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Dense Inception V5 Convolution Neural Network for Liver Tumor Classification into multi abnormal instances and staging of the Disease using LiTS-CT images

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Abstract -Liver Cancer is one among the deadliest form of the cancer disease which owing to abnormal development of cells in the liver and its surrounding tissue. Hence identification and classification of the liver lesion or malignant growth through manual observation is highly challenging due to complex boundaries and features with high degree of intraclass variation and low degree of interclass variations. Machine learning based unsupervised algorithm has been employed to automatically classify the diseases on basis of the lesion appearance and its characteristics but those models consume more processing time and will lead to reduced scalability and reliability. In order to tackle those limitations, deep learning architecture has been exploited as it is more advantageous in discriminating the liver lesions features efficiently and accurately in order to prevent cancer cells from multiplying and spreading. In this paper, a novel dense Inception V4 Convolution Neural Network for liver cancer classification and staging of the disease on processing of the CT images has been proposed. Initially selective median filter and contrast limited adaptive histogram equalization on CT images employed as preprocessing technique to improve the results of the image segmentation through noise removal, contrast enhancement and normalization of the images. Next, region growing segmentation has been employed to pre-processed images to segment the region of the interest and lesion boundaries effectively. Those segmented image has been employed to principle component analysis which acts feature extraction technique to extract the normalized multiple lesion feature of the liver cancer region. Extracted feature has been employed to the model of the generate the learning model on the employing Dense Inception V4 Convolution Neural Network Classifier for label smoothing on disease classification with 7*7 convolutions on optimizing the hyperparameter for filter vector outputs. Further proposed model minimize the complexity of the network and enhances the computing efficiency. Experimental results of the proposed model have been evaluated in the MATLAB software on using LiTs dataset. Performance analysis of the proposed model 3 classes of the disease as basal hepatocellular carcinoma, hemangioma and liver metastasis with 98.75% accuracy, 98.46 specificity and 99% sensitivity respectively on comparing against conventional classifiers

Keywords: Liver Cancer, Deep Learning, Dense Inception v4 Convolution Neural Network, , Segmentation, Feature extraction, CT images

1. Introduction

Liver Cancer is a world's sixth most deadly common cancer of primarily due to uncertain and gathering of the hepatitis infection. Hepatitis infection in liver develops on change of mutation in DNA cells and it becomes malignant in form of lesion with irregular shape, appearance and boundaries [1]. Diagnosis of the Liver cancer can be carried out using invasive technique such as laboratory screening, clinical screening, biopsy and imaging test. Imaging test includes the magnetic resonance imaging (MRI) scans, and computed tomography (CT) scans which capture the cancer region and provide the report in DICOM format. However, manual processing of the liver cancer classification of liver lesion is hard, cumbersome and complicated due to heterogeneous appearance, non uniform shapes and segments of lesions [2]. Manual recognition and classification of the lesion is highly intensive and challenging on features with high degree of intraclass variation and low degree of interclass variations [3].

Machine learning based on supervised and unsupervised algorithm such K Nearest Neighbour [4], Random Forest [5], Artificial Neural Network [6] has been employed to automatically classify the diseases on basis of the lesion appearance and its characteristics on shape, size and border into various classes of the lesion malignancies. Further Machine learning model is incapable in staging the malignant features and these models are time consuming and it lead to reduced scalability and reliability. In addition, these model process limited discriminative capability and less adaptable to lesion boundary changes on the various categories of the lesion features of the skin cells. To mitigate those limitations, deep learning architecture has been exploited as it is more advantageous in discriminating the features of the liver lesions efficiently and accurately [7].

In this paper, a novel dense Inception V4 convolution neutral network for liver cancer classification and staging of the disease to the CT images has been proposed. Initially Image preprocessing, segmentation and feature extraction has been employed for noise removal, Image enhancement and region of the interest extraction with coarse appearance and lesion boundary and to extract the features lesion in the ROI on basis of the correlation and covariance matrix of the principle component analysis. The feature vector generated on process of the PCA has been employed to the Dense Inception V4 Convolution Neural Network for label smoothing on disease classes with 7*7 convolutions on optimizing the hyperparameter for filter vector outputs into classes of the disease as basal hepatocellular carcinoma, hemangioma and liver metastasis [8] on hyper parameter optimization to minimize the complexity of the network and enhances the computing efficiency.

