

# Kidney Tumor Detection and Classification using Machine Learning Algorithm

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## Abstract :

Kidney cancer is difficult to detect, and it is also difficult for doctors to diagnose. Disease classification/detection helps early disease diagnosis by supporting pathologists and doctors' decisions. Machine learning technology is one of the emerging fields that can be used in the health sector to diagnose different diseases. This study helped the early diagnosis of kidney disease by supporting the decisions of pathologists and doctors. In this role, the use of machine learning algorithms in MATLAB achieved the best results in the classification of kidney tumors. There are four steps involved in this study, they are image processing ,segmentation, feature extraction and classification. FCM algorithm is used as a segmentation algorithm for the recognition of the Kidney region. SVM will be used for the classification of benign and malignant tumor . The goal of the project is to detect kidney tumors and classify tumor stages and predict the accuracy of the system. This project is implemented in MATLAB. MATLAB is the best tool for image processing and analysis of medical images.

**Keywords-** Kidney Tumor, Machine Learning, Support Vector Machine, Fuzzy C-Means, MATLAB.

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## I. Introduction

Detecting diseases in the benign stage is a challenging task. This problem is solved by machine learning technology. Let's first understand the information about kidney tumors. Kidney cancer cells grow out of control and form masses called tumors in the kidneys. This stage of the tumor can be benign or malignant. If not treated early, the tumor will grow and spread to other internal parts of the body, this type of tumor called malignant tumor. .

Image segmentation is the process of dividing a digital image into multiple segments or pixel sets. The goal of image segmentation is to group pixels into prominent image areas. Medical image segmentation is one of the most important topics in medical technology. It helps doctors in various aspects, such as analysis and diagnosis of different diseases, research on anatomical structures, and treatment planning. It refers to the process of deriving from medical images the important areas with uniform local image features (such as edges, textures, colors, etc.). This paper initially applied different image processing techniques, such as grayscale RGB, histogram equalization, binarization, and ROI extraction. Morphological operation for segmentation, using GLCM for feature extraction and support vector machine for classification.

## II. RELATED WORK

In this study, they used the empirical analysis of ML technology to classify the kidney patient data set as CKD or NOTCKD [1]. They Use seven machine learning techniques as well as NBTtree, J48, support vector machine, logistic regression, multi-layer perceptron, naive Bayes, and Composite Hypercube on Iterated Random Projection(CHIRP) and use unique evaluation measures, such as mean absolute error (MAE), Root Mean Square Error (RMSE), Relative Absolute Error (RAE), Root Relative Square Error (RRSE), Recovery Rate, Precision, F-measure, and Accuracy.

In this study [2], a computer-aided tool was proposed to classify kidney pathology through ultrasound processing and analysis of kidney images. Kidney ultrasound images are divided into four categories: normal, cyst, stone and tumor. Obtain a kidney scan ultrasound image (US) and use the knowledge related to common pathologies from the perspective of a urologist as input for classification. The image is preprocessed by applying Gaussian and median filters to remove speckle noise. The optimal threshold segmentation algorithm is used to obtain the region of interest. Extracts a set of first-order statistical characteristics. These characteristics are used as input to train and test probabilistic neural network classifiers. The retention method is adopted, where 50% of the images are used for training and the remaining 50% for testing. Finally, the efficiency of the classifier is evaluated. A classification rate of 93.5% was obtained. The results obtained by are based on performance index calculations and are very satisfactory.

In this study [3], they aimed to extract the characteristics of different kidney abnormalities to distinguish between normal and abnormal conditions. Two filters, median filter and Wiener filter are used to remove speckle noise in images (ultrasound). Implement image quality performance technique to identify image quality. peak-to-signal noise ratio (PSNR) and root mean square error (MSR) are used to verify the enhanced image. Then use FCM (Fuzzy Media Clustering Technology) to segment the preprocessed image, which will produce better results when finding a region of interest (ROI). Extract and analyze statistical features as well as Scale Invariant Feature Transform (SIFT) features and texture features. The energy, variance, and kurtosis in normal kidney images are found to be higher than in abnormal kidney images. These features can be used to distinguish between normal and abnormal kidney conditions. The developed system is expected to provide decision support for physicians to provide better medical care.

