

DETECTION OF LIVER CANCER USING IMAGE PROCESSING TECHNIQUES

Submitted in partial fulfillment of the requirements for the award of
Master of Technology degree in Biomedical Engineering.

By

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SCHOOL OF BIO AND CHEMICAL ENGINEERING**

SATHYABAMA

**INSTITUTE OF SCIENCE AND TECHNOLOGY
(DEEMED TO BE UNIVERSITY)**

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BONAFIDE CERTIFICATE

This is to certify that this Project Report is the bonafide work of B.HARSHAVARDHINI (39380002) who carried out the project entitled “**DETECTION OF LIVER CANCER USING IMAGE PROCESSING TECHNIQUES**” under my supervision from October 2020 to April 2021

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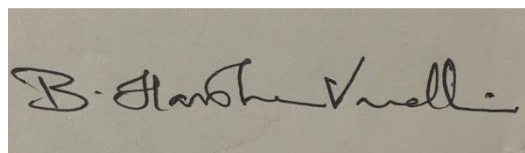
Submitted for Vivavoce Examination held on

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DECLARATION

I, **HARSHAVARDHINI B (39440001)** hereby declare that the Project Report entitled **“DETECTION OF LIVER CANCER USING IMAGE PROCESSING TECHNIQUES”** done by us under the guidance of **Mr. G. UMASHANKAR, M.Tech., (Ph. D).**, is submitted in partial fulfilment of the requirements for the award of Master of Technology degree in Medical Instrumentation engineering.

A rectangular box containing a handwritten signature in black ink. The signature appears to be 'B. Harshavardhini' written in a cursive style.

DATE :

PLACE:CHENNAI

SIGNATURE OF THE CANDIDATE

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ABSTRACT

Now –a- days liver Cancer is growing anonymously in huge rate because this liver cancer has low survival rate even symptoms do not appear until the cancer in the advanced stage. if disease caught late the average person survive only a year. so we propose the cancer detection using feature extraction and classification. In this we go with the three phases of detection processing phase, pre-processing phase and detection phase through feature extraction and classified using extracted features for the normal and abnormal stages of the tumor. The diagnosis method consists of four stages, pre-processing of MRI images, feature extraction, and classification. After pre-processing of image, the segmentation is done with fuzzy C means clustering and levelset segmenter. also the features are extracted based on Texture Analysis Using the Gray-Level Co-Occurrence Matrix (GLCM). In the last stage, KNN classifier are employed to classify the Normal and abnormal liver.

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CHAPTER-1

INTRODUCTION

1.1 INTRODUCTION

Cancer is the abnormal growth of the tissue in an organ. Liver cancer is a type of cancer which affects the largest organ of the abdomen, liver. It is of two types namely Primary Liver Cancer and Secondary Liver Cancer. Primary Liver Cancer originates in the liver itself and is known as Hepatocellular Carcinoma (HCC) or Hepatoma. Secondary Liver Cancer is a type growth of cancer cell where the cancer cell originates from different organ and spread to liver.

The first step is to find an image to do the further processing. MRI is a high quality imaging technique which produces the structure of human organ in more defined manner and useful for diagnosis of diseases and Biological Research . The results of an MRI image are greatly enhanced by automotive and accurate classification of image. The second step includes several enhancement technique to get best quality of the image by removing the unwanted noise from the image. The third stage segment or detect the cancer cell using segmentation.

1.2 LIVER CANCER

Liver cancer is one of the major death factor in the world and also known as hepatic cancer; it is a cancer which starts in the liver, and not from another organ which ultimately travels to the liver. In other words, there may be cancers which start from somewhere else and end up in the liver – those are not (primary) liver cancers. Cancers that originate in the liver are known as primary liver cancers. Liver cancer comprises of malignant hepatic tumors (growths) in or on the liver. The most common type of liver cancer is hepatocellular carcinoma (or hepatoma or HCC), and it tends to affect males more than females.

Early detection and accurate presentation of liver cancer is a significant issue in practical radiology. Liver lesions refer to those abnormal tissue cell that are found in the liver. Liver lesions are a wound or injury in the tissue areas of the body due to harm caused by a wound or disease. These lesions can be identified in a CT scan by a difference in pixel intensity from other regions of the liver. For proper clinical treatment, manual segmentation of this CT scan is difficult and excessively time consuming task. Alternatively, automatic segmentation is very challenging task,

due to numerous issues, including liver stretch over 150 slices in a CT image, poor intensity contrast between lesions and other nearby similar tissues and indefinite form of the lesions.

MRI scans can be very helpful in looking at liver tumors. Sometimes they can tell a benign tumor from a malignant one. They can also be used to look at blood vessels in and around the liver to see any blockages, and can help show if liver cancer has spread to other parts of the body.

Like CT scans, MRI scans provide detailed images of soft tissues in the body. But MRI scans use radio waves and strong magnets instead of x-rays. MRI scans can be very helpful in looking at liver tumors. Sometimes they can tell a benign tumor from a malignant one. They can also be used to look at blood vessels in and around the liver to see any blockages, and can help show if liver cancer has spread to other parts of the body.

1.3 HEPATOCELLULAR CARCINOMA

The most common malignant liver lesion in the setting of a chronic liver disease is hepatocellular carcinoma (HCC); however, these patients are also at increased risk for cholangiocarcinoma (CCA) and combined HCC–CCA. The hepatocarcinogenesis sequence accounts for the development of HCC. As the hepatocytes regenerate to replace cells lost to necrosis and apoptosis, deoxyribonucleic acid (DNA) mutations cause nodules to become dysplastic and eventually malignant. As these nodules undergo malignant transformation, tumoral neovascularity transforms the nodule blood supply from primarily portal venous supply to a predominantly hepatic arterial supply, and these arterial vessels are often abnormal. This process of malignant degeneration occurs across a continuum, and the diffuse regenerative nodularity of the liver parenchyma that occurs during cirrhosis can make the identification of small lesions challenging if a meticulous imaging technique is not used. The American Association for the Study of Liver Diseases (AASLD) recommends surveillance using an ultrasound every six months for patients with cirrhosis of any cause or for patients with chronic hepatitis B, even without findings of cirrhosis. It is challenging to distinguish small HCC from regenerative nodules by ultrasound. Nodules less than one cm can be followed with

more frequent ultrasounds, but nodules that grow or measure greater than one cm should be further characterized with contrast-enhanced cross-sectional imaging such as MRI.

Unlike many malignancies, HCC can be diagnosed by its imaging features without the need for histologic confirmation if an appropriate imaging technique is utilized. The administration of intravenous contrast is critical to diagnosis, and multiple phases of contrast timing are required for the complete characterization of the liver mass enhancement pattern. Regenerative nodules tend to have a T1 signal intensity similar to or brighter than the adjacent parenchyma and the T2 signal same as the liver. The nodules are usually not well identified after contrast because they enhance the same as the surrounding liver unless there are surrounding fibrotic bands with delayed enhancement.

CHAPTER 2

LITERATURE REVIEW

2.1 LITERATURE REVIEW

Patient suffering from Liver Tumors are facing a lot of difficulties and challenges starting from day one of admission till leaving the hospital. Liver tumor ablation by minimal invasive treatment is done by radio frequency ablation and the process of this technique take several stages. Therefore, applying lean methodology thinking helps cancer patient in his treatment with delivery of therapy without any delay time, minimizing process complications, and eliminating unnecessary steps. Thus, by applying Lean concept and Fish Bone Cause Effect study we can decrease the Liver Tumor Ablation process from 8 days to one day, save hospital time so more patients can be treated, saving cost and Intensive Care Unit bed availability.

In minimally invasive interventions for liver cancer treatment, image registration is a powerful technique to align diagnostic information, such as tumors and vessels, to the interventional images. In this paper, we investigate how the contrast-enhanced features in computed tomography (CT) images i.e. the tumors and the vessels, help the registration. For this, we de-enhance the contrast-enhanced CT image (iDECT) of the liver acquired during the intervention; and then we compare the accuracy of the registration between the diagnostic contrastenhance CT image (dCECT) and the original interventional contrast-enhanced image (iCECT) versus the dCECT image and the de-enhanced image (iDECT). In addition, we use a rigidity term to improve the registration using the de-enhanced image. The method is evaluated on 11 clinical datasets.

Directional association measured by functional dependency can answer important questions on relationships between variables, for example, in discovery of molecular interactions in biological systems. However, when one has no prior information about the functional form of a directional association, there is not a widely established statistical procedure to detect such an association.

To address this issue, here we introduce an exact functional test for directional association by examining the strength of functional dependency. It is effective in

promoting functional patterns by reducing statistical power on non-functional patterns. We designed an algorithm to carry out the test using a fast branch-and-bound strategy, which achieved a substantial speedup over brute-force enumeration. On data from an epidemiological study of liver cancer, the test identified the hepatitis status of a subject as the most influential risk factor among others for the cancer phenotype. On human lung cancer transcriptome data, the test selected 1068 transcription start sites of putative noncoding RNAs directionally associated with lung cancers, stronger than 95% TSSs of 694 curated cancer genes. These predictions include non-monotonic interaction patterns, to which other routine tests were insensitive. Complementing symmetric (non-directional) association methods such as Fisher's exact test, the exact functional test is a unique exact statistical test for evaluating evidence for causal relationships.

Direction Liver cancer is a mass that develops in the liver tissue due to uncontrolled cell division of the liver cells. Hepatocellular carcinoma is the commonest type of liver cancer, others include cholangiocarcinoma and angiosarcoma. Although this cancer type is rare, studies have shown that it has claimed so many lives. The causes of liver cancer are directly linked to diseases such as liver cirrhosis, hepatitis B and C. The major liver cancer therapy techniques are tumor ablation, tumor embolization, radiotherapy, surgery, chemotherapy, immunotherapy and targeted therapy. The choice of a particular therapy technique depends on certain disease-related factors such as the stage of the disease, its severity, the extent of the damage, patient health status etc. However, other factors are related to the therapy technique and they greatly influence the choice of treatment option. This study focuses on the therapy-related factors which include survival rate, side effects, treatment duration, cost of treatment and comfortability. The various primary liver cancer therapy techniques were evaluated based on the above-listed factors using Fuzzy PROMETHEE decision making theory. The ranking result showed that Tumor Ablation is the best treatment alternative for primary liver cancer upon selected criteria and weights based on desired application. The outcome of this study will benefit both the oncologist and the patients while trying to choose from a variety of alternatives in different scenarios.