The remaining of the article has been sectioned as follows; section 2 details the problem statement and review of literature for liver lesion classification. In Section 3, the proposed dense Inception V4 convolution neural network architecture for disease classification on lesion features into types and stages has been provided. Experimental analysis of the proposed methodology on the disease dataset has been carried out in section 4 along performance analysis on numerous measures like accuracy, recall and precision on the confusion matrix. Finally section 5 concludes the work with future suggestions.

2. Related work

In this part, numerous conventional models have been employed for Liver Lesion identification and classification as automated system on analysis of CT images by utilizing machine learning model has been detailed as follows.

2.1. Liver Lesion Classification using Probabilistic Neural Network

Probabilistic Neural Network is most effective in detecting and classifying the liver lesion classification especially Hepatocellular carcinoma (HCC) in the liver which is basically a malignant tumor. The process of the identifying the HCC has been carried in addition to images preprocessing of using histogram equalization [9]. Next, Pre-processed image is segmented using Graph Cut model to segment the lesions region in the images. Linear discriminant analysis [10] applied to extract the multiple features on segmented images. Those computed feature are employed to train the probabilistic neural network. Neural Network to classify the feature into various liver disease classes into malignant class or benign class including Hepatocellular carcinoma (HCC) .

2.2. Random Forest Classification model for Skin Lesion Classification

Random Forest classification model is employed to identify the liver lesions and segment it into normal and benign including the Hepatocellular carcinoma (HCC) in the liver diseases. The process of classification has been carried out after preprocessing, feature extraction and segmentation of the images using otu's model and Markov Random Field mechanism [11]. Those processes generate the lesion boundaries and effective features for effective classification. Random Forest classifier [12] on extracted features classifies the normal and malignant lesions with high accuracy and efficiency.

3. Proposed model

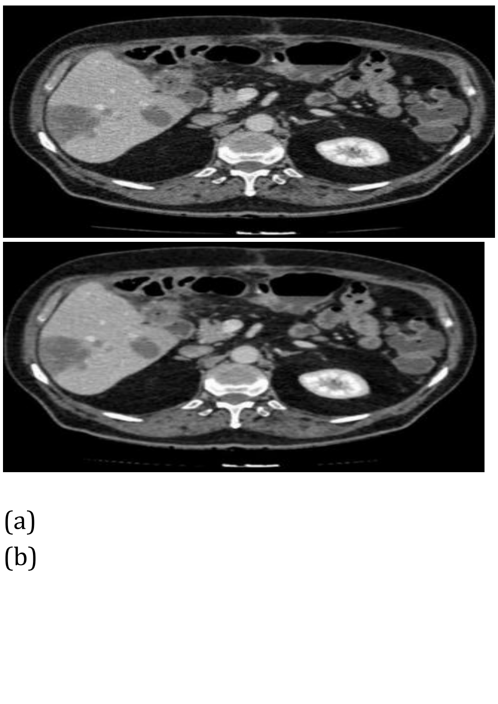
In this section, a new deep learning architecture named Dense Inception V4 Convolution Neural Network architecture has been designed concerning to the liver lesion disease. This architecture is modelled to detect and classifies the severity of disease liver lesion into basal hepatocellular carcinoma, hemangioma and liver metastasis. It is been classified and staged with respect to the lesion features

3.1. Image Preprocessing

Preprocessing of the image is carried out to remove the noise, contrast enhancement and normalization of the image to be classified. The Noise removal is carried out using selective median filter, contrast limited adaptive histogram equalization is employed to enhance the contrast of the image and normalization of the image.