In this study [4], they studied the use of neural network models to predict kidney disease in hypertensive patients. Specifically, they first modeled the prediction problem as a binary classification task. Then, they proposed a hybrid neural network that combines bidirectional long short-term memory (BiLSTM) and an autoencoder network to fully capture the information in the EHR. They built a data set based on a large amount of raw EHR data. The data set contains a total of 35,332 records of hypertensive patients. The experimental results show that the proposed neural model achieves a precision of 89.7 in the task.

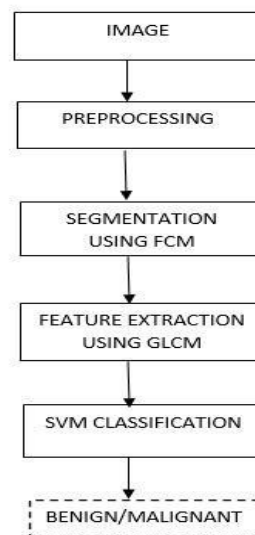
In this study [5], they proposed an adaptive hybrid deep convolutional neural network (AHDCNN) for early prediction and diagnosis of chronic kidney disease (CKD). The deep learning system is used to identify unique lesion subtypes from CT images of kidney cancer. The collected data will undergo preliminary analysis, and missing values will be replaced by estimates of median values. Different features related to kidney disease are determined from noise-free data and input into the implemented classifier to identify changes in kidney patterns. When measuring weights and bias values, system training appears in each hidden layer. The multiple layers of the deep belief network further teach the trained features to identify irregular patterns. Effective use of learning and activation mechanisms is a dual training method to effectively avoid kidney disease. Then determine the regression study and distribution of the data. The proposed method is based on deep learning, and the ROIs given by radiologists show promising results in the classification of renal cell subtypes.

This work [6] proposed a workflow to predict CKD status based on clinical data, combining data preprocessing, missing value processing methods, collaborative filtering, and attribute selection. Among the 11 machine learning methods considered, the additional tree classifiers and the random forest classifiers showed the highest precision and smallest attribute deviations. The study

also considered the practicalities of data collection and emphasized the importance of incorporating domain knowledge when using machine learning for prediction of CKD status.

### III. METHODOLOGY

The program code will be written and modeled in MATLAB image processing tools with the help of existing algorithms. The method followed is shown in Figure 1.



**Figure 1. Kidney tumor Prediction System**

#### A. IMAGE DATASET

Image Acquisition Toolbox simplifies the acquisition process by providing a consistent interface between MATLAB and Simulink hardware devices. Collect different sizes of kidney ultrasound image database. It can be a color image or a black and white image. The collected images are used as input for further processing.

#### B. IMAGE PREPROCESSING

Image Processing Toolbox provides a set of reference standard algorithms and workflow applications for image algorithm development, analysis, visualization, and processing. The Image Processing Toolbox application allows you to automate common image processing workflows. You can interactively segment image data, compare image registration techniques, and batch process large data sets. Visualization features and applications let you explore images, 3D volumes, and videos, adjust contrast, create

histograms, and manipulate regions of interest (ROI). In this study, images of the kidneys are provided as input. MATLAB supports dicom images, so the input image is in dicom format. The image processing steps in this document are as follows:

### 1. INPUT IMAGE

Image acquisition is a basic task and very important for any image analysis. In this project, image processing techniques such as grayscale conversion, edge detection, and image segmentation are introduced. All these techniques are applied for the input medical image by using Matlab source code and display the results.

