International Journal of Engineering Trends and Technology
ISSN: 2231–5381 / https://doi.org/10.14445/22315381/IJETT-V72I8P105

Volume 72 Issue 8, 37-43, August 2024

Original Article

Stage Identification of Malignant Liver Tumors Using Multiclass Classifiers

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Received: 18 December 2023 Revised: 15 June 2024 Accepted: 31 July 2024 Published: 28 August 2024

Abstract *- The work here focuses on the stage-wise classification of liver tumors identified as malignant based on appropriate features. Liver tumors normally progress from stage one to stage four, which indicates the severity of the disease. It is very much essential to identify the stage of cancer to proceed with the treatment by domain experts. In this work, to carry out the stage identification process after recognizing malignant tumors present in the liver, Histogram of Oriented Gradients (HOG) features have been selected and extracted. Prior to this, segmentation of tumors from a liver, validation of tumors and classification of tumors as benign or malignant was carried out. Out of 2640 scans, 1384 scans were classified as containing malignant tumors, and these tumor scans were fed as input to the multiclass classification algorithms such as Random Forest, Naïve Bayes, K-Nearest Neighbor and Convolutional Neural Network to identify stages. The performance of all these classifiers is measured with parameters such as Accuracy, Precision, Recall and F1-Score. It is observed that the CNN has performed better with respect to all parameters. The results obtained are discussed and tabulated.*

Keywords *- Liver tumors, Cancer stages, Accuracy, Precision, Recall, F1-Score.*

1. Introduction

Liver cancer is one of the leading causes of death. To reduce the mortality rate, it is required to identify the stages of cancer and proceed with the necessary treatments. To perform this, it is required first to extract the liver region from the abdominal CT image and then segment the tumors. The segmented tumors are then classified as benign or malignant. The benign tumors are non-cancerous, and malignant tumors are cancerous, and then it is a prerequisite for treatment to identify the stages of cancer of the malignant tumors. Figure 1 shows the original input CT image, preprocessed image and segmented liver. Figure 2 shows the liver image as input, segmented and validated tumors. Figure 3 shows the sample validated tumors that are used for classification as benign or malignant. Later, only malignant tumors are used for identification of stages and this is the main focus of this work.

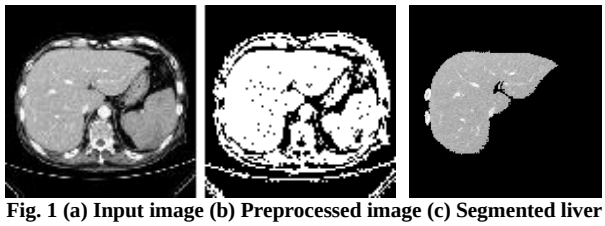

Fig. 1 (a) Input image (b) Preprocessed image (c) Segmented liver

Fig. 2 (a) Input image (b) Segmented tumor (c) Validated tumor

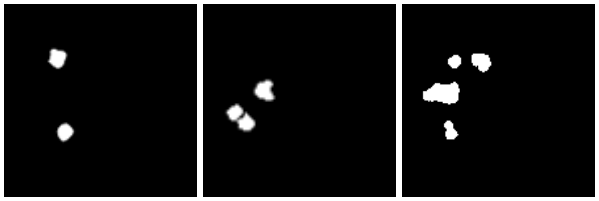

Fig. 3 Sample validated tumors

In this proposed work, Histogram of Oriented Gradients (HOG) are considered as features and fed as input to the machine learning classification algorithms, whereas the CNN model automatically extracts the features and carries out the classification. The HOG is a feature descriptor which focuses on the shape of an object in an image i.e., tumors in this case. The gradients are the minute changes in the x and y directions of the image. It calculates the gradient for every pixel in an

image. The HOG feature descriptor decomposes an image into small squared cells, computes histograms of oriented gradients in each block, stabilizes the result using a block-wise form, and returns a descriptor for each cell. It also counts the occurrences of gradient orientation in confined slices of an image.

