initialize a fuzzy partition and set the weight W
(for all Wij)

(2) Repeat

a) Calculate the center of clusters using the fuzzy partition.

b) Update the fuzzy partition, i.e., Wij.

(3) Until the centers do not change.

$$w_{ij} = \frac{1}{\sum_{k=1}^{c}\left(\frac{\|X_i - c_j\|}{\|X_i - c_k\|}\right)^{\frac{2}{m-1}}}$$

$$c_j = \frac{\sum_{i=1}^{N} w_{ij}^m . x_i}{\sum_{i=1}^{N} w_{ij}^m}$$

3)Adaptive K-Means: This adaptive K-Means method which proposed recently was originally based on the standard K-Means algorithm for better segmentation [27]. During initialization step, the placement of the k-centroids is very crucial because different location will give different result. The standard K-Means method uses the randomly choose k-centroids which leads to accuracy degradation in segmentation. This may cause inconsistent result in the image segmentation. Despite of using the normal randomly choose initial k-centroids, this adaptive method manipulates the local minimum and maximum values based on the RGB color space during the initialization step. The enhanced initialization method returns a two-element array with minimum and maximum RGB values from the whole pixel area. The operator computes the maximum and minimum pixel values for each band of a rendered image within the region of interest. The adaptive method is an iteration-based clustering that produces an optimal value of initial k-centroids by minimizing the objective function. The initial k-centroids can be obtained by using the following objective function:

$$\alpha = \sum_{i-1}^{c}\sum_{k-1}^{n} \partial(\mu_{min}, \mu_{max}) \quad (4)$$

where α is the Euclidean distance between minimum RGB value μ_{min} and maximum RGB value μ_{max}, n represent the number of image pixels and c is the total number of cluster. [28]

C. Thresholding Algorithms

Thresholding is one of the simplest and fastest segmentation methods based on the assumption that images are formed from regions with different grey levels.

1)Local Thresholding: Global thresholding does not provide satisfactory results for some type of images such as images which do not have a constant background and have diversity across the object. For this kind of images, thresholding provides a good result in one region but fails in other parts of images [29,30]. In order to find different threshold values for different parts of images, the local thresholding method divides images into sub images and then calculates the threshold value for each part. The results of thresholding for each part of an image are then merged. In this method, an image is divided into vertical and horizontal lines, whereas each part includes a region of both the background and the object. Finally, an interpolation is needed to produce appropriate results.

Different statistical methods are used to select the threshold value for each sub image, for example, mean, standard deviation, mean and standard deviation together, and mean of maximum and minimum.
Local thresholding needs more time to segment an image compared to global thresholding. This method is more useful in the case of images with varying backgrounds.

D. Classification Algorithms

Classification is a pattern recognition technique which uses training data to find the patterns. Training data includes a sample of image features with their target labels. This technique is known as the supervised learning technique, because it involves training data which are segmented manually and then presented to the automatic process [34-36]

1) k-Nearest Neighbor: K-nearest-neighbor (k-nn) is a regular non-parametric and commonly used classification method. This method is known as a non-parametric method because the k-nn algorithm does not need any information about statistical properties of pixels. The k-nn algorithm needs a great amount of sample data which are labelled as training data. In this algorithm, k is the number of nearest neighbors.

Below, we explain the k-nn algorithm.

Algorithm:

a) Set labelled training data $X_D = \{x_1, \ldots, x_{n_D}\}$ where $X_D \in M_{func}$.
b) Choose k neighbors to find.
c) Choose d: $R^p * R^p \rightarrow R^+$ any metric (distance measure) on R^p.
d) For any vector z in R^p: using $X_D = \{x_i\}$

Calculate and sort the distances $d(z,x_i)$ as $\{d1 \leq d2 \leq \cdots \leq dk \leq dk+1 \leq \cdots . \leq dnD\}$

Find the column in U_d corresponding to the k-nearest neighbor indices {1, 2, ..., k}.