### 2. RGB TO GRAYSCALE CONVERSION

This study was generally focused on gray scale because it is a preferred format for image processing. The given kidney image is converted to grayscale. In order to better understand the gray scale, you can see here using the image representation in MATLAB. The grayscale image  $m$  Pixel and  $n$  pixel represents as Matrix  $m \times n$ . The element value (such as  $\text{img}(m, n)$ ) represents the grayscale intensity of pixels with 0 = black and 1 = white.

### 3. HISTOGRAM EQUALIZATION

The first-order global feature of the kidney image is its grayscale histogram. The grayscale histogram of an image is a graph that lists all the gray levels used in the image on the horizontal axis and the number of pixels at each level on the vertical axis [11]. The grayscale histogram of the image is displayed as the right frame. A grayscale image is usually composed of 256 levels of gray, so the horizontal axis of the histogram ranges from 0 to 255. The vertical axis changes the grayscale according to the number of pixels in the image and the distribution of values. A group of techniques called grayscale histogram modification is used to improve the visual appearance of images.

### 4. BINARIZATION (CONVERSION OF GRAYSCALE TO BINARY)

Binarization is the process of converting each pixel in an image to a bit. The value is specified as "1" or "0" depending on the average value of all pixels. The simplest way to use image binarization is to select a threshold value and classify all pixels above that threshold as white and all other pixels as black. gray levels represent the quantization range in gray image processing. Currently, the most widely used storage method is 8-bit storage. 8-bit gray image has 256 levels of gray, the intensity of each pixel can be from 0 to 255, 0 is being black, 255 being white.

There are two gray levels, 0 is black and 1 is white are binary images, which are often used in medical imaging and are called binary images [12]. Because binary images are easy to operate, images in other storage formats are also converted to binary images, which will be used for enhancement or edge detection. Thresholding gives an easy and convenient method to achieve this binarization on the basis of colors in the foreground and background regions of an image [22].

For the binarization of equalized image a thresholding technique is used as shown below:

Binarized Image  $b_i, j = 255$  if  $e(i, j) > T$  Where  $e(i, j)$  is the equalized MRI image and  $T$  is threshold resultant for the equalized image.

### C. SEGMENTATION

In the image, the unwanted region has eliminated by selecting an interesting area in that image. Useful area in the image is called interested region. After applying the following techniques such as RGB to gray, histogram equalization, then the given kidney image is ready for ROI extraction. So, ROI algorithm is used to eliminate the unwanted region and to get the only required kidney region using ROI function. In ROI, we need only two bean shaped kidney blobs is required for the segmentation. Hence following steps are taken to extract the required region.

- i. Remove the pixels touching the border.
- ii. Remove smaller objects present in the image.
- iii. Extract two largest blobs of an image.
- iv. If any very smaller holes present in the blobs, then fill those holes.

After doing all above procedures, then this image is ready for the image segmentation.

FCM [5] proposed by Bezdek in 1973, is a clustering technique. FCM employs fuzzy partitioning such that data point can belong to all groups with different degrees of membership between 0 and 1. FCM is an iterative algorithm. The purpose of the FCM is to find a cluster center (called centroids) to minimize the functions of non-similarity. The aim of FCM is to find cluster centers (called as centroids) that minimize a dissimilarity function. FCM is employed to segment the required Kidney part for the further image processing. Once we get the required kidney image then we can extract the tumor from the kidney image.

The introduction of fuzzy partitions, the membership matrix ( $U$ ) is initialized randomly according to formula [15].

$$\sum_{i=1}^c u_{ij} = 1, \quad x_j = 1, \dots, n \quad \text{eq. 1}$$

The dissimilarity function, used in FCM is given Equation

$$J(U, c_1, c_2, \dots, c_c) = \sum_{i=1}^c \sum_{j=1}^n u_{ij}^m d_{ij}^2 \quad \text{eq.2}$$

$U_{ij}$  is between 0 and 1

$C_{ij}$  is the centroid of  $i$  cluster

$d_{ij}$  is the Euclidean distance between centroid and  $j$ th data point.