The stage of cancer indicates how distant it has spread into nearby tissues or additional parts of the body. The various stage identification methods are implemented to identify and classify the cancer stages. Some of the multiclass classification algorithms such as Random Forest (RF), Naïve Bayes, K-Nearest Neighbour (KNN) and Convolutional Neural Network (CNN) classifiers are implemented, and it has been discussed in this paper. The outline of the paper takes in related work, methodology, results and discussions, and conclusions.

2. Related work

The research work carried out with respect to various segmentation and classification techniques is discussed here. Many imaging techniques like Magnetic Resonance Imaging (MRI), Positron Emission Tomography (PET), Ultrasound (US), Computed Tomography (CT) and so on are available [1]. A human liver typically weighs about 1.5 kg and measures about 15 cm in width [2]. The liver's primary functions are bile production and excretion. It also filters the blood from the digestive strip, and later, it is distributed to the remainder of the body. It also detoxifies the chemicals and metabolizes medicines. The liver also generates proteins which is necessary for the blood clot and also for further functions. A novel CNN is designed and trained on 34 patients' MRI data and has achieved 83% accuracy [3].

The liver tumor classification using GoogleNet has gained an efficient classification accuracy of 93.63% [4]. The CLAHE method [5] has been used to classify the cancer as benign or malignant and has achieved an accuracy of 97%. The benefit of the level set method [6] is that it is robust to topological variations of the object. The level set method, with its firmness and topologically unrelated nature, resolves the problem of splitting the curvature and joining of curvatures. The energy function makes the level set points to reach the object of interest and is associated with the curve defined in an image. The superpixels (grid) are an image area which is well aligned with intensity edges and is generated as a cluster of similar intensity pixels [7]. The superpixels share similar visual properties, and this technique works on a group of pixels rather than a single pixel. Some K numbers of superpixels are generated, and cluster centre S for each superpixel are computed. The gene expression with DNA methylation data is combined and produces a merged system where the stages of KIRC (Kidney Renal Cell Carcinoma) are identified in a better way. The network-based LASSO Label Prediction (NLLP) [8] method is used to predict the KIRC stages. An accuracy of 85.2% is achieved for the KIRC cancer stage prediction using the fused network. In [10], 160 evaluable events arose in 48 patients during the 4-year continuation. The overall survival of the cohort was 7.03 years. Comparative survival analysis showed the beneficial effect of DC vaccine beyond 2 years from initial diagnosis (HR = 0.53, P = .048) or in patients with disease control (HR = 0.16, P = .00053). A trend for synergistic effect with metronomic cyclophosphamide and/or vinblastine was indicated (HR = 0.60 P = .225). A strong synergistic effect was found for immune checkpoint inhibitors (ICIs) after priming with the DC vaccine (HR = 0.40, P = .0047)

The automatic classification methods [10] are essential to classify the identified liver tumors as benign or malignant by extracting certain properties from tumor areas. A hybrid strategy in which the liver shape model is constructed from different ground truth data consists of three steps: i) Statistical Shape Model (SSM) subspace initialization by intensity and gradient profile, (ii) localization of the liver-shaped model in CT utilizing 3-D generalized Hough Transform (iii) employing graph theory to alter the shape model for changing the liver edge using an optimal-surface-detection approach. A Statistical Shape Model (SSM) for liver segmentation has been proposed, which is based on a cubic Hermite mesh with a small number of elements. The proposed technique has achieved 92.3% JSC [11].

In [12], This study proposes a sufficient method for liver and tumors segmentation from CT images using a hybrid ResUNet model. The two overlapping models were used in this study to segment the liver and for Region of Interest (ROI) assessment. Based on the experimental study, the accuracy for liver segmentation was found to be approximately 99.55%, 97.85%, and 98.16%.

The textural information extracted from each suspicious tumor in CT abdominal images was used to train the Probabilistic Neural Network (PNN) [13] to classify the tumor. In [14], The try is to progress the existing cancer detection techniques using DCNN by filtering out malignant CT scans from the medical dataset and segmenting those images for stage identification. Segmentation is done using UNET++ architecture and stage recognition is done by taking into consideration the "size" (T) parameter from the internationally accepted standard named "TNM staging" for classifying the spread of each malignant nodule as T1-T4. An accuracy of 99.83 % is achieved in lung cancer classification using VGG-16.