3.1.1. Median Filter – Noise Removal

In this part, Usually CT images in DICOM format containing noise which can be removed using the median filter. Median filter measures the average intensity of the selected window in image and associate with the variation characteristic of the other windows in the image. Those selected image will associates with center to produce the similar characteristics on the entire images. Image processing of the filter is depicted in the figure 1

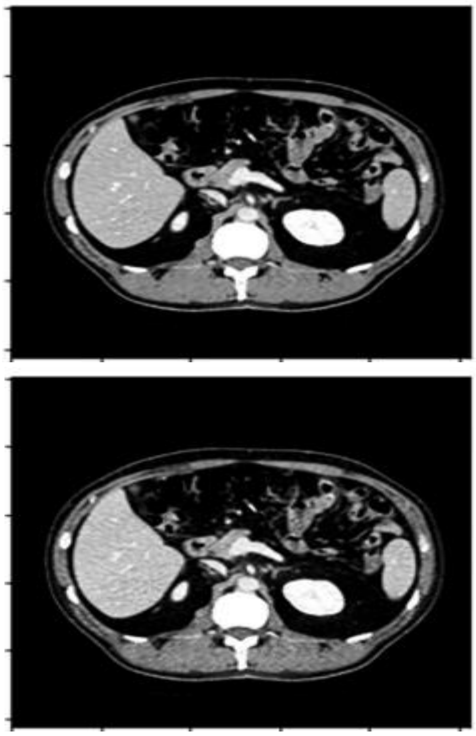


(a)
(b)

Figure 1: Noise Removal using Median Filter (a) Input CT image (b) Noise Filtered Image

3.1.2. Contrast limited adaptive histogram equalization- Enhancement and Normalization

CLAHE has considered as image quality enhancing mechanism to enlarge the contrast of the lesion (disease) features in the images. It is framed on basis of the partition of the expected image to definite non-overlapping regions of similar sizes. CLAHE is framed with partition of the targeted image of equal sizes. Image histogram for each region of the image has to be computed on basis of limit for contrast enlargement. Then computed histogram is redistributed on a condition that its height should not vary beyond the clip limit.



(a)
(b)

Figure 2: Constrast Enhancement and Normalization using CLAHE (a) Noise Removed Image (b) Constrast Enhanced Image

Estimation of Cumulative Distribution Function is used for histogram equalization. These histogram functions of the Cumulative

Distribution function are employed to transform into a uniform density function from the input grayscale density function. On employing the CLAHE technique, every image pixel has been mapped straightly on merging the mapping regions of segment outcomes of the four nearest regions. Further it requires some primary consideration to the regions in CR and BR groups. When the leaves images noises are removed, then image improving techniques are applied to extend the image quality.

3.2. Image Segmentation – Region Growing Technique

In this segmentation, seed representing distinct image regions of the maize plant has been initialized and allowed to increase until it reaches the entire image. A segmentation rule represents the growth mechanism and a rule verifies the homogeneity of the feature regions after each growth process has been constructed. The growth step at each stage k and for selected region unfermented pixels in the 8-neighbourhood of all pixel of the region edge and border. Homogeneity of the region is verified for class of seed as follows

Homogeneity verification of seed points

If (pixel intensity is close to the region mean value |I(j,d) – M(i)| <= T(i))

Threshold Ti changes on basis of the region Rn and the intensity of the pixel I(j,d).

The region obtained using segmentation using homogeneity verification is processed further for classification. Figure 3 represents the region of interest by image segmentation process is represented with red contour.

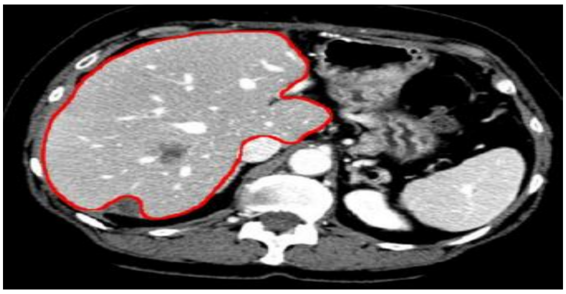


Figure 3: Region of Interest Segmentation using Region growing segmentation

3.3. Feature Extraction – Principle Component Analysis

Principal component analysis (PCA) is employed for extract the feature which is highly discriminating features among features on the region of the interest contoured by region growing segmentation. PCA employed for examining the samples objects, computing the features and defining the features to mention their variations. Each principle component of the contour highlighted represents the largest amount of variance. Since the contour or region of interest can be complex to compute the feature consist of large high dimension, PCA achieve feature determination effectively on minimizing the dimensions without more loss of feature information.