$m \in [1, \infty]$  is a fuzziness parameter.

To reach a minimum of dissimilarity function, there are two conditions. These are given in equation 3 and equation 4.

$$c_i = \frac{\sum_{j=1}^n u_{ij}^m x_j}{\sum_{j=1}^n u_{ij}^m} \quad \text{eq.3}$$

$$u_{ij} = \frac{1}{\sum_{k=1}^c \left( \frac{d_{ij}}{d_{kj}} \right)^{2/(m-1)}} \quad \text{eq.4}$$

Initially the  $U_{ij}$  and the centers of the clusters are randomly assigned, then  $U_{ij}$  is updated in each iteration. The iterative process stops when

$$\|U^{(s)} - U^{(s-1)}\| = \max |U_{ij}^{(s)} - U_{ij}^{(s-1)}| < \varepsilon \quad \text{eq. 5}$$

This algorithm determines the following steps.

- i. Randomly initialize the membership matrix ( $U$ ) that has constraints in equation one
- ii. Calculate centroids ( $c_i$ ) by using equation three.
- iii. Calculate dissimilarity between centroids and data points using equation two.

Stop if its improvement over previous iteration is below a threshold

Step4. Compute a new  $U$  using Equation (4). If condition (5) is False Go to Step 2.

By iteratively update the cluster centers and the membership grades for each data point, FCM iteratively moves the cluster centers to the "right" location within a data set. FCM does not ensure that it converges to an optimal solution, because of cluster centers (centroids) are initialize using  $U$  that randomly initialized. (Equation 3).

By using FCM segmentation you can be able to segment the kidney part which is required to detect the tumor in it. FCM segmentation yields best segmentation result.

### EXTRACT EDGES

Edge detection is the process of quickly finding contrast in image intensity. This process helps in retain the most of the important structural features of the image. In this project, canny edge detection is used to identify the edges of kidney images. It will locate obvious discontinuities in kidney images [16] and helps to preserve important statistical features in kidney images. Canny provides an optimal edge detector [18], which is mainly used for two-dimensional images. The canny operator can give edge information of intensity and direction.

### IMAGE ENHANCEMENT

Medical images require image enhancement, is an image processing category that can provide better visualization and make diagnostic more accurate. The histogram equalization is the best accepted method which is not productive when image contrast differs across the image. AHE prevent this limitation by developing the mapping for each pixel from the histogram[19]. The advantage of Adapthisteq is that it divides the image into small rectangular areas called tiles and adjusts their local histograms to increase the contrast of these areas. This method is also called Contrast Limited Adaptive Histogram Equalization (CLAHE) [20]. Like almost all other MATLAB functions, adapthisteq can be used on a single input (image) and set all other parameters to default values.

Adaptive histogram equalization (AHE) is a computer image processing technology used to improve contrast in kidney images. It is different from ordinary histogram equalization in the respect that the adaptive method computes several histograms and each corresponding to a distinct section of the image and uses them to redistribute the lightness values of the image. It is therefore suitable for improving the local contrast and enhancing the definitions of edges in each region of kidney image. It will improve the brightness of the image. Thus, it enhances the local contrast of the input image and results in better quality for visualization.

#### **D. FEATURE EXTRACTION**

In statistical texture analysis, the characteristics of the texture are calculated based on the statistical distribution of the intensity combinations. Based on the number of intensity points (pixels) in each combination, the statistics are divided into first-order, second order, and higher-order statistics. The Gray Level Co-occurrence Matrix (GLCM) method is a method to extract second-order statistical texture features [21]. This method has been used in many applications. GLCM is a matrix in which the number of rows and columns is equal to the number of gray levels in image G. The Gray Level Co-occurrence Matrix (GLCM) has been used in many works to extract texture information from kidney images. GLCM is the most widely used texture analysis method in biological images because it can capture the spatial dependence of gray values in the image. GLCM is a useful method to improve details. It is often used to defining an image. It is a list of the frequencies of different combinations of pixel brightness values (grayscale) that appear within the image. GLCM represents the frequency of a group of pixels located at the same distance and direction of the displacement vector.