A few of the classification algorithms [15], like Support Vector Machine, Decision Tree, K - Nearest Neighbor, Artificial Neural Network and Convolutional Neural Network (CNN), are discussed, and a comparative study shows that CNN is the more efficient classification algorithm. The multilayer perceptron is used to classify the objects. The textural information obtained was used to train the

Probabilistic Neural Network (PNN) [16] to categorize the tumor. The Back-Propagation Neural Network (BPNN) [17] and Support Vector Machine (SVM) to perform the classification of liver cancer is carried out. The comparative result shows that the BPNN classifier has achieved an accuracy of 73.23%, which outdoes the SVM classifier, which achieves 63.11%.

The multilayer perceptron and the C4.5 decision tree algorithms successfully detected the lesion with 89.15 percent accuracy and 95.02 percent accuracy, respectively, using 123 CT scan images [18]. The convolutional layers in a Convolutional Neural Network (CNN) apply learned filters to input images and follow with max pooling in a systematic manner to create feature maps [19]. The automated extraction of essential features in deep learning techniques has contributed much towards gaining efficient classification accuracy [20].

In medical image processing, removing unwanted noise from an image is critical. Because the edges are crucial for visual appearance and edge recognition techniques, noise removal with edge preservation will be an added benefit. The Weiner filter is used to remove to noise in the images and apply morphological operations to segment the required image [21].

The GLCM textural features are obtained that exist in the tumor and non-tumor regions. The SVM is utilized to categorize the tumors based on these characteristics [22]. The K-Nearest Neighbour algorithm is a supervised learning technique that has been applied in data mining, pattern recognition, classification and other applications. The authors of the research paper have extracted ACHLAC features and used a KNN classifier to classify the data [23]. In [24], Biomarkers improve drug development and clinical trials by identifying appropriate patients and accelerating the endorsement method. A range of biomarkers appropriate for cancer recognition and analysis, such as imaging-based diagnosis (CT, SPECT, MRI, and PET), blood-based biomarkers (proteins, genes, mRNA, and peptides), cell imaging-based diagnosis (needle biopsy and CTC), tissue imaging-based diagnosis (IHC), and genetic-based biomarkers (RNAseq, scRNAseq, and spatial transcriptomics) are discussed.

3. Methodology

The malignant tumors are classified into any one of the four stages by applying NB, RF and KNN classifiers. Later, CNN is also used for the same purpose.

3.1. Naïve Bayes Classifier

Naive Bayes is a type of classifier that makes use of Bayes Theorem. It calculates probabilities for every single class, which finds the possibility that a given input belongs to a particular class. The class that has the maximum probability value is considered to be the most probable one. Naive Bayes is the probability model where the test instance that is to be classified is represented by a vector $x = (x_1, x_2, \ldots. x_n)$ containing some n features. The posterior probabilities with respect to all the class labels, that is, P(Stage 1|x), P(Stage 2|x), P(Stage 3|x) and P(Stage 4|x) has to be computed. The Bayes theorem can be used where the posterior probability P(S|x) is calculated by taking the product of prior probability and class conditional probability P(x|S) with respect to each class label as given in equation (1).

$$P(S|x) = P(x|S).P(S) \tag{1}$$

The prior probabilities of all the class labels are estimated by estimating the ratio of training data of each class and the total number of training data as shown in Equation (2).

$$P(S) = \frac{y}{N} \tag{2}$$

Where y represents the total number of training data of each class label and N represents the total number of training data. The class conditional probability is calculated by taking the product of the conditional probability of mean and variance of all the feature values of all the features with respect to each class label, as shown in equation (3).

$$P(x|S) = \prod_{i=1}^{n} P(x_i|S) \tag{3}$$

Where, x_i represents n features of test instance x.