Finally it composed of feature vectors of the feature of the lesion components. Provided CT image of size N x N, initially it mentions the image to a 1D vector U. Vector consists of large variance values. Variance for specified feature X in a image is calculated as follows

$$\text{variance}(y) = \frac{\sum_{i=1}^{n} \text{b(yi – y) (yi – y)}}{n-1}$$

Covariance of the features is calculated for the X and Y events which changes together with mean is as represented as

$$\text{Covariance}(y,x) = \frac{\sum_{i=1}^{n} \text{a(yi – y) (xi – x)}}{n-1}$$

In this computation eigen vector of M_{ij} is a feature vector consist of principle feature group with feature values as eigen value can used for classification of the disease features. Figure 4 represent the distribution of principle feature pixel as dot in the region of interest

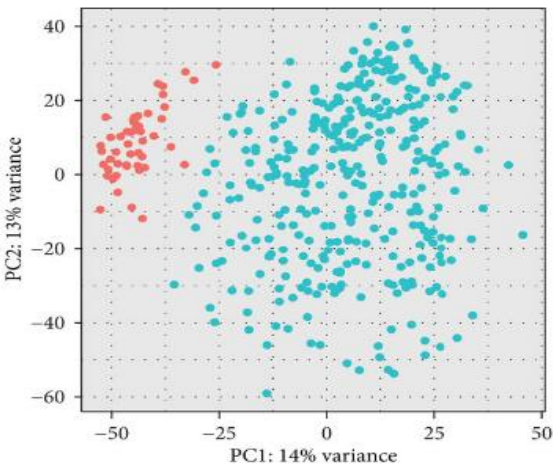


Figure 4: Representation of Feature using PCA extraction

3.4. Dense Inception v4 Convolution Neural Network

In this part, extracted features from PCA extractor has been employed to the Dense Inception V4 Convolution Neural Network Architecture. It processes the feature vector to produce the disease type and stages such as basal hepatocellular carcinoma, hemangioma and liver metastasis. Inception v4 architecture [16] is to produce a set of feature map with the smallest resolution as it is mixture of the convolution layer consist 7*7 convolutions, pooling layer activation layer, loss layer and fully connected layer which represents classification layer with fine tuning of the hyper-parameters through hamming distances. Hence, in total 42 learnable layers are included in Inception v3 CNN model

- **Convolution layer**

In this convolution layer with kernel size of 7*7 has been utilized to process the features. It constructs the feature map from the feature vectors using V4 Inception. Figure 3 represents the feature map generation in the convolution layer.

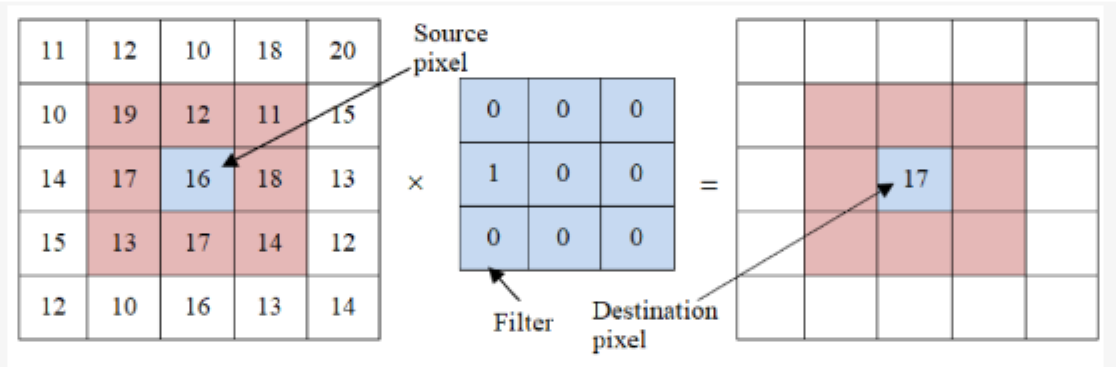


Figure 5: Feature Map of the Liver lesion features vectors

- **Max pooling layer**

In this layer, feature vector in form feature map is down-sampled by half on computing the relationship the features of the lesion and creates the pooling index for the features to control the over fitting issues using the filter and stride value. The pooling operation obtains the small grid segment which represents the down sampling. Stride refers to number of shifts in pixel over the input image matrix. The max pooled layer extracted features which has high-level representations on the feature vector constructed. The feature map is given in the figure 6