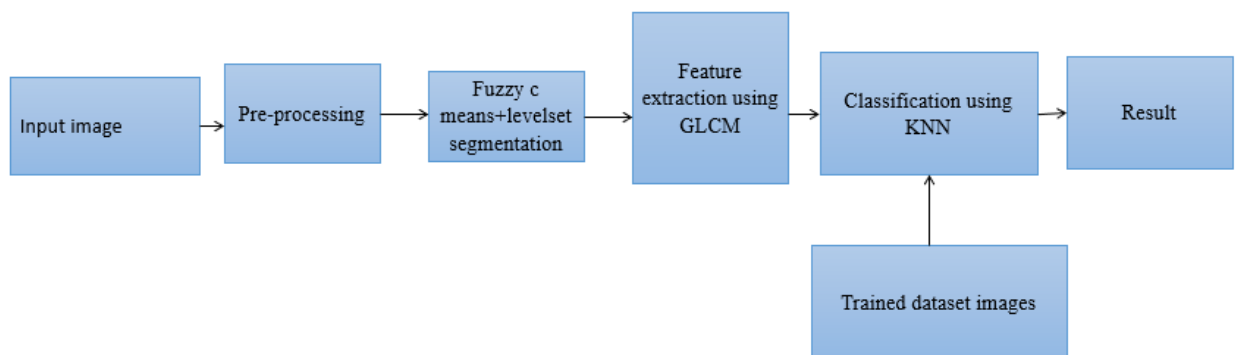
Predicting cancer disease state is an important problem in the cancer discovery process. For example, discriminating between benign and malignant tumors improves the medical diagnosis of cancer. Although technological advancing led to the generation of data pertaining to patients with different disease states, evaluating the prediction performance of machine learning algorithms would be an important step. In this paper, we propose using machine learning algorithms such as a variant of Ada Boost, deep boost, xg boost and support vector machines and evaluate them using area under curve and accuracy on real clinical data related to thyroid cancer, colon cancer and liver cancer. Experimental results show the good performance of SVM.

CHAPTER -3

PROPOSED METHOD

3.1 PROPOSED SYSTEM

The proposed approach consists of three successive stages. Firstly, image noises removed through pre-processing stage, to improve the quality of the input images. The second stage is feature extraction and selection through HOG algorithm to extract the main features of the tooth object . Finally, the KNN classifier is employed to classify the liver images as cancer or healthy.



3.1 PROPOSED BLOCK DIAGRAM

3.2 SYSTEM DESIGN

In system design a general description about the module and various components used along with their corresponding diagrammatic representation using UML are discussed.

3.2.1 DESIGN REPRESENTATION

The design can be represented by means of UML diagrams. In this, We are going to represent the design by using unified modeling language.

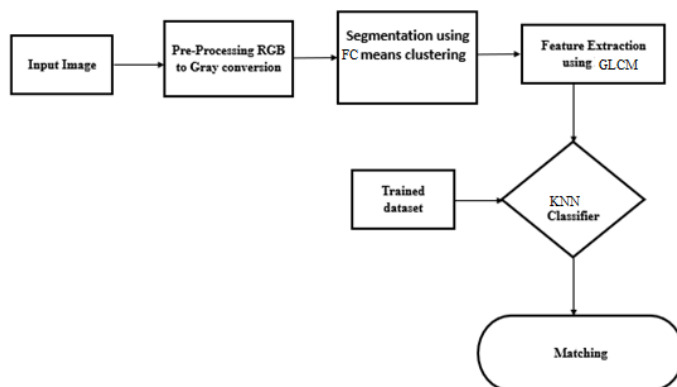
3.2.2 UNIFIED MODELLING LANGUAGE(UML)

UML is a standard language for specifying, visualizing and documenting of software system and created by object management group (OMG) in 1997. There are three types of modelling , structural model, behavioural model, and architectural model. To model a system the most important aspect is to capture the dynamic behaviour which has some internal or external factors for making the interactions. These internal or external agents are known actors. It consists of actors, use cases and their relationship among several other useful and important features. The UML diagrams are,

- Flow diagram
- Component Diagram

3.2.2.1 FLOW DIAGRAM

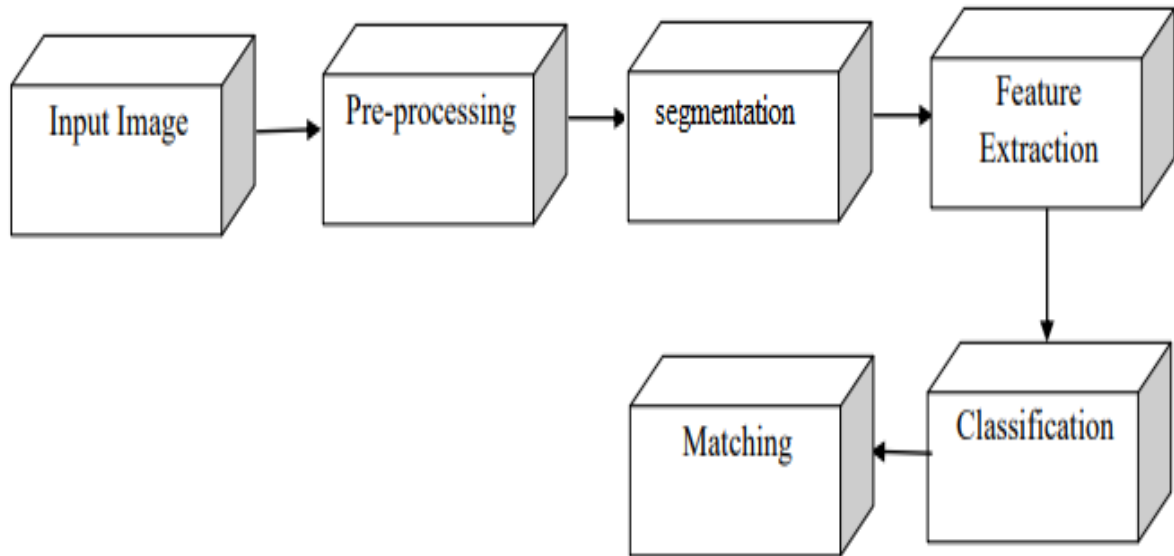
Users are able to visualize how the system will operate, what the system will accomplish, and how the system will be implemented is represented in figure 3.2 Flow diagram is a collective term for a diagram representing a flow or set of dynamic relationships in a system.



3.2.2.1 FLOW BLOCK DIAGRAM

3.2.2..2 COMPONENT DIAGRAM

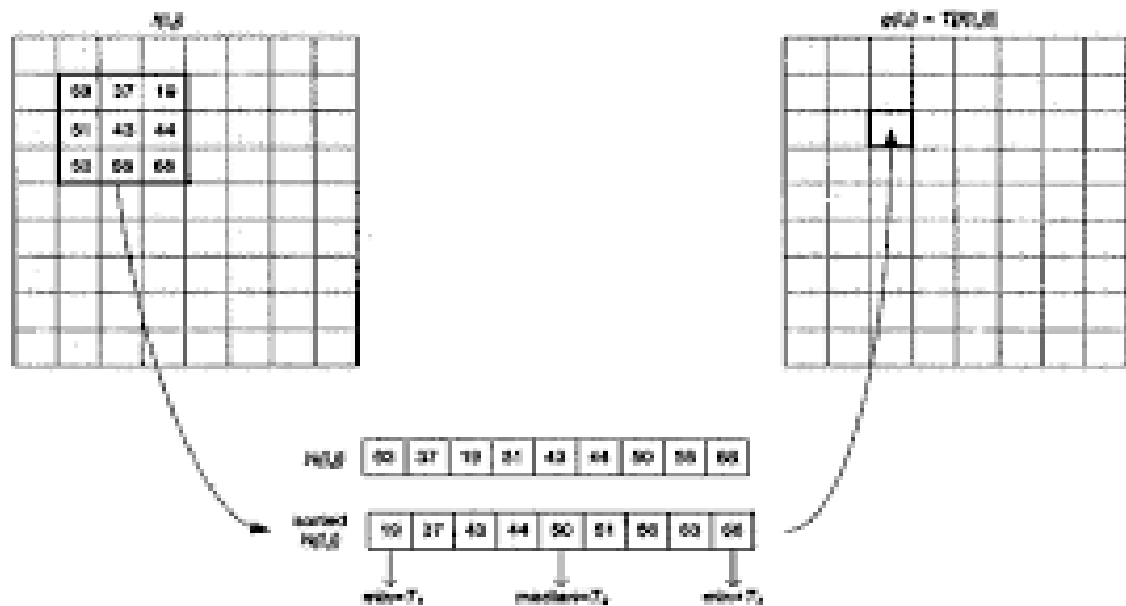
component diagram displays the structural relationship of components of a software system. These are mostly used when working with complex systems that has many components such as sensor nodes, cluster head and base station.



3.2.2.2 COMPONENT BLOCK DIAGRAM

3.3 PRE-PROCESSING

This step is important as acquired image is noisy. The pre-processing includes series of operations performed on acquired input dental image. Each of the acquired dental images is first subjected to rgb to gray conversion . A gray image is a digital image that has only possible values for pixel i.e. 0-255.image resized to 500*500.image is filtered using median filter. The Median Filter is a non-linear digital filtering technique, often used to remove noise from an image or signal. Such noise reduction is a typical pre-processing step to improve the results of later processing (for example, edge detection on an image).



3.3 PRE-PROCESSING DIAGRAM

3.3.1 MEDIAN FILTER

The median filter is a non-linear digital filtering technique, often used to remove noise from an image or signal. Such noise reduction is a typical pre-processing step to improve the results of later processing (for example, edge detection on an image).

The median filter is normally used to reduce noise in an image, somewhat like the mean filter. However, it often does a better job than the mean filter of preserving useful detail in the image.