Finally, the posterior probabilities for each class label using Equation (1) are computed and the new instance is classified to the class label for which the posterior probability is greater.

Algorithm 1: Naïve Bayes Classifier

Step 1: Feed malignant tumor images as input.
Step 2: Extract HoG features.
Step 3: Feed the extracted features into Naïve Bayes classifier model.
Step 4: Find the sample mean and variance of the feature vectors with respect to each class label of the training set.
Step 5: Prior probability of each class label is computed.
Step 6: Next, the posterior probability of the test dataset with respect to all class labels is computed with the help of values computed in Step 4.
Step 7: Combine prior probability and posterior probability values and compute conditional probability values for each class labels.
Step 8: Naïve Bayes classifier model classifies the test dataset to the class label for which the condition probability value is higher.

3.2. RF Classifier

Random Forest is a classifier that contains several decision trees on different subsets of the given dataset. As a substitute for relying on one decision tree, the random forest takes the output from each tree, and based on the majority votes, classification is done. The greater number of trees results in higher accuracy and prevents the problem of overfitting. The RF is an ensemble learning method which makes use of Bagging and Boosting.

The bagging combines the results of multiple models, but if all the models are constructed using the same dataset, then it is of no use. So, another solution under bagging is to use Bootstrapping, where a sampling technique is used, which creates subsets of datasets with replacement. The bagging will make use of these subsets, and different classifier models will be created. The final prediction is made by combining the predictions of all these models. Boosting is an ensemble method that tries to build a strong classifier from a large number of weak classifiers.

Algorithm 2: RF Classifier

Step 1: Read malignant tumor images as input.
Step 2: Extract HoG features from the malignant tumor dataset.
Step 3: Input feature vector to RF model.
Step 4: The model randomly samples the training data and selects a subset of features.
Step 5: Then, the model constructs many decision trees.
Step 6: The RF model predicts the class label based on majority voting.

3.3. KNN Classifier

The KNN classifier finds the similarity between the feature vectors of the new instance and the existing one and places the new instance in the category that is most similar to the existing categories. The similarity is identified by computing Euclidean distance using equation (4), where q and g are two feature vectors. The target distance value is set to 0.09, where if the distance is less than or equal to the set value, then the similarity could be found.

$$ED(q, g) = \sqrt{\sum_{j=1}^{n} (f_j(q) - f_j(g))^2} \quad (4)$$

Algorithm 3: KNN Classifier

Step 1: Read malignant tumor images as input
Step 2: Extract HoG features from the malignant tumor dataset.
Step 3: Input feature vector to KNN classifier.
Step 4: The classifier gets trained by learning the features.
Step 5: The classifier computes the Euclidean distance between every test image and training image.
Step 6: The classifier predicts the class label based on a smaller distance.

3.4. CNN Model

The convolutional layers in a CNN apply learned filters to input images and follow with max pooling in a systematic manner to create feature maps. The input images of size 224x224 are convoluted using 64 filters of size 3x3 and are followed with max pooling using a 2x2 filter of stride 2. The resultant images are convoluted using 256 filters and are followed with max pooling. Again the resultant images are convoluted using 128 filters and are followed with max pooling. Each convolution makes use of the ReLU activation function and Adam optimizer with a learning rate of 0.001. The output of the max pooling layer after the last convolution layer is flattened and fed into the fully connected layer, which comprises 5000 neurons. As the model is built for multiclass identification, the softmax activation function is used in the last layer. The fully connected layer is connected to the softmax function, which is used to perform multiple classifications as the output of the model is to predict one among four stages of cancer.

Algorithm 4: CNN

Step 1: Convolute the input images using 64 filters of size 3x3.
Step 2: Apply the ReLU activation function.
Step 3: Perform Max Pooling with stride 2 using a 2x2 filter.
Step 4: Repeat Steps 1 to 3 using 128 filters.
Step 5: Flatten the output obtained to form a feature vector.
Step 6: Connect feature vectors to the Fully Connected (FC)layer.
Step 7: Finally, fed the output of the FC layer into the softmax function to perform classification.