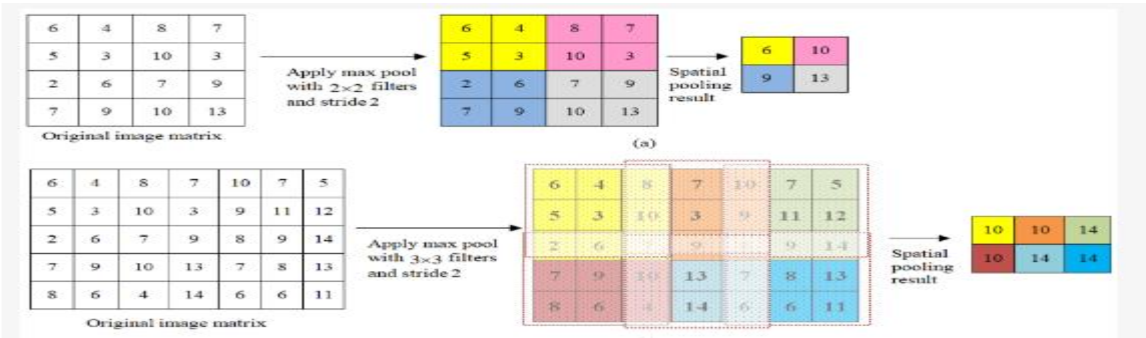


Figure 6: Max pooling with different filters and stride values

- **Activation Layer**

The architecture employs the rectified linear units (ReLU) activation function which improves the training stage to minimize the errors and introduces non-linearity among the max pooled feature vector. Each activation function is followed by batch normalization, the over fitting and improves the system generalization by normalizing the output of the activation function with convolution operation of diseases for staging labels. Figure 7 illustrates the proposed architecture of the Dense Inception v4 Convolution Neural Network.

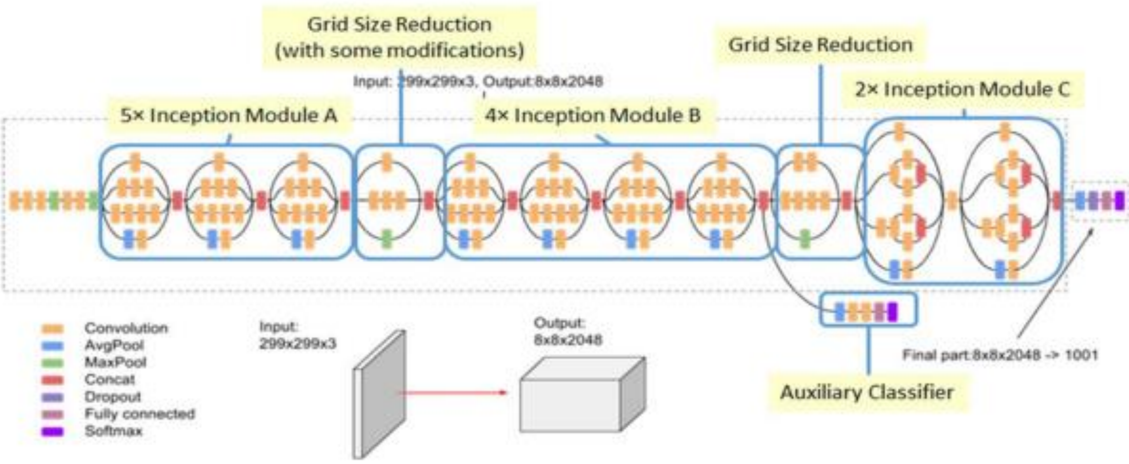


Figure 7: Representation of the Processing of Dense Inception V4 Convolution Neural Network

- **Fully Connected layer**

Fully connected layer is represented as decision layer processes in the flattened manner on learning the most discriminative features of the feature map to construct a class. Classes containing the feature vector are transformed into 1 dimensional data. The produced output represents the categorical probability distribution.