Compute the label vector

$U(*|z) = (u(1|z), u(2|z), \ldots, u(c|z))^T$ with k-nn labels from U_d:

$$u(i|z) = \sum_{j=1}^{k} \frac{u_{D,ij}}{k} \quad for\ i = 1,2,\ldots,c$$

Decide $x \in i \Leftrightarrow D_{mk}(z) = e_i \Leftrightarrow u(i|z) = \max\{u(i|z)\}$

where z is the new data, X_D is the training data, R^p is the domain, and p is the dimension of data. The term d is the Euclidean distance between two vectors in R^p and is declared as follows:

$$d(z,x_i) = \|z,x_i\| = \sqrt{(z,x_i)^T(z,x_i)}.$$

Here we present the standard k-nn. Three parameters which affect the k-nn results are as follows: (1) finding a suitable k to classify the data, (2) selecting the measurement for distance (like Euclidean distance), and (3) the method of counting votes [37-39]

a) Advantages

i. K-NN is an unbiased algorithm and need not have any assumption of the data under consideration.
ii. It is very popular because of its simplicity and ease of implementation plus effectiveness.

iii. Robust to noisy training data
iv. Effective if training data is large.

b) Disadvantages

i. k-NN does not create model, hence, the process of abstraction is not included.
ii. It requires high time to prepare data to design a robust system.
iii. Need to determine the value of parameter K(number of nearest neighbours).
iv. Computation cost is high because we need to compute the distance from each of the instance to all training samples.

2) Support Vector Machine: The core mechanism of SVM is to find the optimal classification hyperplane satisfying the classification requirements. So that the hyperplane is able to not only guarantee the classification accuracy but also maximize the blank area beside the hyperplane. But in order to maximize the segmentation accuracy, we combine the SVM and ISODATA algorithm. And as an unsupervised method, ISODATA permits diverse number of clusters [23, 24] to be specified rather than requiring that is known as a priori so that we can use it to correct the pixels which have been identified into incorrect parts. Then the improved SVM algorithm calculates the Euclidean distance between each pixel and the cluster centres which are determined by the hyperplane so it can correct the miss-identified pixels by putting them into the minimum Euclidean distance cluster using the adaptive method of unsupervised ISODATA. A training sample set $(X_i, Y_i), i = 1,2 \ldots,1, X \in R^n, -1 \leq Y \leq 1$ was given, and the algorithm is as follows:

Step1: In order to make the hyperplane
$(\vec{w} \bullet \vec{x}) + b = 0$ suitable for every point in the training sample sets, we set the constraint condition
$Y_i[(\vec{w} \bullet \vec{x}) + b] \geq 1$. The margin of two classes is
$1/2\|w\|$

Step2: Lagrange is added to solve the optimization problem by the equation (6)

$$L(\vec{w}, b, a) = \frac{1}{2}\|w\| - a\left(y\left((\vec{w} \bullet \vec{x}) + b\right) - 1\right)$$

Step3: The problem is solved when partial derivative is zero which can convert the quadratic programming into relevant dual problem shown in the equation (7)

$$Q(a) = \sum_{j=1}^{l} a_j - \frac{1}{2}\sum_{i=1}^{l}\sum_{j=1}^{l} a_i a_j y_i y_j (\vec{x_i} \bullet \vec{x_j})$$

$$s.t. \sum_{j=1}^{l} a_j y_j = 0, j \epsilon [1, l], a_j > 0$$

Step4: Equation (8) represents the final function for classification

$$c(x) = sgn\left\{\left[\sum_{j=1}^{l} a_j^* y_j (x_j \bullet x_i) + b^*\right]\right\}$$

Step5: Suppose that through the above steps we have K classes, and P denotes the spectrums of the images. Define $M_{ik, jk, p}$ as the (i, j) pixel of the K class. Define $Z_{k, p}$ as the cluster center of every class and it is calculated by the equation (9)

$$Z_{k,p} = \frac{\sum_{i=0}^{M}\sum_{j=0}^{N} M_{ik,jk,p}}{N_k} \quad (9)$$

where N_k is the total pixels of the image in the cluster φ_k.