4. Results and Discussions

The performance of Naïve Bayes, RF, KNN and CNN cancer stage identification methods are measured using Accuracy, Precision, Recall and F1-Score metrics. The green color caption represents the correct prediction where, and the red color represents the wrong prediction. The sample output images obtained after applying Naïve Bayes, Random Forest and KNN classifiers are given in Figures 4, 5 and 6, respectively.

From Figure 4, it is observed that, stage 1 in green color indicates that it is correctly identified as stage 1. However, stage 1 in red color indicates the wrong prediction. Similarly, we have to interpret other scans as well, given in Figures 4, 5 and 6. Based on the results obtained, all models with respect to metrics have been tabulated by considering all scans.

The sample output images obtained after applying Random Forest are shown in Figure 5. The sample output images obtained after applying the KNN classifier are shown in Figure 6. The training and validation accuracy of the CNN model is shown in Figure 7. The model is trained for 30 epochs and has achieved an average training and validation accuracy of 96% and 80%, respectively.

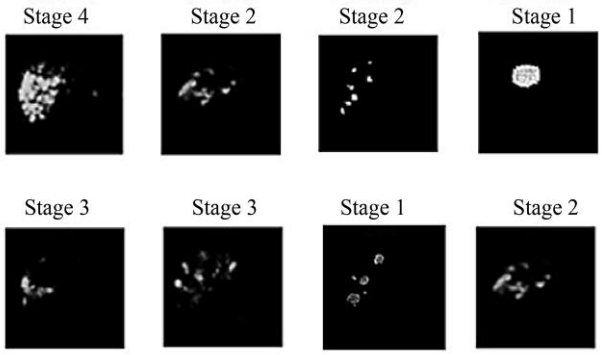

Fig. 4 Sample output of Naïve Bayes classifier

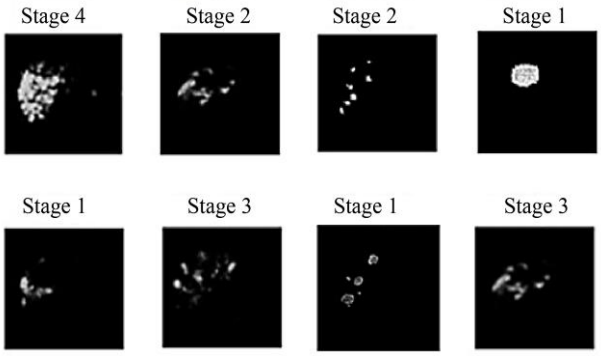

Fig. 5 Output of random forest classifier

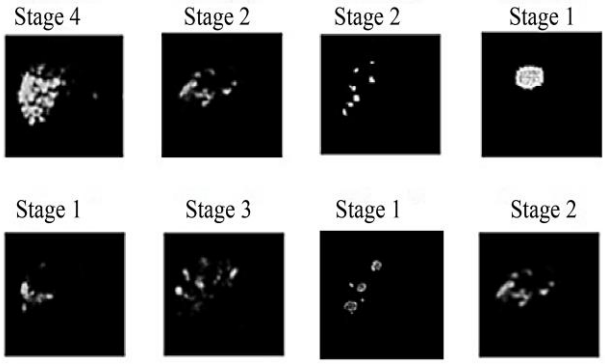

Fig. 6 Output of KNN classifier

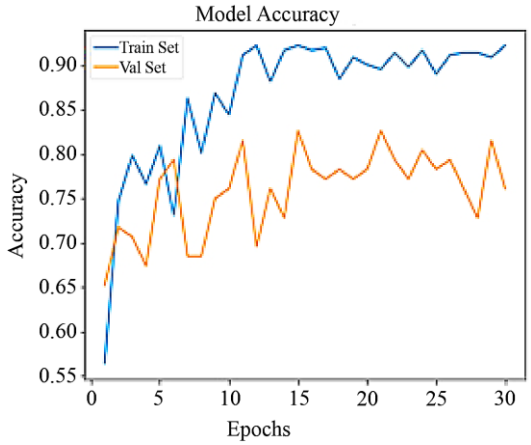

Fig. 7 Training and Validation accuracy of the CNN model

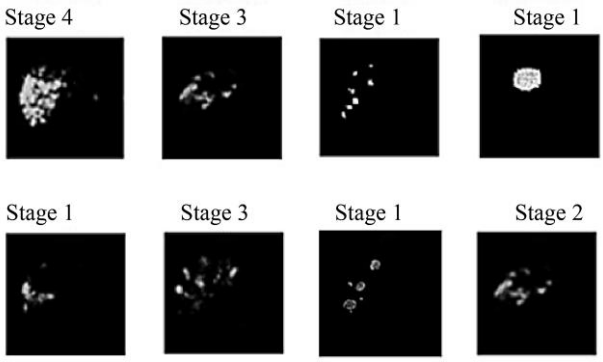

Fig. 8 Output of CNN model

Table 1. Self-relative study

Sl. No.	Method	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)
1	Naïve Bayes	84.05	82.98	83.48	83.22
2	Random Forest	85.50	82.96	82.82	82.88
3	KNN	86.95	86.33	86.25	86.28
4	CNN	90.94	90.51	90.48	90.64