HOW IT WORKS:

Like the mean filter, the median filter considers each pixel in the image in turn and looks at its nearby neighbors to decide whether or not it is representative of its surroundings. Instead of simply replacing the pixel value with the mean of neighboring pixel values, it replaces it with the median of those values. The median is calculated by first sorting all the pixel values from the surrounding neighborhood into numerical order and then replacing the pixel being considered with the middle pixel value. (If the neighborhood under consideration contains an even number of pixels, the average of the two middle pixel values is used.) Figure illustrates an example calculation.

123	125	126	130	140
122	124	126	127	135
118	120	150	125	134
119	115	119	123	133
111	116	110	120	130

Neighbourhood values:

115, 119, 120, 123, 124,
125, 126, 127, 150

Median value: 124

3.3. 1MEDIAN VALUES& NEIGHBOURHOOD VALUES TABLE

As can be seen, the central pixel value of 150 is rather unrepresentative of the surrounding pixels and is replaced with the median value: 124. A 3×3 square neighbour hood is used here larger neighbour hoods will produce more severe smoothing.

3.4 FUZZY C-MEANS (FCM)

Segmentation for our project is k means clustering. FC-means clustering is one of the simplest and popular unsupervised machine learning algorithms. The 'means' in the FC-means refers to averaging of the data; that is, finding the centroid. Fuzzy c-means (FCM) is a method of clustering which allows one piece of data to belong to two or more clusters. In pattern recognition and image processing, Fuzzy C denotes a clustering methodology that allocate a fragment of information into two or more clusters. Many algorithms are supported fuzzy theory. Fuzzy C-explains a cluster rule that used relationship degree to work out every datum belongs to an explicit cluster. Fuzzy separated the 'n' vectors and X_r where $r = 1, 2, 3, \dots, n$ into fuzzy cluster and evaluated every center cluster creating worth perform of non-similarity index to realize the minimum. The selection of associate acceptable objective function is that the key to the success of the cluster analysis and to get higher quality cluster results.

Segmentation is an important step in many medical imaging applications and a variety of image segmentation techniques exist. One group of segmentation algorithms is based on clustering concepts. In this chapter we provide an overview of several fuzzy c-means based clustering approaches and their application to medical imaging. In particular we evaluate the conventional hard c-means and fuzzy c-means (FCM) approaches as well as three computationally more efficient derivatives of fuzzy c-means: fast FCM with random sampling, fast generalised FCM, and a new anisotropic mean shift based FCM.

input image conversion to feature space is applied clustering. In our case, we have chosen fuzzy c-means clustering method, settings are in experiments section. After these two steps (input image conversion to feature space of clustering method and accomplishing clustering method) is accomplished next segmentation method.

Assumptions: Image transformed into feature space, number of clusters c , stop condition ϵ , fuzziness parameter m .

Step 1: Cluster image in feature space, with next conditions: number of clusters is c , fuzziness index is m and stop condition is ϵ .

Step 2: Repeat for each pixel a_{ij} of image I .

Step 2.1: Find out, into which cluster CA belongs pixel a_{ij} at most. Step

2.2: Find out, whether in the closest surroundings of pixel a_{ij} exists segment R_k , which points belong to same cluster CA .

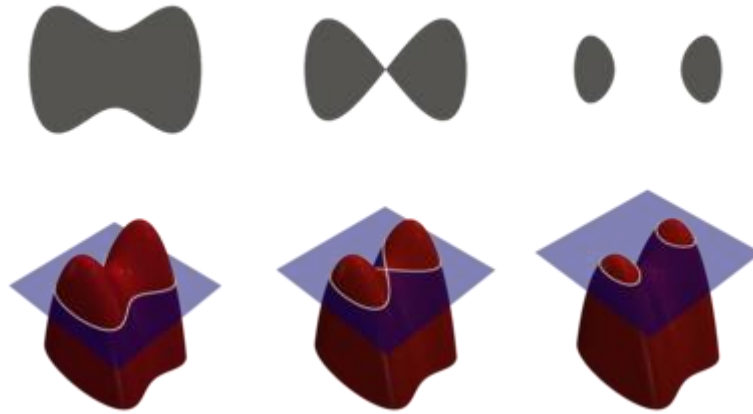
Step 2.3: If such segment R_k exists, than pixel a_{ij} add to segment R_k , else create new segment R_n and add pixel a_{ij} to new segment R_n .

Step 3: Merge all segments, which belong to one cluster and are neighbors. Step 4: Arrange borders of all segments.

3.4.1 LEVELSET SEGMENTATION

Level-set methods (LSM) are a conceptual framework for using level sets as a tool for numerical analysis of surfaces and shapes. The advantage of the level-set model is that one can perform numerical computations involving curves and surfaces on a fixed Cartesian grid without having to parameterize these objects (this is called the Eulerian approach). Also, the level-set method makes it very easy to follow shapes that change topology, for example, when a shape splits in two, develops holes, or the reverse of these operations. All these make the level-set method a great tool for modeling time-varying objects, like inflation of an airbag, or a drop of oil floating in water.

The figure on the right illustrates several important ideas about the level-set method. In the upper-left corner we see a shape; that is, a bounded region with a well-behaved boundary. Below it, the red surface is the graph of a level set function φ determining this shape, and the flat blue region represents the xy plane. The boundary of the shape is then the zero-level set of φ , while the shape itself is the set of points in the plane for which φ is positive (interior of the shape) or zero (at the boundary).



3.4.1 LEVEL SEGEMENTATION DIAGRAM

3.4.2 THE LEVEL-SET EQUATION

If the curve $\{\displaystyle \Gamma\}$ moves in the normal direction with a speed $\{\displaystyle v\}$, then the level-set function $\{\displaystyle \varphi\}$ satisfies the level-set equation

$$\frac{\partial \varphi}{\partial t} = v |\nabla \varphi|.$$

Here, $\{\displaystyle |\cdot|\}$ is the Euclidean norm (denoted customarily by single bars in PDEs), and $\{\displaystyle t\}$ is time. This is a partial differential equation, in particular a Hamilton–Jacobi equation, and can be solved numerically, for example, by using finite differences on a Cartesian grid.[2][3]

The numerical solution of the level-set equation, however, requires sophisticated techniques. Simple finite-difference methods fail quickly. Upwinding methods, such as the Godunov method, fare better; however, the level-set method does not guarantee the conservation of the volume and the shape of the level set in an advection field that does conserve the shape and size, for example, uniform or rotational velocity field. Instead, the shape of the level set may get severely distorted, and the level set may vanish over several time steps. For this reason,

high-order finite-difference schemes are generally required, such as high-order essentially non-oscillatory (ENO) schemes, and even then the feasibility of long-time simulations is questionable. Further sophisticated methods to deal with this difficulty have been developed, e.g., combinations of the level-set method with tracing marker particles advected by the velocity field.

3.4.3 FEATURE EXTRACTION

GLCM

In statistical texture analysis, texture features are computed from the statistical distribution of observed combinations of intensities at specified positions relative to each other in the image. According to the number of intensity points (pixels) in each combination, statistics are classified into first-order, second order and higher-order statistics. The Gray Level Cooccurrence Matrix (GLCM) method is a way of extracting second order statistical texture features. The approach has been used in a number of applications, Third and higher order textures consider the relationships among three or more pixels.

In statistical texture analysis, texture features are computed from the statistical distribution of observed combinations of intensities at specified positions relative to each other in the image. According to the number of intensity points (pixels) in each combination, statistics are classified into first-order, second order and higher-order statistics. The Gray Level Cooccurrence Matrix (GLCM) method is a way of extracting second order statistical texture features. The approach has been used in a number of applications, Third and higher order textures consider the relationships among three or more pixels. These are theoretically possible but not commonly implemented due to calculation time and interpretation difficulty. A GLCM is a matrix where the number of rows and columns is equal to the number of gray levels, G , in the image. The matrix element $P(i, j | \Delta x, \Delta y)$ is the relative frequency with which two pixels, separated by a pixel distance $(\Delta x, \Delta y)$, occur within a given neighborhood, one with intensity 'i' and the other with intensity 'j'. The matrix element $P(i, j | d, \theta)$ contains the second order statistical probability values for changes between gray levels 'i' and 'j' at a particular displacement distance d and at a particular angle (θ) . Using a large number of intensity levels G

implies storing a lot of temporary data, i.e. a $G \times G$ matrix for each combination of $(\Delta x, \Delta y)$ or (d, θ) . Due to their large dimensionality, the GLCM's are very sensitive to the size of the texture samples on which they are estimated. Thus, the number of gray levels is often reduced. GLCM matrix formulation can be explained with the example illustrated in fig 2.1 for four different gray levels. Here one pixel offset is used (a reference pixel and its immediate neighbour). If the window is large enough, using a larger offset is possible. The top left cell will be filled with the number of times the combination 0,0 occurs, i.e. how many time within the image area a pixel with grey level 0 (neighbour pixel) falls to the right of another pixel with grey level 0(reference pixel).

The MATLAB code used for the GLCM is

```
q1 = imread ('Jerry.jpg');
```

```
w1 = rgb2gray (q1);
```

```
e1 = imresize (w1, [128 128]);
```

```
r1 = graycomatrix (e1);
```

```
disp (r1); t1 = imhist (e1);
```

```
figure, imshow (e1),
```

title ('transformed gray Jerry .jpg in gray'); The output will be an 8*8matrix which is a GLCM of input image.