Step6: Sum up the Euclidean distance between each pixel $M_{ik, jk, p}$ and each cluster center $Z_{k, p}$ of all the bands, represents as $D_{ik, jk}$

$$D_{ik,jk} = \sum_{p=1}^{P} (M_{ik,jk,p} - Z_{k,p})^2 \quad (10)$$

Step7: For pixels $M_{ik, jk, p}$, if $D_{ik, jk} < D_{ik', jk'}$ where $D_{ik', jk'}$ represents the previous distance, then $M_{ik, jk, p}$, $\in \varphi_k$, φ_k means the cluster k. Equation (11) calculates the new value $Z_{k,, p}$

$$Z_{k,p} = \frac{1}{N_k} \sum_{M_{ik,jk,p} \in q_k} M_{ik,jk,p} \quad (11)$$

Step8: Execute the step6 to sept7, then LP=LP-1 where LP is the iteration. If LP>1 or $\vec{Z}_{k,p}^{L+1} \neq \vec{Z}_{k,p}^{L}$, then go through the algorithm from step B; else LP=1 or $\vec{Z}_{k,p}^{L+1} = \vec{Z}_{k,p}^{L}$, then stop the iteration. [25]

a) Advantages

i. It gains flexibility in the choice of the form of the threshold.
ii. Contains a nonlinear transformation.
iii. It provides a good generalization capability.
iv. The problem of over fitting is eliminated.
v. Reduction in computational complexity.
vi. Simple to manage decision rule complexity and Error frequency.

b) Disadvantages

i. Result transparency is low.
ii. Training is time consuming.
iii. Structure of algorithm is difficult to understand
iv. Determination of optimal parameters is not easy when there is nonlinearly separable training data.

3) Maximum Likelihood: Maximum Likelihood classifier is one of the most popular methods of classification where a pixel with the maximum likelihood is classified into the corresponding class. The likelihood L_k is defined as the posterior probability of a pixel belonging to class k.

$$L_k = P\left(k/_X\right) = \frac{P(k) * P(X/k)}{\sum P(i) * P(X/i)}$$

where $P(k)$: prior probability of class k

$P(X/k)$: conditional probability to observe X from class k, or probability density function

Usually $P(k)$ are assumed to be equal to each other and $\sum P(i) * P(X/i)$ is also common to all classes. Therefore, L_k depends on $P(X/k)$ or the probability density function.

Maximum likelihood estimates the parameter of a statistical model. In this method, it is supposed that there is a huge volume of data and we just have a sample set of these data. Finding the distribution of original data is not possible or the cost of it is not reasonable. Thus, we need to find a distribution parameter based on existing data. One of the popularly used distributions is Gaussian distribution. Therefore, we can find the mean and variance of sample data and use it to estimate the original data model. This method tries to find the best estimation for sample data to produce a nearest data model to original data. [21, 22, 31-33]

a) Advantages

i. Maximum Likelihood can be used in a wide range of estimation situations. For example, it can be performed on each sample of original Data with various censoring models
ii. Approximation of normal distributions and approximation of sample variances that can be applied to produce confidence bounds and suggestion tests for the parameters

b) Disadvantages

i. When the distribution of the population does not allow the normal distribution, the maximum likelihood method cannot be applied.
ii. Maximum likelihood estimation cannot be applied with small samples of data.

4) Artificial Neural Networks

Artificial neural network is a type of artificial intelligence that emits some functions of the human mind. An ANN is having a sequence of layers. Each layer of neural network system consists of a set of neurons. Neurons of all layers are linked by weighted connections to all neurons of the preceding and succeeding layers. The accuracy depends on the number of input and structure of the network. ANN is non-parametric approach. In this method, the classification of the input is very fast, but the training process is slow. Choosing correct architecture is tough. [41]

A neural network model is similar to human nervous system. As the human learn things by experience and practice or by repetition, to develop the human like behavior in machine we use artificial intelligence and neural network model uses the concept of artificial intelligence that's why it called as artificial neural network. The artificial neural network is taught through a dataset. This dataset may be known to us then ANN is trained in a supervised manner, and it learns precisely and quickly about the pattern buried in dataset. And Trained ANN is used to identify the patterns for which it is trained. But if the dataset is not known to us in advance then the unsupervised training is used. The neural network is consist of neurons that are correlated together to convert inputs into useful output. [40]

a) Advantages

i. It is a non-parametric classifier.
ii. It is a universal functional approximator with arbitrary accuracy.
iii. capable to present functions such as OR, AND, NOT
iv. It is a data driven self adaptive technique
v. efficiently handles noisy inputs
vi. Computation rate is high

b) Disadvantages

i. It is semantically poor.
ii. The training of ANN is time taking.
iii. There exists a problem of over fitting.
iv. Difficult in choosing the type network architecture.