The GLCM features are :

##### Mean

The mean value estimates the value at which the central grouping occurs in the image. The mean value can be calculated using the following formula:

$$\mu = \frac{1}{MN} \sum_{i=1}^M \sum_{j=1}^N p(i, j)$$

Where  $p(i,j)$  is pixel value at point  $(i,j)$  of an image of size  $M \times N$ .

##### Variance

The intensity of the pixels depends on the characteristics of the kidney image. This change can be used to classify tumor, which can be estimated as follows:

$$\sigma^2 = \sum_{i,j} \frac{(x_{i,j} - \mu)^2}{N}$$

##### Standard deviation

The standard deviation  $\sigma$  is the estimated value of the mean square deviation of the gray pixel value  $p(i, j)$  from its mean value. The standard deviation describes the dispersion within a local area. It is determined by the following formula:

$$S = \sqrt{\sigma^2} = \sigma$$

#### Smoothness

Relative smoothness,  $R$  is a measure of gray contrast level, which can be used to set the relative smoothness descriptor. The smoothness is determined by the formula

$$R = 1 - \frac{1}{1 + \sigma^2}$$

Where  $\sigma$  is the standard deviation of the image

#### Energy

The energy of the image is calculated by squaring and summing the pixels in the transformed image, and is given by the following formula:

$$E = \sum_x \sum_y I(x, y)^2,$$

Where  $I$  is the intensity of pixel value at  $x, y$

#### Contrast

Extracted contrast features are used in classification to locate tumor in the image. Contrast information is estimated as:

$$C = \sum_x \sum_y (x - y)^2 I(x, y).$$

#### Entropy

The statistical evaluation of randomness which will characterizes the texture features present in image is said to be entropy and is given by:

$$E_n = - \sum_x \sum_y p(x, y) \log[p(x, y)],$$

Where  $p$  is the probability of occurrence of a particular pixel value.

#### Homogeneity

Closeness of the distribution in pixel elements of ROI in image is computed using homogeneity and is given as:



$$H = - \sum_x \sum_y \frac{p(x, y)}{1 + (x - y)^2}.$$

#### Kurtosis

Estimated kurtosis value can be distinguish between the benign and malignant tumor through peaks and flat probability distribution which is given by:

$$K = \sum_{i=1}^N \frac{(I_i(x - y) - m_k)^4}{(N - 1)\sigma^4},$$

Where  $I(x-y)$  represent intensity of pixel,  $N$  represents the number of samples in circle lines,  $\sigma$  represents standard deviation and  $m_k$  represents the mean of sub-bands. For benign tumor the distribution appears to be flat and for malignant , it appears to be peak.

#### Correlation

Nearby pixels of image are highly correlated which helps in identifying the similar regions. Correlation is estimated as:

$$Correlation = \sum_{i,j} \frac{(i - \mu_j)(j - \mu_j)p(i, j)}{\sigma_i \sigma_j}.$$

#### Skewness

This parameter indicates the lack of symmetry in distribution of pixels. This estimation gives an idea about symmetry and lack of symmetry within ROI in image. Skewness is estimated as:

$$Skewness = \sum_{i=1}^N \frac{(I_i(x, y) - m_k)^3}{(N - 1)\sigma^3}.$$

#### Sensitivity

Ability of a classifier to identify the positive results quantitatively is evaluated:

$$Sensitivity = \frac{TP}{TP + FN}$$

#### Accuracy

Accuracy is the efficiency of classifier in terms of true positive and true negatives indicating the proportion of true results:

$$Accuracy = \frac{TP + TN}{TP + FP + TN + FN}$$

## E. CLASSIFICATION

The support vector machine (SVM) is a binary linear classification whose decision boundary is explicitly constructed to minimize generalization error. If the observed classification is "linearly separable", SVM conforms to a "decision boundary" defined by the maximum margin between the closest points in each class. This is commonly known as the "Maximum Margin Hyperplane (MMH)". The support vector machine is a supervised learning model with related learning algorithms that analyze data and recognize patterns. For each given input, it predicts which of the two categories constitutes the input, making it a non-probabilistic binary linear classifier. From a given set of training samples, each sample is marked as belonging to one of two categories, the SVM training algorithm creates a model and assigns new samples to one category or another. In the proposed method, we use a linear classifier. The best hyperplane is the one that represents the largest separation or margin between two classes. So, we choose the hyperplane to maximize the distance from it to the nearest data point on each side. If such a hyperplane exists, it is called the maximum boundary hyperplane, and the linear classifier defined by it is called the maximum classifier.

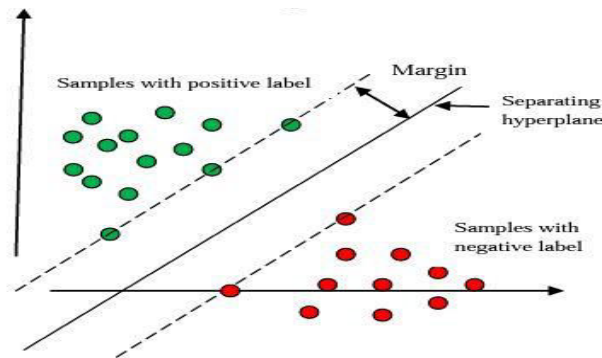
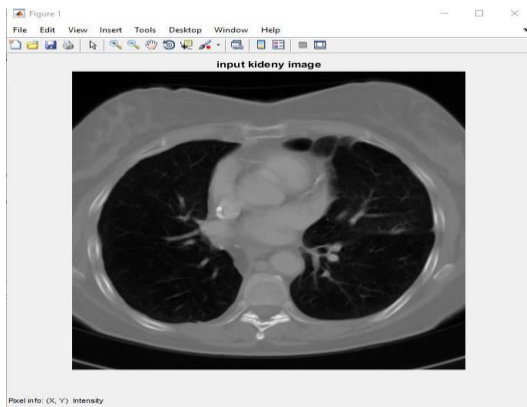


Figure 2. SVM

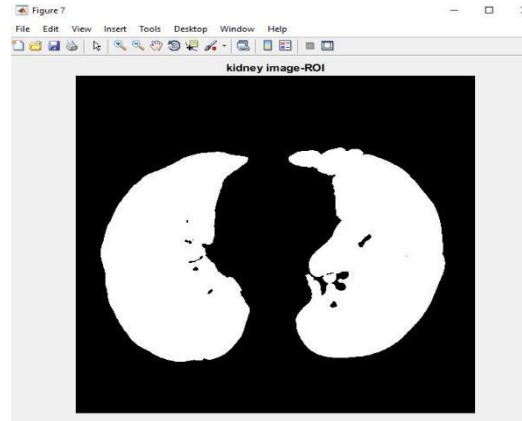
The mixed data of kidney CT images are provided as input. In SVM algorithm the input images are trained, and the results are predicted by tuning the various parameters. Input images undergo feature extraction. At the training the various SVM parameters are tuned, and then the predictions are made using the hyper plane of SVM. In the testing phase the tumor in the kidney is classified as benign or malignant tumor. Initially the input images are pre-processed. Later SVM operation takes place. The cancer images undergo testing processes and estimates whether the tumor in image is malignant or benign.