3.4.4 Entropy

Entropy shows the amount of information of the image that is needed for the image compression. Entropy measures the loss of information or message in a transmitted signal and also measures the image information.

$$\text{ENTROPY} = \sum_{i=0}^{Ng-1} \sum_{j=0}^{Ng-1} -P_{ij} * \log P_{ij}$$

3.4.5 Correlation

Correlation measures the linear dependency of grey levels of neighboring pixels. Digital Image Correlation is an optical method that employs tracking & image registration techniques for accurate 2D and 3D measurements of changes in images. This is often used to measure deformation, displacement, strain and optical flow, but it is widely applied in many areas of science and engineering. One very common application is for measuring the motion of an optical mouse

$$\text{Correlation} = \frac{\sum_{i=0}^{Ng-1} \sum_{j=0}^{Ng-1} (i, j) p(i, j) - \mu_x \mu_y}{\sigma_x \sigma_y}$$

Sl.No	GLCM Feature	Formula
1.	<i>Contrast</i>	$\sum_{i,j=0}^{N-1} P_{i,j} (i - j)^2$
2.	<i>Correlation</i>	$\sum_{i,j=0}^{N-1} P_{i,j} \left[\frac{(i - \mu_i)(j - \mu_j)}{\sqrt{(\sigma_i^2)(\sigma_j^2)}} \right]$
3.	<i>Dissimilarity</i>	$\sum_{i,j=0}^{N-1} P_{i,j} i - j $
4.	<i>Energy</i>	$\sum_{i,j=0}^{N-1} P_{i,j}^2$
5.	<i>Entropy</i>	$\sum_{i,j=0}^{N-1} P_{i,j} (-\ln P_{i,j})$
6.	<i>Homogeneity</i>	$\sum_{i,j=0}^{N-1} \frac{P_{i,j}}{1 + (i - j)^2}$

3.4.1 TABLE FORMULA FOR CORRELATION

3.5 CLASSIFICATION

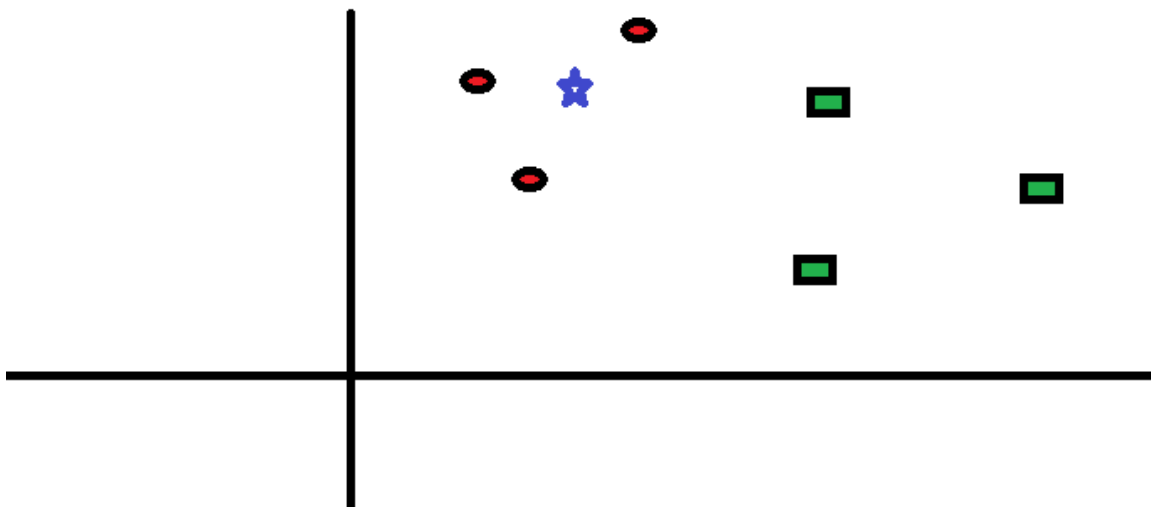
KNN

KNN can be used for both classification and regression predictive problems. However, it is more widely used in classification problems in the industry. To evaluate any technique we generally look at 3 important aspects:

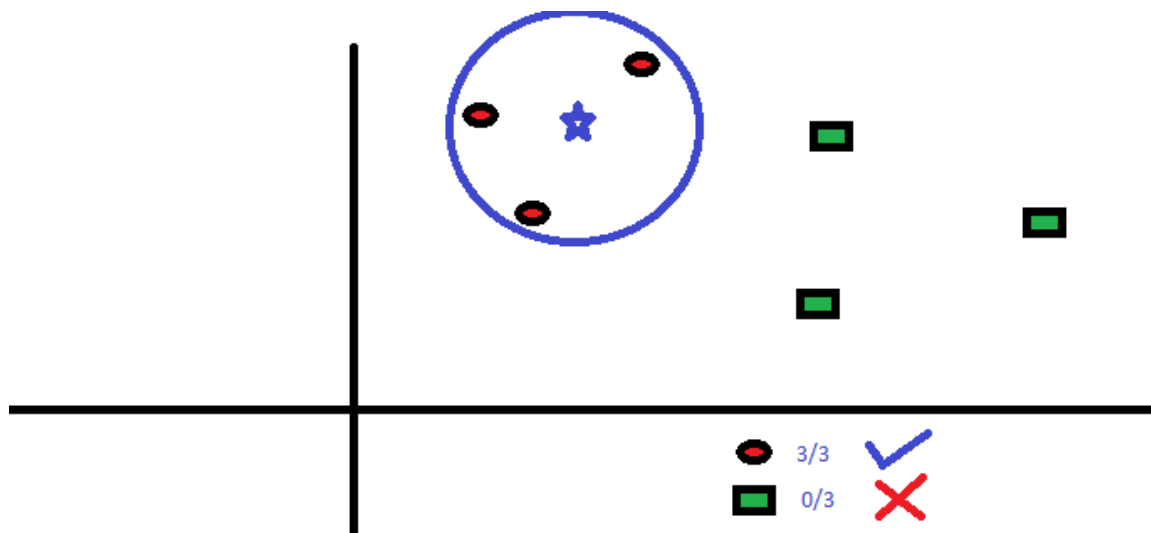
1. Ease to interpret output
2. Calculation time
3. Predictive Power

3.5.1 HOW DOES THE KNN ALGORITHM WORK?

Let's take a simple case to understand this algorithm. Following is a spread of red circles (RC) and green squares (GS) :



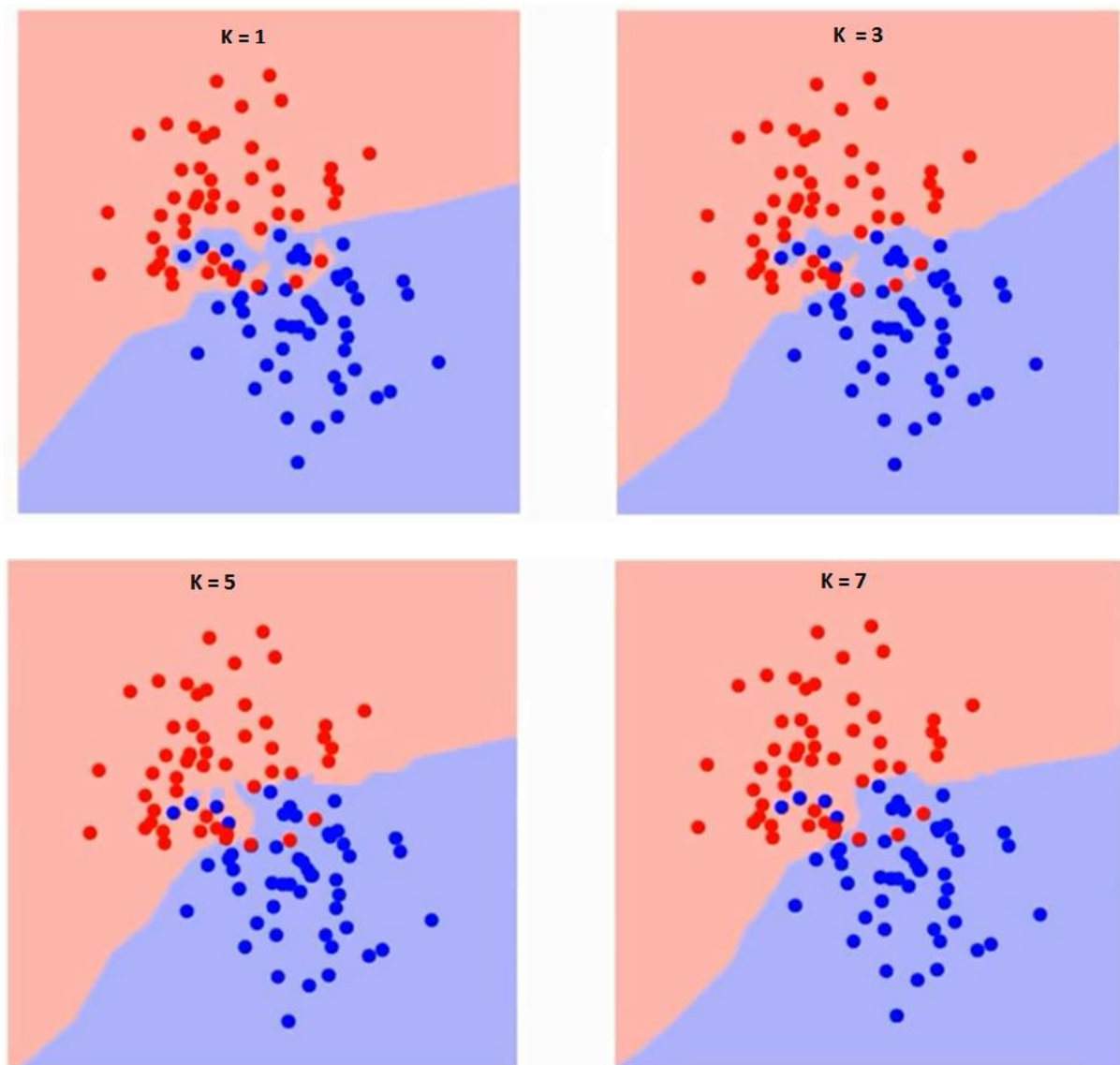
You intend to find out the class of the blue star (BS) . BS can either be RC or GS and nothing else. The “K” in KNN algorithm is the nearest neighbors we wish to take vote from. Let's say $K = 3$. Hence, we will now make a circle with BS as center just as big as to enclose only three datapoints on the plane. Refer to following diagram for more details:



The three closest points to BS is all RC. Hence, with good confidence level we can say that the BS should belong to the class RC. Here, the choice became very obvious as all three votes from the closest neighbors went to RC. The choice of the parameter K is very crucial in this algorithm. Next we will understand what are the factors to be considered to conclude the best K.