5) Genetic Algorithm

Genetic Algorithm (GA) is an optimization-based method that uses population for solving optimization problems. It is been effectively applied in image segmentation and enhancement of images. It mainly helps in improving the quality of the images and gives the better visual perception to the images to produce better outcomes. It is one of the evolutionary problems [42]. GA works best on practical problems. It has two parameters such as crossover and mutation and works well than common image enhancement techniques. A typical genetic algorithm requires: 1. A genetic representation of the solution domain. 2. A fitness function to evaluate the solution domain This step starts with producing generations using Selection, Crossover and Mutation. Selection – it randomly chooses a value from the database, Crossover- it chooses a value from the input image and from the n^{th} generation, which consists of the characteristics' value, and combines it, Mutation – it chooses a random value based from the range of the characteristics' value. Then using any combinations of selection, crossover and mutation, it searches an acceptable value based from the fitness value. [43]

Algorithm:

```
initialize population;
evaluate population;
while termination criterion not reached
[
   select solutions for next population;
   perform cross-over and mutation;
  evaluate population;
 ]
```

6)Decision Tree

Decision tree is a tree-like graph of decisions. Each branch represents the decisions to be made graphically. It is a non-parametric supervised approach. It partitions input into uniform classes. This method permits the acceptation and rejection of class label at each intermediate stage. This method gives the set of rules after classification that should be understood.

The decision-tree classifier is hierarchically based classifier which compares the data with a range of properly selected features. The selection of features is determined from an assessment of the spectral distributions or separability of the classes. There is no generally established procedure. Therefore, each decision-tree or set of rules should be designed by an expert. When a decision-tree provides only two outcomes at each stage, the classifier is called binary decision-tree classifier.

a) Advantages

i. Computing time is less than the maximum likelihood classifier and by comparison statistical errors are avoided.
ii. Can handle nonparametric training data
iii. Does not require an extensive design and training.
iv. Provides hierarchical associations between input variables to forecast class membership and provides a set of rules n are easy to interpret.
v. Simple and computational efficiency is good.

b) Disadvantages

i. The usage of hyperplane decision boundaries parallel to the feature axes may restrict their use in which classes are clearly distinguishable.
ii. Becomes complex calculation when various values are undecided and/or when various outcomes are correlated.
iii. The accuracy fully depends on design of decision-tree and selected features.
iv. Splits are very sensitive to training data set.

7) Minimum Distance Classifier

The minimum distance classifier is used to classify unknown image data to classes which minimize the distance between the classes in multi-feature space. The distance is defined as an index of similarity so that the minimum distance is identical to the maximum similarity. The following distances are often used in this procedure:

a) Euclidean distance

$d_k^2 = (X - \mu_k)^t . (X - \mu_k)$ is used in cases where the variances of the population classes are different to each other. The Euclidean distance is theoretically identical to the similarity index.

b) Normalized Euclidean distance

The normalized Euclidean distance is proportional to the similarity index, in the case of difference variance.

$d_k^2 = (X - \mu_k)^t . \sigma_k^{-1} . (X - \mu_k)$

c) Mahalanobis distance

In cases where there is correlation between access in feature space, the mahalanobis distance with variance-covariance matrix should be used as

$d_k^2 = (X - \mu_k)^t . \Sigma_k^{-1} . (X - \mu_k)$

where X: vector of image data

μ_k : mean of the k[th] class

σ_k : variance matrix

Σ_k: variance-covariance matrix

a) Advantages

i. Minimum distance classifier is fast compared to other classifiers.
ii. Minimum distance classifiers do not contain unclassified pixels.

b) Disadvantages

i. This classifier does not incorporate variability of signatures.
ii. It is useful only when distance between means is large when compared to randomness of each class with respect to its mean.

