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# Comparative Analysis on Performance of Different Classification Models for Accurate Liver Tumor Segmentation and Classification



*Abstract:* - One of the most common cancer disease is the occurrence of tumors in liver organ. Hepatocellular carcinoma is one of the most common type of cancer found in liver organ which causes most mortality in the world. The imaging technique mostly used to detect these type of cancer is Computed Tomography (CT) scans. In this paper we have proposed computer aided diagnostic system for detection of tumors in liver organ and its classification model to grade the tumor stage in the liver organ on the basis of tumor volume. We have made a comparative analysis of the different classification model used for this proposed model. The classification techniques used are SVM, KNN, Random Forest classifier, Naïve Bayes classifier and linear discriminant analysis. A total of 11 patients CT scans are considered for this study and real world datasets are collected from a diagnostic center in Guwahati, Assam. Each patient dataset consists of 800 to 1200 CT images captured at different contrast levels to enhance the quality of the image captured. The analysis of the classification model is done by considering the accuracy of the model and volumetric error overlap(VOE). It has been found from the result analysis that SVM outperforms all other classifiers in terms of accuracy and VOE.

*Keywords:* ROI, Segmentation, tumor, CT image, SVM, KNN, Random Forest classifier, Naïve Bayes classifier, linear discriminant analysis.

#### Introduction:

Hepatocellular carcinoma is one of the deadliest disease in recent times [1]. Image segmentation plays a crucial role in the image guided detection and diagnosis of liver tumors in medical field. Among all imaging modalities, CT scan is widely adopted for this diagnosis because of its high imaging speed, excellent spatial resolution, and relatively low cost. CT images are two-dimensional slices of specific human body organs. Tumors in CT images appear as a continuous series. The difference in intensity between normal and tumor tissues in CT images aids in the detection and classification of these abnormalities. Segmentation in abdominal computed tomography (CT) images is particularly challenging due to overlapping organs that share similar intensity ranges and are located close to each other anatomically. Consequently, accurately defining the boundaries of organs, vessels, and lesions cannot be achieved with simple threshold-based segmentation methods. There are no clear boundaries defined which differentiate the organs in the abdomen. Hence image segmentation is performed to identify the characteristic region of interest (ROI) from the CT scan image analyzed. The ROI is characterized by position, texture, volume and spatial relation to other objects in the image. Capturing images in different contrast increases the characterization of the images. Therefore, it is best to use contrast enhanced computed tomography (CECT) images for the liver tumor detection and treatment monitoring [2].

The raw CT images might consist of some unwanted noise elements in them [3]. In order to make them noise free, a preprocessing step is followed before the actual segmentation of the image takes place. This method helps to enhance the quality and features of images. This process in return makes it easier for segmentation algorithms to accurately identify and segment the regions of interest. So preprocessing techniques are crucial for improving the accuracy of segmentation algorithms. One of the most used technique in medical imaging is median filter. Median filter replaces each pixel's value with the median value of the neighboring pixels to remove salt-and-pepper noise while preserving edges. Edge detection and preservation serves as a valid point to use it in detecting the ROI in the abdomen scan. Another technique known as gaussian filter uses a gaussian function to smooth the image and reducing random noise from the image. There are numerous other preprocessing techniques which help in contrast enhancement, image resizing and rescaling, edge enhancement, image restoration and intensity normalization, to name a few [2,4]. The preprocessed images are then segmented using image segmentation technique to identify the ROI on the basis of tumor volume. Marker controlled watershed transform [5,6] is implemented to segment

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the tumor tissues from the entire liver organ. This method has a comparatively low computational cost and it also preserve the boundaries of the ROI. According to the RECIST standard [7], the maximum axis of the tumors must first be measured. Only tumors with an axis greater than 10 mm should be considered, while smaller tumors should be disregarded. Hence all the tumors with volume less than 10mm are considered as benign tumors while tumors with 10mm volume or more are categorized as malignant tumors. After the image has been segmented, the next process is feature extraction. There are many feature extraction techniques which contribute to the identification of some important features which effectively and efficiently characterize an image on the dataset [8,9]. The main idea here is to implement an algorithm which extracts certain important attributes which are more than enough to define the image. Finally, the pool of extracted features is fed into the classifier for classification of the components into tumored or unhealthy tissues and untumored or healthy tissues.

## Literature Review:

Many researchers have used various classification model to efficiently categorize the tumored cells and untumored cells present in a specified organ of a human body. A Krishan and D Mittal [10] proposed a methodology to identify the presence of tumor cells in the liver organ using CT images. They have classified the cells into tumor and normal classes. Further they had also categorized the tumor classes into Hepatocellular Carcinoma and Metastases. They combined six different classifiers to form a multi-level ensemble model which classifies the tumored tissues with 88.98% accuracy.

In another research paper [11], authors implemented a two-stage random forest-based classifier to categorize liver tumors as benign, intermediate, or malignant cells. Moreover, they had also proposed a technique to grade the tumor existence as LR1, LR2,LR3,LR4 and LR5 achieving an accuracy of  $88\% \pm 5\%$ ,  $85\% \pm 2\%$ ,  $78\% \pm 3\%$ ,  $83\% \pm 4\%$ , and  $79\% \pm 3\%$  respectively.