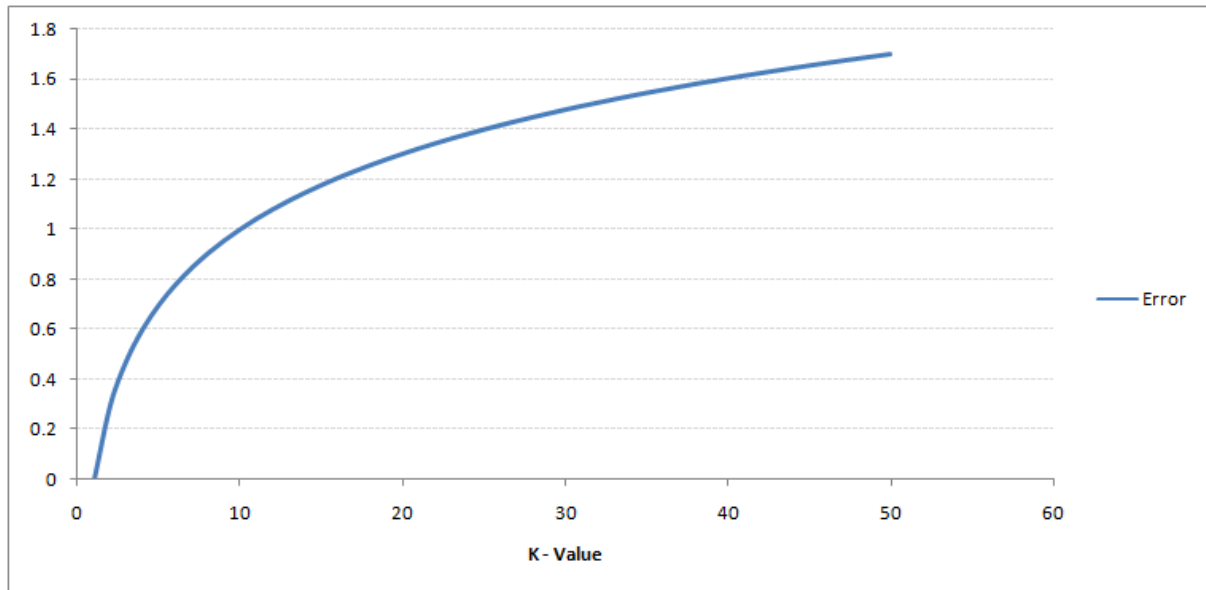
3.5.2 HOW DO WE CHOOSE THE FACTOR K?

First let us try to understand what exactly does K influence in the algorithm. If we see the last example, given that all the 6 training observations remain constant, with a given K value we can make boundaries of each class. These boundaries will segregate RC from GS. The same way, let's try to see the effect of value "K" on the class boundaries. Following are the different boundaries separating the two classes with different values of K.



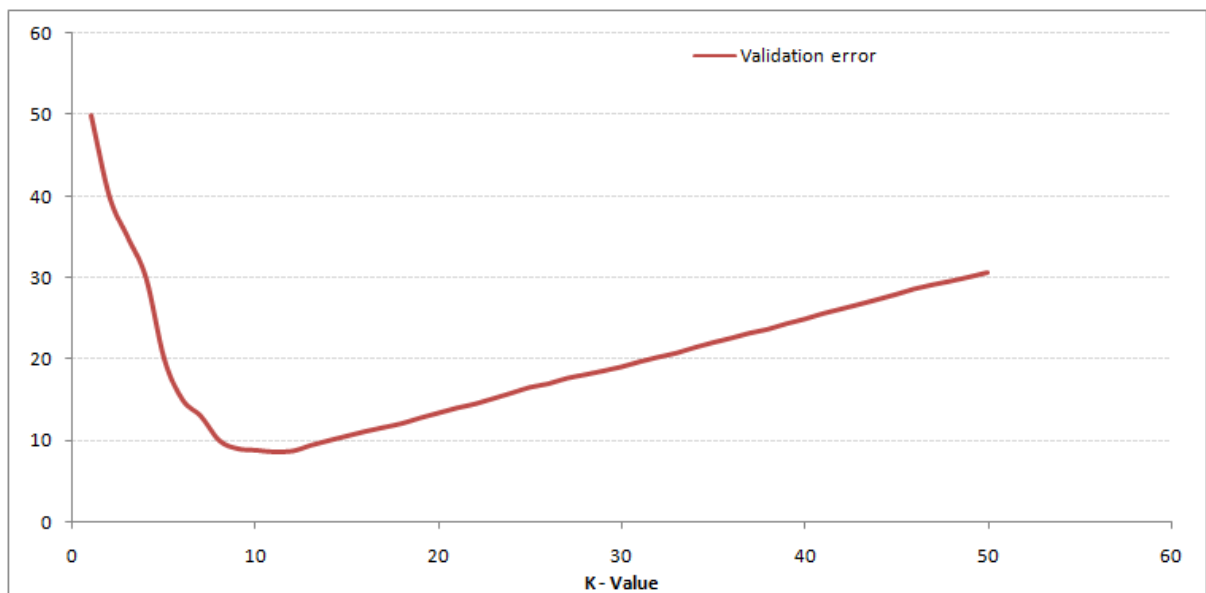
3.5.2 *K* FACTOR DIFFERENT VALUES

If you watch carefully, you can see that the boundary becomes smoother with increasing value of K . With K increasing to infinity it finally becomes all blue or all red depending on the total majority. The training error rate and the validation error rate are two parameters we need to access on different K -value. Following is the curve for the training error rate with varying value of K :



3.5.2.1 ERROR OF K VALUE

As you can see, the error rate at $K=1$ is always zero for the training sample. This is because the closest point to any training data point is itself. Hence the prediction is always accurate with $K=1$. If validation error curve would have been similar, our choice of K would have been 1. Following is the validation error curve with varying value of K :



3.5.2.2 VALIDATION VALE OF K

This makes the story more clear. At $K=1$, we were overfitting the boundaries. Hence, error rate initially decreases and reaches a minima. After the minima point, it then increase with increasing K . To get the optimal value of K , you can segregate the training and validation from the initial dataset. Now plot the validation error curve to get the optimal value of K . This value of K should be used for all predictions.

3.5.3 BREAKING IT DOWN – PSEUDO CODE of KNN

We can implement a KNN model by following the below steps:

1. Load the data
2. Initialise the value of k
3. For getting the predicted class, iterate from 1 to total number of training data points
 1. Calculate the distance between test data and each row of training data. Here we will use Euclidean distance as our distance metric since it's the most popular method. The other metrics that can be used are Chebyshev, cosine, etc.
 2. Sort the calculated distances in ascending order based on distance values
 3. Get top k rows from the sorted array
 4. Get the most frequent class of these rows Return the predicted class

3.6 SUPPORT VECTOR MACHINE

Support vector machines (SVMs, also support vector networks) are supervised learning models with associated learning algorithms that analyze data used for classification and regression analysis. Given a set of training examples, each marked as belonging to one or the other of two categories, an SVM training algorithm builds a model that assigns new examples to one category or the other,

making it a non-probabilistic binary linear classifier. An SVM model is a representation of the examples as points in space, mapped so that the examples of the separate categories are divided by a clear gap that is as wide as possible. New examples are then mapped into that same space and predicted to belong to a category based on which side of the gap they fall on.

In addition to performing linear classification, SVMs can efficiently perform a non-linear classification using what is called the kernel trick, implicitly mapping their inputs into high-dimensional feature spaces.

When data are not labeled, supervised learning is not possible, and an unsupervised learning approach is required, which attempts to find natural clustering of the data to groups, and then map new data to these formed groups. The clustering algorithm which provides an improvement to the support vector machines is called support vector clustering and is often used in industrial applications either when data are not labeled or when only some data are labeled as a preprocessing for a classification pass.

3.6.1 MOTIVATION

Classifying data is a common task in machine learning. Suppose some given data points each belong to one of two classes, and the goal is to decide which class a new data point will be in. In the case of support vector machines, a data point is viewed as a p -dimensional vector (a list of p numbers), and we want to know whether we can separate such points with a $(p - 1)$ dimensional hyperplane. This is called a linear classifier. There are many hyper planes that might classify the data. One reasonable choice as the best hyper plane is the one that represents the largest separation, or margin, between the two classes. So we choose the hyper plane so that the distance from it to the nearest data point on each side is maximized. If such a hyper plane exists, it is known as the maximum-margin hyper plane and the linear classifier it defines is known as a maximum margin classifier; or equivalently, the perceptron of optimal stability.

3.6.2 DEFINITION

More formally, a support vector machine constructs a hyper plane or set of hyper planes in a high- or infinite-dimensional space, which can be used for

classification, regression, or other tasks. Intuitively, a good separation is achieved by the hyper plane that has the largest distance to the nearest training-data point of any class (so-called functional margin), since in general the larger the margin the lower the generalization error of the classifier.

Whereas the original problem may be stated in a finite dimensional space, it often happens that the sets to discriminate are not linearly separable in that space. For this reason, it was proposed that the original finite-dimensional space be mapped into a much higher-dimensional space, presumably making the separation easier in that space. To keep the computational load reasonable, the mappings used by SVM schemes are designed to ensure that dot products may be computed easily in terms of the variables in the original space, by defining them in terms of a kernel function $k(x, y)$ selected to suit the problem. The hyper planes in the higher-dimensional space are defined as the set of points whose dot product with a vector in that space is constant. The vectors defining the hyper planes can be chosen to be linear combinations with parameters α_i of images of feature vectors x_i that occur in the data base. With this choice of a hyper plane, the points x in the feature space that are mapped into the hyper plane are defined by the relation: $\sum_i \alpha_i k(x_i, x) = \text{constant}$. Note that if $k(x, y)$ becomes small as y grows further away from x , each term in the sum measures the degree of closeness of the test point x to the corresponding data base point x_i . In this way, the sum of kernels above can be used to measure the relative nearness of each test point to the data points originating in one or the other of the sets to be discriminated. Note the fact that the set of points x mapped into any hyper plane can be quite convoluted as a result, allowing much more complex discrimination between sets which are not convex at all in the original space.

SVMs can be used to solve various real world problems:

- SVMs are helpful in text and hypertext categorization as their application can significantly reduce the need for labeled training instances in both the standard inductive and transductive settings.
- Classification of images can also be performed using SVMs. Experimental results show that SVMs achieve significantly higher search accuracy than traditional query refinement schemes after just three to four rounds of

relevance feedback. This is also true of image segmentation systems, including those using a modified version SVM that uses the privileged approach as suggested by Vapnik.