III.CONCLUSIONS

In this paper, diverse algorithms that could be applied in the area of image processing are discussed. Any image processing requires the following stages which include: Pre-processing, segmentation, classification. The algorithms for certain important stages are discussed briefly. They include Local thresholding for thresholding mechanism, K-means, Fuzzy C-Means (FCM), and Adaptive K-Means for segmentation, and finally K-nearest algorithm, Support Vector Machines (SVM), Maximum Likelihood, Artificial Neural networks (ANN), Genetic Algorithm, Decision Tree, and Minimum Distance Classifier as classification algorithms. The above

listed are some of the well-known algorithms, however, there are many more algorithms that can be used depending on the requirements.

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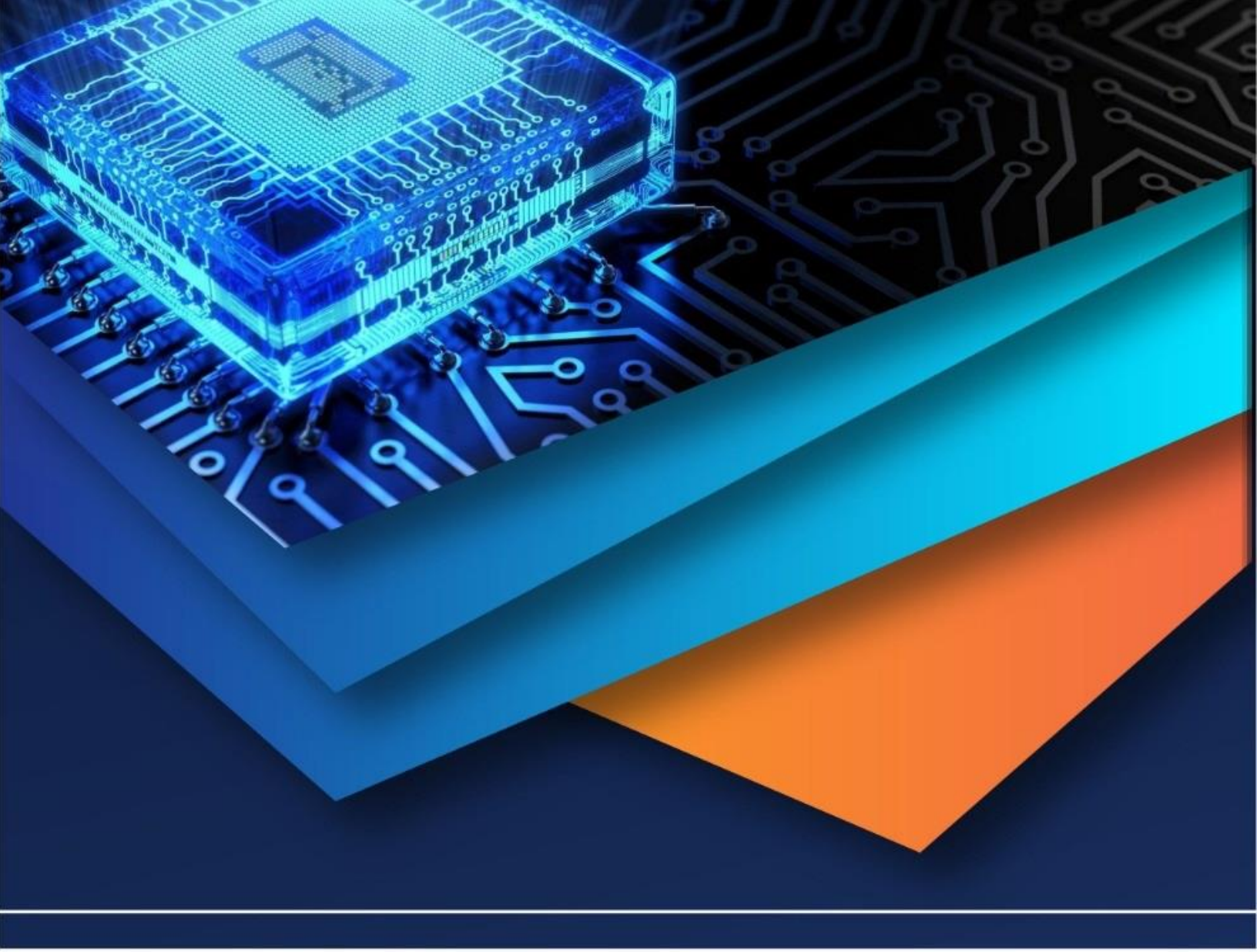

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