M Rela et. al. [12] proposed different machine learning algorithms to classify the tumor tissues into liver abscess(LA) and Hepatocellular Carcinoma(HCC). The techniques used for classification are SVM, Decision Tree, KNN, NB and ensemble model. It was found that SVM outperforms all the other classification model with an accuracy of 85% to predict the tumor tissues correctly whereas DT and ensemble had the lowest accuracy rate.

P Devi and P Dabas [13] proposed a comparative analysis of two classification model for liver cancer classification using CT images. They used back propagation neural network and support vector machine algorithm to classify between benign and malignant tumors. It was found from their research that BPNN with an accuracy of 73.23% outperforms SVM which gave an accuracy of 63.11%.

In another research study [14] for extraction of texture features of tumor cells in liver organ using computed tomography, SVM was used to predict the treatment of tumor. Once the texture features are extracted from the tumor image, it was combined with the medical records of the patient. Thereafter, on the basis of the dataset integrated, treatment predictions are done which comprises of surgery, radio frequency ablation, transcatheter arterial chemoembolization, Percutaneous Ethanol Injection if the tumor is malignant, and no treatment if the tumor is benign.

Authors in [15] proposed a convolutional neural network(CNN) to implement a deep learning system to classify liver tumors using magnetic resonance imaging(MRI) technique. The accuracy of this technique was very satisfactory as with unenhanced MRI images it was capable of categorizing the benign and malignant tumors effectively.

Authors in [16] proposed a two deep encoder-decoder convolutional neural networks (EDCNN) to segment and classify the liver tumor and lesions accurately.

## **Materials and Methods:**

In order to implement these classification models, image preprocessing and segmentation techniques are implemented first using MATLAB R2019a and then classifier is implemented using Python programming language. A median filter is applied as a preprocessing step to remove unwanted noise from the images. Thereafter, segmentation of the CT images is done using segmentation algorithm. The important and necessary

features are extracted from the organ using various feature extraction algorithms. Finally, the classification models are trained and tested to validate the comparative analysis of the various classifiers used. The dataset comprises real-time data of patients with liver tumors, collected from Primus Diagnostics Centre, Guwahati, Assam. CT scans are used to evaluate the proposed model, capturing the patient tumor images at different enhancement phases. The CT images used in this research have a resolution of 1024 x 512 pixels. A total of 11 patient data are collected and each of the patient CT scans are captured at different contrast levels and hence the total number of CT images of each patient ranges from 800 to 1200 CECT images. The total number of CT images used for this research is 10488 CT scans.

The outcome of the feature extraction algorithms is fed as an input to the classification models. Each of the classification model is trained for a specific set of datasets and the test results are validated. This process is computed using Python programming. The classification models used for this research are namely SVM, KNN, Random Forest classifier, Naïve Bayes classifier and linear discriminant analysis.

## **Proposed methodology:**

The proposed model execution starts with the acquirement of the contrast enhanced computed tomography scans of the patients. The clinically acquired images is ought to contain certain noisy elements within it. These disturbances might affect the working of the segmentation process and the classification model might generate more false predictions. Hence it is crucial to enhance the quality of the scans before we start the process of image segmentation. In our research, we have used a nonlinear statistical filtering technique known as the median filter, to eliminate the unwanted noisy components from the CT scan. Median filter works as a smoothing technique and it helps in preserving and enhancing the edges of the ROI. Hence, it is widely used in medical image preprocessing.

# Median Filter:

This filtering method replaces the current pixel value with the median value of pixels in the surrounding region [17,18].

- It first constructs a cumulative histogram for the neighboring region.
- It then identifies the first index that surpasses half the total number of pixels in the histogram. Instead of computing the actual histogram, this method iteratively narrows down the histogram range that contains the median value.
- In each iteration, the current valid range is split into two halves, and the half with the greater number of pixels is selected for the next round.
- This process repeats until the range converges to a single bin.

For instance, 8-bit image (256 bins) needs only eight iterations to find the median.

After enhancing the images, the next crucial step is to segment the images using segmentation algorithm. There are numerous segmentation techniques used over couple of years to detect and identify the area of interest from a specific component in the image. If we consider the medical image processing field, a single segmentation method is not sufficient enough to accurately divide the image into multiple segments and detect the region of interest, which can be a cancerous cell, tumor tissues or may be lesions. Hence we need to choose an algorithm which would accurately extract the tumors from the liver which are of the same intensity levels. The decision making process regarding which algorithm to consider still remains a challenging task. In this study we have used Marker controlled watershed transform for segmentation. The main idea behind this usage is that this technique overcomes the drawback of oversegmentation found in some segmentation algorithms. It can also extract ROI with boundaries having low contrast [19].

# Marker controlled watershed transform:

- It starts with defining a marker function which predetermines the number and possible localization of the region of interest.
- Next we compute the foreground and the background markers. Foreground are of dark intensity signifying the objects to extract and background are of low intensity signifying the neighboring organs and the normal tissues.