This model has given better training and testing accuracy of 96% and 90.94%, respectively. The sample output images obtained after applying the CNN model are shown in Figure 8. The results obtained after the completion of all the methods are given in Table 1. Here, it is observed from a self-relative study that the CNN model has given better results of 90.94%, 90.51%, 90.48% and 90.64% with respect to Accuracy, Precision, Recall and F1-Score, respectively. The CNN model, compared to the KNN classifier, shows an improvement of 3.99%, 4.18%, 4.23% and 4.36% with respect to Accuracy, Precision, Recall and F1-Score, respectively. The graphical representation of the same is shown in Figure 9.

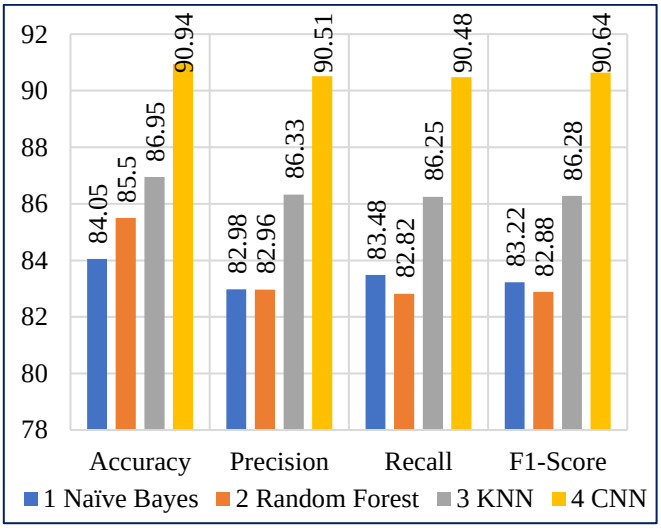

Fig. 9 Graphical representation of self-relative study

5. Conclusion

This paper focused on the identification of cancer stages from the extracted liver malignant tumors. The Naïve Bayes classifier, Random Forest classifier, KNN classifier and CNN model were used to identify cancer stages. This was carried out by extracting HOG features and these were fed as input to the proposed classifiers except CNN. The CNN extracted features on its own and classified the tumors stage-wise. The performances of all the above-discussed techniques have been evaluated and tabulated with respect to parameters such as Accuracy, Precision, Recall and F1-Score. It is observed from the relative comparison with respect to all parameters that the CNN model has given improved results, and thus, the CNN model is considered the proposed method. In future, various other Deep Learning models can be employed for still better performance.

Authors Contribution Statement

MVS and HN contributed towards the concept, literature review, methodology, implementation and Results. MVS and HN wrote the manuscript. 'BGN and KSA contributed towards data analysis, interpretation of results and critical revisions of results. All authors have read and approved the manuscript.

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