- Hand-written characters can be recognized using SVM.
- The SVM algorithm has been widely applied in the biological and other sciences. They have been used to classify proteins with up to 90% of the compounds classified correctly. Permutation tests based on SVM weights have been suggested as a mechanism for interpretation of SVM models. Support vector machine weights have also been used to interpret SVM models in the past. Posthoc interpretation of support vector machine models in order to identify features used by the model to make predictions is a relatively new area of research with special significance in the biological sciences.

3.6.3 PROPERTIES

SVMs belong to a family of generalized linear classifiers and can be interpreted as an extension of the perceptron. They can also be considered a special case of Tikhonov regularization. A special property is that they simultaneously minimize the empirical classification error and maximize the geometric margin; hence they are also known as maximum margin classifiers.

A comparison of the SVM to other classifiers has been made by Meyer, Leisch and Hornik.

3.6.4 PARAMETER SELECTION

The effectiveness of SVM depends on the selection of kernel, the kernel's parameters, and soft margin parameter C . A common choice is a Gaussian kernel, which has a single parameter γ . The best combination of C and γ is often selected by a grid search with exponentially growing sequences of C and γ , for example, $C \in \{2^{-5}, 2^{-3}, \dots, 2^{13}, 2^{15}\}$. Typically, each combination of parameter choices is checked using cross validation, and the parameters with best cross-validation accuracy are picked. Alternatively, recent work in Bayesian optimization can be used to select C and γ , often requiring the evaluation of far fewer parameter combinations than grid search. The final model, which is used for testing and for

classifying new data, is then trained on the whole training set using the selected parameters.

3.6.5 Issues

Potential drawbacks of the SVM include the following aspects:

- Requires full labeling of input data
- Uncalibrated class membership probabilities
- The SVM is only directly applicable for two-class tasks. Therefore, algorithms that reduce the multi-class task to several binary problems have to be applied; see the multi-class SVM section.
- Parameters of a solved model are difficult to interpret.

3.6.7 EXTENSIONS

SUPPORT VECTOR CLUSTERING (SVC)

SVC is a similar method that also builds on kernel functions but is appropriate for unsupervised learning and data-mining. It is considered a fundamental method in data science.

MULTICLASS SVM

Multiclass SVM aims to assign labels to instances by using support vector machines, where the labels are drawn from a finite set of several elements.

The dominant approach for doing so is to reduce the single multiclass problem into multiple binary classification problems. Common methods for such reduction include:

- Building binary classifiers which distinguish (i) between one of the labels and the rest (one-versus-all) or (ii) between every pair of classes (one-versus-one). Classification of new instances for the one-versus-all case is done by a winner-takes-all strategy, in which the classifier with the highest output function assigns the class (it is important that the output functions be calibrated to produce comparable scores). For the one-versus-one approach, classification is done by a max-wins voting strategy, in which every classifier assigns the instance to one of the two classes, then the

vote for the assigned class is increased by one vote, and finally the class with the most votes determines the instance classification.

- Directed acyclic graph SVM (DAGSVM)
- Error-correcting output codes

Crammer and Singer proposed a multiclass SVM method which casts the multiclass classification problem into a single optimization problem, rather than decomposing it into multiple binary classification problems. See also Lee, Lin and Wahba.

3.6.8 STRUCTURED SVM

SVMs have been generalized to structured SVMs, where the label space is structured and of possibly infinite size.

3.6.9 IMPLEMENTATION

The parameters of the maximum-margin hyperplane are derived by solving the optimization. There exist several specialized algorithms for quickly solving the QP problem that arises from SVMs, mostly relying on heuristics for breaking the problem down into smaller, more-manageable chunks.

Another approach is to use an interior point method that uses Newton-like iterations to find a solution of the Karush–Kuhn–Tucker conditions of the primal and dual problems. Instead of solving a sequence of broken down problems, this approach directly solves the problem altogether. To avoid solving a linear system involving the large kernel matrix, a low rank approximation to the matrix is often used in the kernel trick.

Another common method is Platt's sequential minimal optimization (SMO) algorithm, which breaks the problem down into 2-dimensional sub-problems that are solved analytically, eliminating the need for a numerical optimization algorithm and matrix storage. This algorithm is conceptually simple, easy to implement, generally faster, and has better scaling properties for difficult SVM problems.

The special case of linear support vector machines can be solved more efficiently by the same kind of algorithms used to optimize its close cousin, logistic regression; this class of algorithms includes sub-gradient descent (e.g., PEGASOS)

and coordinate descent (e.g., LIBLINEAR). LIBLINEAR has some attractive training time properties. Each convergence iteration takes time linear in the time taken to read the train data and the iterations also have a Q-Linear Convergence property, making the algorithm extremely fast.

The general kernel SVMs can also be solved more efficiently using sub-gradient descent (e.g. P-pack SVM), especially when parallelization is allowed.

Kernel SVMs are available in many machine learning toolkits, including LIBSVM, MATLAB, SAS, SVM light, Shogun, Shark, J Kernel Machines, Open CV and others.

CHAPTER-4

SOFTWARE

4.1 SYSTEM REQUIREMENTS FOR MATLAB

Operating Systems

Windows 10

Windows 8.1

Windows 8

Windows 7 Service Pack 1

Windows Server 2016

Windows Server 2012

Windows Server 2008 R2 Service Pack 1

Processors

Any Intel or AMD x86-64 processor

AVX2 instruction set support is recommended

With Polyspace, 4 cores is recommended

Disk Space

2 GB for MATLAB only,

4–6 GB for a typical installation.

RAM

2 GB

With Simulink, 4 GB is required

With Polyspace, 4 GB per core is recommended

4.2 Graphics

No specific graphics card is required.

Hardware accelerated graphics card supporting OpenGL 3.3 with 1GB GPU memory is recommended.

4.2 MATLAB

What Is MATLAB?

MATLAB is a high-performance language for technical computing. It integrates computation, visualization, and programming in an easy-to-use environment where problems and solutions are expressed in familiar mathematical notation. Typical uses include:

- Math and computation
- Algorithm development
- Modeling, simulation, and prototyping
- Data analysis, exploration, and visualization
- Scientific and engineering graphics
- Application development, including graphical user interface building

MATLAB is an interactive system whose basic data element is an array that does not require dimensioning. This allows you to solve many technical computing problems, especially those with matrix and vector formulations, in a fraction of the time it would take to write a program in a scalar noninteractive language such as C or Fortran.

The name MATLAB stands for *matrix laboratory*. MATLAB was originally written to provide easy access to matrix software developed by the LINPACK and EISPACK projects. Today, MATLAB uses software developed by the LAPACK and ARPACK projects, which together represent the state-of-the-art in software for matrix computation. MATLAB has evolved over a period of years with input from many users. In university environments, it is the standard instructional tool for introductory and advanced courses in mathematics, engineering, and science. In industry, MATLAB is the tool of choice for high-productivity research, development, and analysis.

4.2.1 TOOLBOXES

MATLAB features a family of application-specific solutions called *toolboxes*. Very important to most users of MATLAB, toolboxes allow you to *learn* and *apply* specialized technology. Toolboxes are comprehensive collections of MATLAB functions (M-files) that extend the MATLAB environment to solve particular classes of problems. Areas in which toolboxes are available include signal processing, control systems, neural networks, fuzzy logic, wavelets, simulation, and many others.

4.2.2 THE MATLAB SYSTEM

The MATLAB system consists of five main parts:

4.2.3 DEVELOPMENT ENVIRONMENT

This is the set of tools and facilities that help you use MATLAB functions and files. Many of these tools are graphical user interfaces.

It includes the MATLAB desktop and Command Window, a command history, and browsers for viewing help, the workspace, files, and the search path.

4.2.4 THE MATLAB MATHEMATICAL FUNCTION LIBRARY

This is a vast collection of computational algorithms ranging from elementary functions like sum, sine, cosine, and complex arithmetic, to more sophisticated functions like matrix inverse, matrix eigenvalues, Bessel functions, and fast Fourier transforms.

4.2.5 THE MATLAB LANGUAGE

This is a high-level matrix/array language with control flow statements, functions, data structures, input/output, and object-oriented programming features. It allows both “programming in the small” to rapidly create quick and dirty throw-away programs, and “programming in the large” to create complete large and complex application programs.

4.2.6 HANDLE GRAPHICS®

This is the MATLAB graphics system. It includes high-level commands for two-dimensional and three-dimensional data visualization, image processing, animation, and presentation graphics. It also includes low-level commands that allow you to fully customize the appearance of graphics as well as to build complete graphical user interfaces on your MATLAB applications.

4.3 THE MATLAB APPLICATION PROGRAM INTERFACE (API).

This is a library that allows you to write C and Fortran programs that interact with MATLAB. It includes facilities for calling routines from MATLAB (dynamic linking), calling MATLAB as a computational engine, and for reading and writing MAT-files.

4.3.1 IMAGE PROCESSING IN MATLAB

Images and pictures. As we mentioned in the preface, human beings are predominantly visual creatures: we rely heavily on our vision to make sense of the world around us. We not only look at things to identify and classify them, but we can scan for differences, and obtain an overall rough *_feeling_* for a scene with a quick glance. Humans have evolved very precise visual skills: we can identify a face in an instant; we can differentiate colours; we can process a large amount of visual information very quickly.

However, the world is in constant motion: stare at something for long enough and it will change in some way. Even a large solid structure, like a building or a mountain, will change its appearance depending on the time of day (day or night); amount of sunlight (clear or cloudy), or various shadows falling upon it. We are concerned with single images: snapshots, if you like, of a visual scene. Although image processing can deal with changing scenes, we shall not discuss it in any detail in this text.

For our purposes, an image is a single picture which represents something. It may be a picture of a person, of people or animals, or of an outdoor scene, or a microphotograph of an electronic component, or the result of medical imaging. Even if the picture is not immediately recognizable, it will not be just a random blur.

4.4 IMAGE PROCESSING

Image processing involves changing the nature of an image in order to either

1. improve its pictorial information for human interpretation,
2. render it more suitable for autonomous machine perception.

We shall be concerned with digital image processing, which involves using a computer to change the nature of a digital image (see below). It is necessary to realize that these two aspects represent two separate but equally important aspects of image processing. A procedure which satisfies condition,

- (1) A procedure which makes an image look better may be the very worst procedure for satisfying condition
- (2). Humans like their images to be sharp, clear and detailed; machines prefer their images to be simple and uncluttered.