- We then recalculate the marker function so that it only has minima at the foreground and background markers.
- Finally, we compute the watershed transform with the new marker function [20].

The next work is to extract important but essential features from the segmented image. For our research we have used three feature extraction techniques namely, Gray level co-occurrence matrix (GLCM) [21,22], Gray Level Run Length Matrix (GLRLM) [21,22] and Local binary pattern (LBP) [23,24] feature extraction algorithm. The idea behind use of these algorithms is to minimize the complexity of the large dataset which represents the characteristics of an image because large datasets overfits the classification model used. The number of features extracted from GLCM, GLRLM and LBP are 19, 7 and 59 respectively. A total of 85 features are extracted and fed into the different classification model to classify the tumored and untumored tissues in the liver organ.

# Classification Model:

Execution of a classification model in medical image processing requires that we carefully analyze and extract the dataset which would characterize the images, train the model with appropriate predetermined classes and then test the model with the new dataset and validate their classes. Five different classification models are trained and tested and a comparative analysis of their performance in terms of the model accuracy is given as an outcome of this research. The clinical dataset used in all the models are the same with a total of 10488 CT scans and same set of extracted features are fed into the classifiers. Each CT scan has 85 features extracted from it to give it as an input to the classification model. SVM, KNN, Random Forest classifier, Naïve Bayes classifier and linear discriminant analysis are used for this study [12].

SVM is a statistical approach to classifying complex datasets on the basis of a hyperplane. This hyperplane is created by a set of points which is nearest to the support vectors.

K Nearest Neighbor does not require any preprocessing before the segmentation process. It is the process of segmentation where the input y is assigned to the class that is most frequently represented among the K nearest neighbors.

Random Forest is a classifier that consists of multiple decision trees created from various subsets of the dataset. It enhances predictive accuracy by averaging the results of these trees. This method relies on ensemble learning, which combines multiple classifiers to tackle complex problems and boost model performance. The following steps outline the Random

Forest algorithm:

- Randomly select samples from the given data or training set.
- Construct a decision tree for each training subset.
- Aggregate the results of all decision trees through voting.
- The final prediction is determined by selecting the most frequently voted result.

In naïve bayes classifier, the datasets undergo density estimation. Given the class, the algorithm applies Bayes' theorem, assuming that the predictors are conditionally independent. NBC typically provides posterior distributions that are resilient to biased class density estimations, particularly when the posterior is 0.5 (the decision boundary). NBC assigns observations to the most likely class.

Linear discriminant analysis functions by finding a linear combination of features that differentiates between two or more classes of objects or events. It achieves this by projecting multi-dimensional data into a single dimension, making it easier to classify. Consequently, LDA is often referred to as a dimensionality reduction technique. This flexibility allows LDA to be applied to multi-class classification problems as well.



Figure1. Steps involved in proposed methodology

# **Results and Discussion:**

The classification models are trained and tested with total 10488 datasets consisting of CT scans of liver with tumored cells as well as healthy cells. The performance of these models are calculated on the basis of two statistical parameters, accuracy and volumetric overlap error(VOE). Accuracy of the model is calculated using the formula:

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

While volumetric overlap error(VOE) is calculated by using the formula:

$$VOE = 1 - \frac{TP}{TP + FP + FN}$$

where,

TP means true positive which predicts tumor tissues correctly

TN means true negative which predicts untumored tissues correctly

FP means false positive which predicts tumor tissues incorrectly

FN means false negative which predicts untumored tissues incorrectly

The table 1 determines the accuracy and VOE in percentage of all the classifiers executed in this research. It can be analyzed from the results that SVM outperforms all the other models in terms of accuracy with 92% accuracy. While KNN, Random Forest classifier, Naïve Bayes classifier and linear discriminant analysis gives an accuracy of 77%, 83%, 61.5% and 77% respectively. Also when we analyze the VOE, SVM has the least volumetric overlap

error with 8.21% followed by RN classifier with 17.1%, KNN and LDA with 23.07% and NB classifier with 38.4%. Figure 2 determines the statistical representation of the performance analysis of all the classifiers.

Classification Model	Accuracy	VOE
Support Vector Machine	92%	8.21%
K-Nearest Neighbor	77%	23.07%
Random Forest classifier	83%	17.1%
Naïve Bayes classifier	61.5%	38.4%
Linear discriminant analysis	77%	23.07%



Table1. Accuracy and VOE of different classification models



Figure 2: Performance Analysis of SVM, KNN, Random Forest classifier, Naïve Bayes classifier and linear discriminant analysis on the basis of (a)-(b) Accuracy (c)-(d) VOE

#### **Conclusion:**

The proposed methodology uses five classifiers for performance analysis on the basis of accuracy and VOE. There are a total of 10488 CT scans used as a dataset and each image is being represented by 85 features which has been extracted using GLCM, GLRLM and LBP feature extraction techniques. It has been concluded from the research that classification of the tumors into benign and malignant has been most accurate with minimum error in case of support vector machine. This methodology can be used by the medical experts for detection of tumors in patients and plan the treatment and diagnosis of the patient accordingly. Thus it can be concluded that support vector machine can increase the effectiveness and efficiency of detection of ROI in medical imaging.

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