## IV. EXPERIMENTAL RESULTS

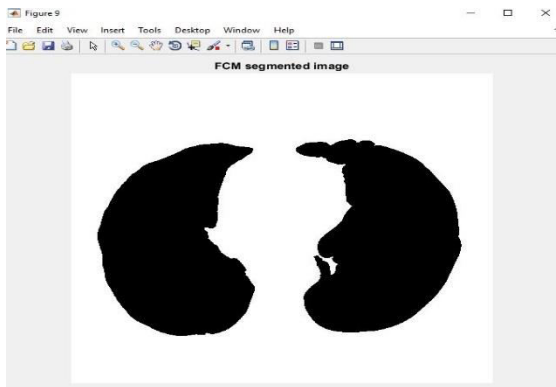
The data set used for study of the proposed system consists of kidney Dicom images. The experimental result is shown below:



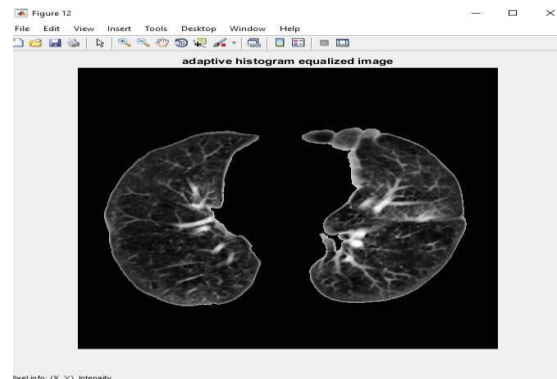
**Figure 3. Input kidney image**



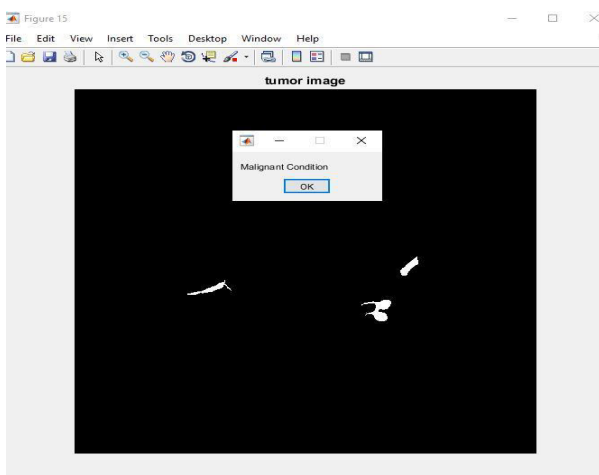
**Figure 4. ROI image**



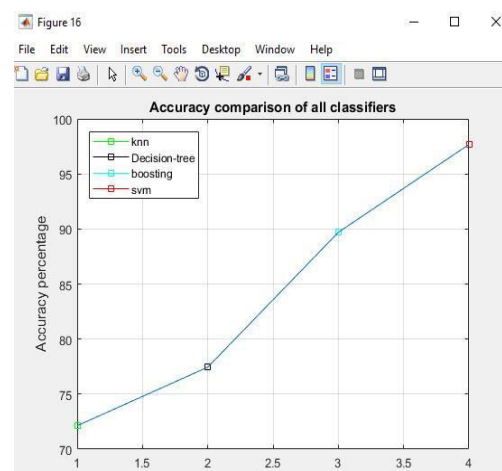
**Figure 5. FCM segmented image**



**Figure 6. AHE image**



**Figure 7. Tumor image**



**Figure 8. Accuracy of Classification**

## V. CONCLUSION

Proposed system helps physician to extract the tumor region and evaluate whether the tumor is benign or malignant. The CT image is used in this paper. SVM provides the accuracy of 97.644%. The accuracy of system can be improved if training is performed by using a very large image database. The different basic image processing techniques are used for prediction purpose. In the first phase the image is preprocessed. In second phase Kidney region is separated from surrounding anatomy. In next phase ROI is extracted, after ROI extraction, then FCM is used to segment the kidney region and then features extraction is performed by GLCM. Finally with the obtained texture features classification is performed to detect the occurrence of tumor.

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