4.4.1 Some applications

Image processing has an enormous range of applications; almost every area of science and technology can make use of image processing methods. Here is a short list just to give some indication of the range of image processing applications.

1. Medicine

Inspection and interpretation of images obtained from X-rays, MRI or CAT scans, analysis of cell images, of chromosome karyotypes.

2. Agriculture

Satellite/aerial views of land, for example to determine how much land is being used for different purposes, or to investigate the suitability of different regions for different crops ,inspection of fruit and vegetables distinguishing good and fresh produce from old.

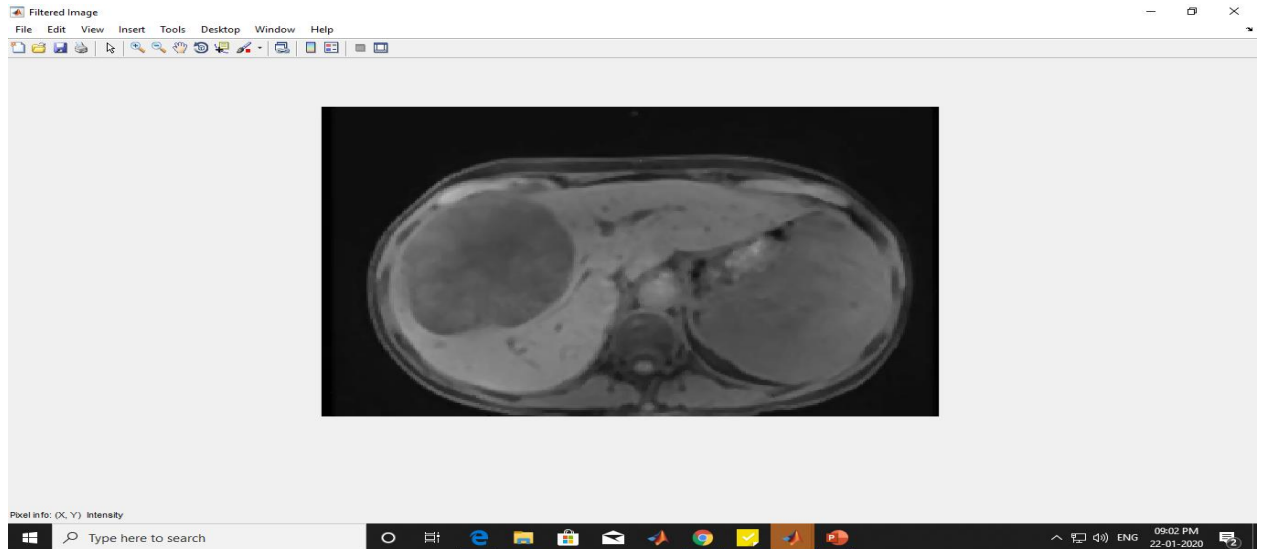
3 Industry

Automatic inspection of items on a production line,
inspection of paper samples.

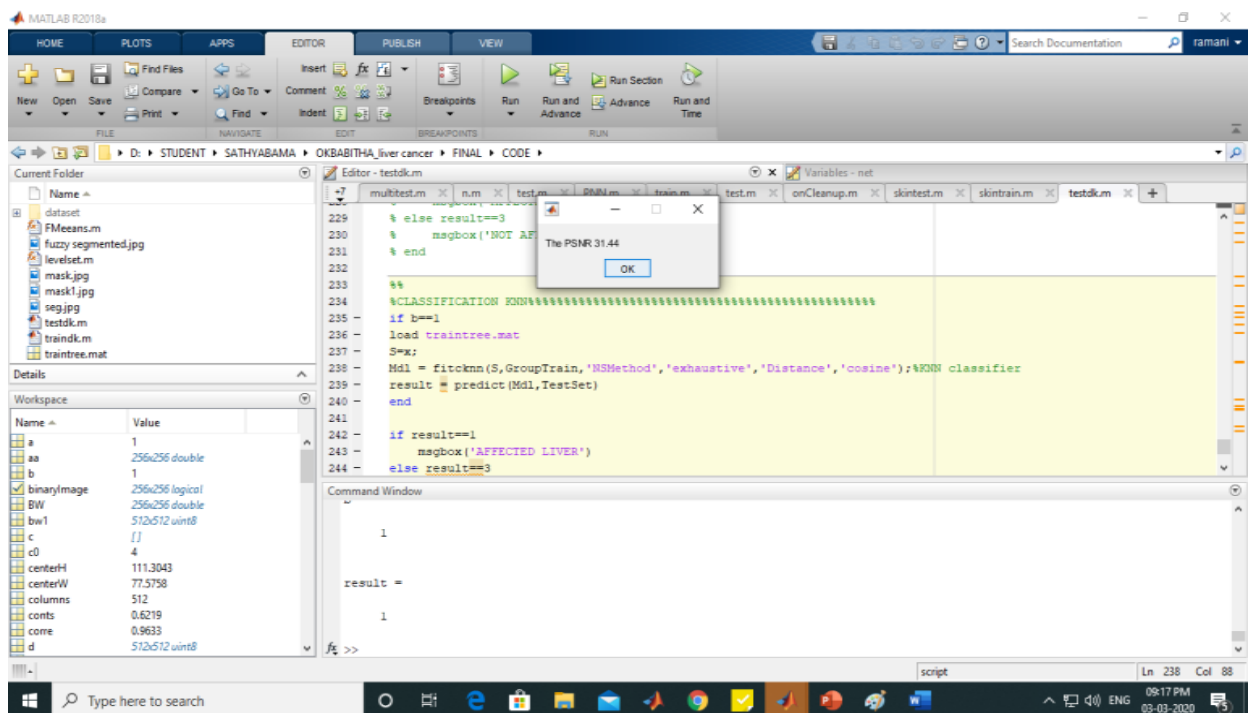
CHAPTER-5

5.1 OUTPUTS

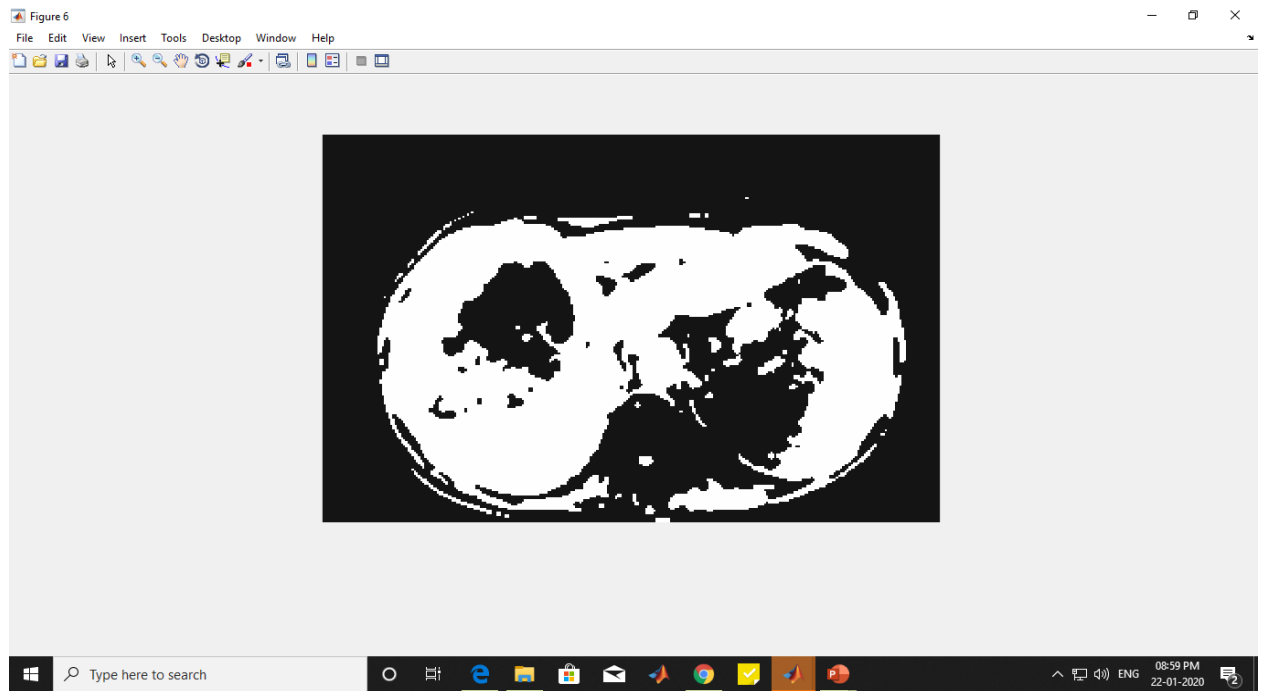
FILTER IMAGE



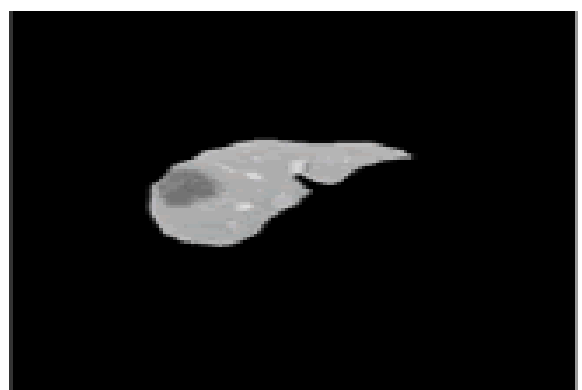
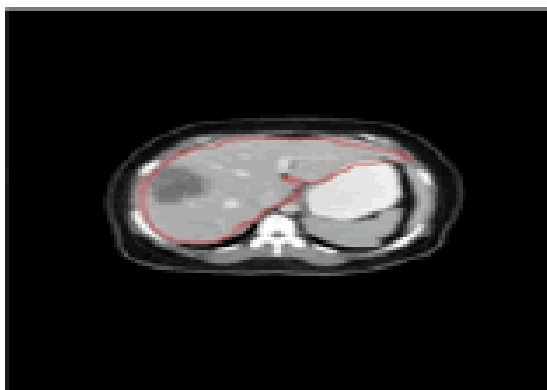
PSNR



FUZZY SEGMENTATION



LEVELSET



FEATURE EXTRACTION

Variables - x

120x9 double

	1	2	3	4	5	6	7	8	9
1	95.2113	44.7004	1.3211e+06	0.1075	2.1760	0.1537	0.9841	0.7280	0.9963
2	109.4191	18.4722	4.6244e+03	-1.1034	7.0511	1.7684	0.8980	0.4718	0.9579
3	114.2262	16.9094	2.7066e+03	-0.0308	7.1003	2.0770	0.8545	0.4461	0.9505
4	75.0385	19.4244	9.1612e+03	-0.0330	4.4377	1.4298	0.9131	0.5050	0.9660
5	75.0386	19.4244	9.1612e+03	-0.0331	4.4378	1.4273	0.9132	0.5050	0.9660
6	113.5937	23.6381	1.0499e+04	-0.4367	3.5860	2.5411	0.8482	0.4694	0.9395
7	100.6561	22.7489	1.1895e+04	-0.3695	8.6939	2.4545	0.8522	0.4752	0.9416
8	85.8354	41.7333	1.0287e+06	-0.1027	3.3040	0.3933	0.9608	0.7107	0.9906
9	104.3482	21.9518	2.6897e+04	-0.2511	4.8410	0.7626	0.9460	0.5868	0.9818
10	90.0731	42.6516	1.1982e+06	-0.3976	4.0343	0.2160	0.9791	0.7075	0.9949
11	121.9621	22.2321	1.5512e+04	-0.9544	3.5900	3.3357	0.8001	0.4525	0.9206
12	112.3160	21.2832	1.6319e+04	-0.7141	4.9871	1.4188	0.9170	0.4876	0.9662
13	87.7054	42.7702	9.5456e+05	-0.1595	2.1685	0.2446	0.9748	0.7238	0.9942
14	116.9264	21.9514	1.4246e+04	-0.6375	3.4343	2.7090	0.8427	0.4521	0.9355
15	95.9313	44.7234	1.5418e+06	-0.2356	2.4677	0.1369	0.9855	0.7335	0.9967
16	89.2365	41.2354	9.9551e+05	-0.3171	2.9675	0.1485	0.9844	0.7314	0.9965
17	125.8567	17.6854	8.2530e+03	-0.1471	1.5373	1.0755	0.9325	0.5282	0.9744
18	120.7341	22.2475	5.8865e+03	-0.3579	6.2803	3.2556	0.8191	0.4177	0.9223
19	108.2432	24.5462	1.2786e+04	-0.0742	2.5085	1.9607	0.8726	0.5305	0.9533
20	102.9731	23.2419	1.1770e+04	-0.4619	5.1332	1.7382	0.8881	0.5224	0.9586
21	102.9731	23.2419	1.1770e+04	-0.4619	5.1333	1.7369	0.8882	0.5226	0.9586
22	101.5007	47.3857	1.6731e+06	-0.1970	2.9483	0.1700	0.9823	0.7290	0.9960
23	115.7041	19.0227	1.0955e+04	-1.7096	6.5155	2.3881	0.8638	0.4511	0.9431
24	116.5371	20.9968	1.0745e+04	-0.7704	3.8460	3.6807	0.7946	0.4535	0.9124

CLASSIFICATION

MATLAB R2018a

Current Folder: D:\STUDENT\SATHYABAMA\OKBABITHA_liver cancer\FINAL\CODE

Workspace:

Name	Value
a	1
aa	256x256 double
b	1
binaryImage	256x256 logical
BW	256x256 double
bw1	512x512 uint8
c	[]
c0	4
centerH	111.3043
centerW	77.5758
columns	512
conts	0.6219
corre	0.9633
d	512x512 uint8

Script: testdk.m

```

229 % else result==3
230 msgbox('NOT AFFECTED LIVER')
231 % end
232
233 %%CLASSIFICATION KNN%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
234 if b==1
235 load traintree.mat
236 S=x;
237 Mdl = fitcknn(S,GroupTrain,'NSMethod','exhaustive','Distance','cosine');%KNN classifier
238 result = predict(Mdl,TestSet)
239 end
240
241
242 if result==1
243 msgbox('AFFECTED LIVER')
244 else result==3

```

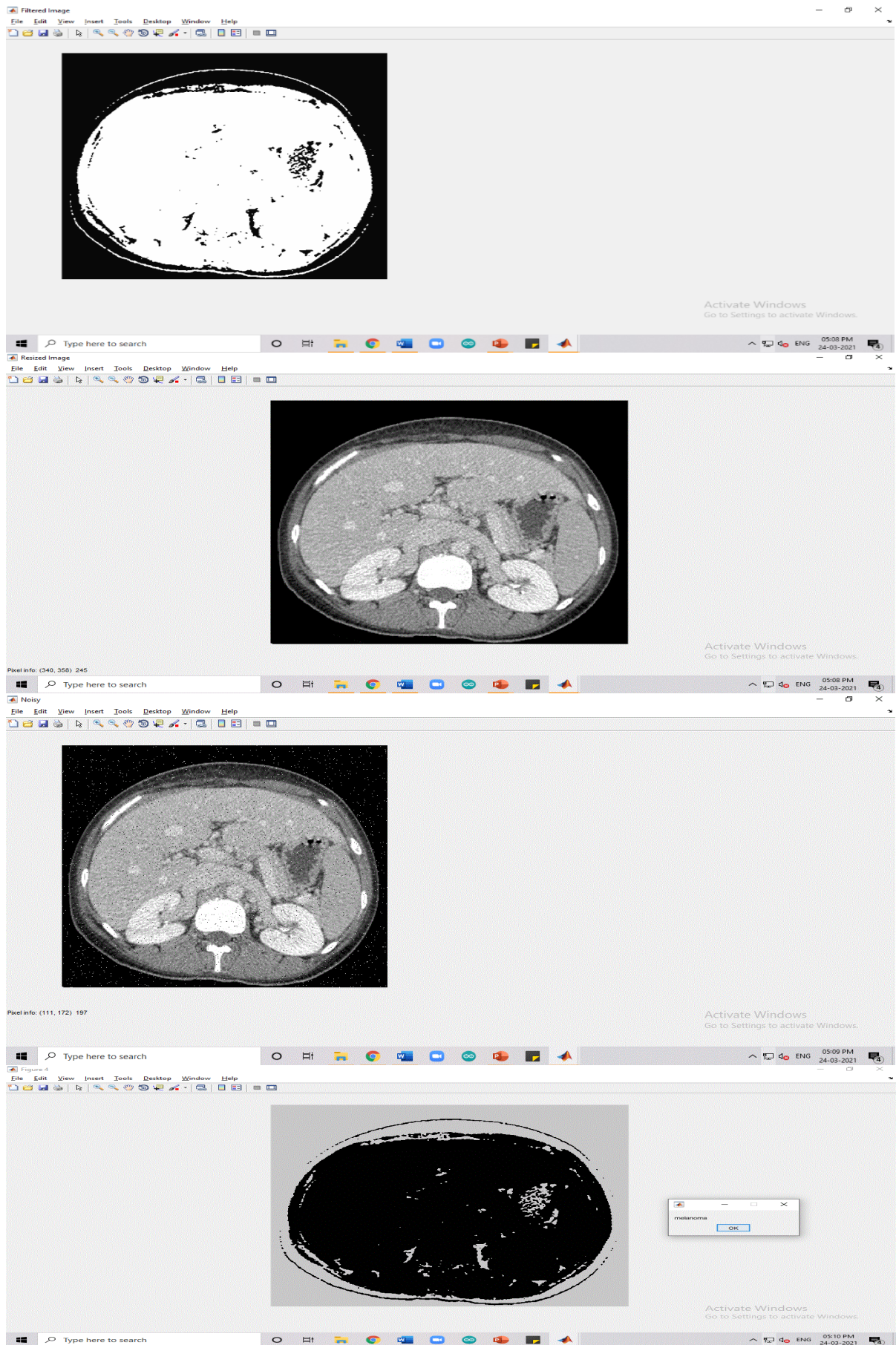
Command Window:

```

1
result =
1

```

Message Box: AFFECTED LIVER



CHAPTER 6

CONCLUSION

The segmentation method presented in this paper is one of the flexibly methods for segmentation. fcMeans and watershed segmentation is comparatively more clear than thresholding segmentation.. In this case also we find infected area. Cancerous region is separated from healthy liver by the method of segmentation. The unique features of the segmented images were extracted using GLCM.

Features are contrast, correlation, Energy, Homogeneity, Std Deviation. On that features knn used to classify. In short the development of knn used is an entirely different from normal algorithms used for learning and knn used provides a new insight into this learning

CHAPTER-7

REFERENCES

- [1] Weimin Huang; Ning Li; Ziping Lin; Guang-Bin Huang; Weiwei Zong; Jiayin Zhou; Yuping Duan, "Liver tumor detection and segmentation using kernel-based extreme learning machine," in Engineering in Medicine and Biology Society (EMBC), 2013 35th Annual International Conference of the IEEE , vol., no., pp.3662- 3665, 3-7 July 2013
- [2] Jie Lu; Defeng Wang; Lin Shi; Pheng Ann Heng, "Automatic liver segmentation in CT images based on Support Vector Machine," in Biomedical and Health Informatics (BHI), 2012 IEEE-EMBS International Conference on , vol., no., pp.333-336, 5-7 Jan. 2012
- [3] R. K. Bhullar and N. K.Walia. A New Hybrid Technique for Detection of Liver Cancer on Itrasound Images. International Journal of Science and Research (IJSR), Vol. 3,No. 10, pp. 1647- 1651, India,2014
- [4] V.v.gomathi and s.karthikeyan. Performance evaluation of hmsk and sqfd algorithms for computer tomography (ct) image segmentation of effective radiotherapy. Journal of Theoretical and Applied Information Technology, Vol. 22,No. 2, pp. 1647- 1651, India,2014
- [5] R.Rajagopal and P.Subbiah. Computer Aided Detection of Liver Tumor using SVM Classifier. International Journal of Advanced Research in Electrical, Electronics and Instrumentation Engineering, Vol. 3,No. 6, pp. 10170- 10177, India, June 2014.