- **Softmax Layer**

Softmax module is employed to map the image pixel to a certain category of liver disease lesion. The softmax classifier identifies the features classes of the image pixel output in an N-channel image of probabilities and the identifies segments related to the class with the maximum probability of every image pixel.

- **Hyperparameter**

Hyperparameter is gradient of the softmax layer containing the feature classes of the liver lesion features.

- **Hyperparameter tuning**

Hyper parameter optimization is represented as hyperparameter tuning to reduce the network complexity and enhances the computing efficiency. In this gradient decent is used as function for hyperparameter tuning. Figure 8 represents the proposed architecture of the work.

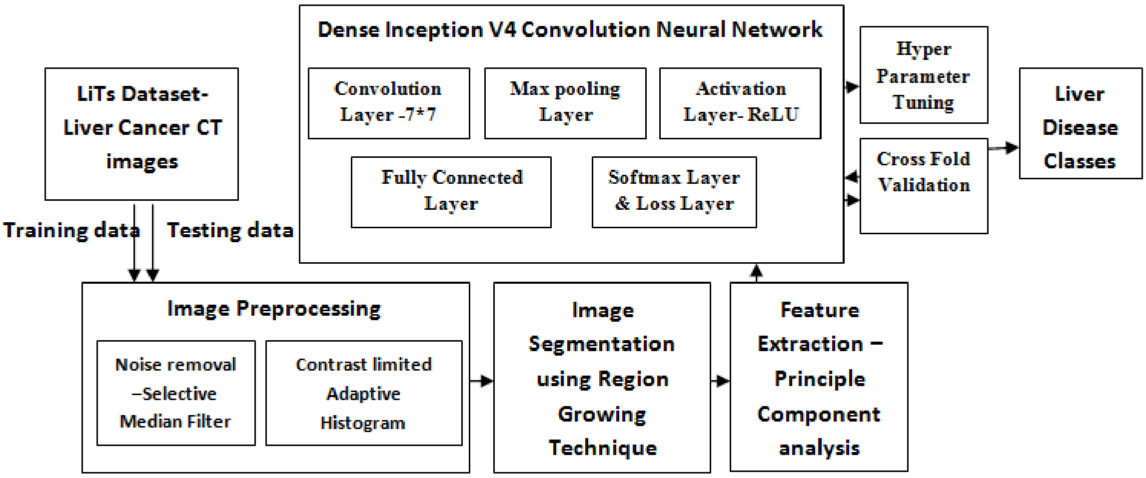


Figure 8: Proposed Architecture of the work

Algorithm : Liver Lesion Classification using Dense Inception V4 CNN

Step 1: Input: Feature Vector V ={v1,v2,...VN}
Step 2 :Output: Disease Class Label D={C1,C2..CN}
Step 3 :Process
Step 4 :Set Convolution Kernel 7*7
Step 5 :Generate the Convolution Feature vector ()

Feature Vector =

3	8	6
4	7	2
9	5	1

Step 6 : Establish Feature Map using Stride value as FM()
Step 7: Activate ReLu() on Pooled vector
FC= Fully Connected(FM)
Class label= Soft_Max(FC)
Step 8. Update Network Parameter θ using gradient descent
Step 9 : Class= { basal hepatocellular carcinoma, hemangioma and liver metastasis }

4. Experimental Results

Experimental outcomes of the proposed model has evaluated in the MATLAB software on using LiTs dataset which contains 2886 CT images in DICOM format [17]. In processing of the image, dataset is portioned into training set, testing set and validation set. In this 10 fold validation has been applied to enhance the performance of the classification and staging of the disease with high scalability and accuracy. The performance of the model has been evaluated with dice Similarity Coefficient, sensitivity, and specificity. Table 1 provide the performance comparison of the Liver cancer classification approaches.

Table 1: Performance Evaluation of Liver Classification Technique Techniques

Disease Classes	Technique	Dice Coefficient	Sensitivity	Specificity
Basal hepatocellular carcinoma-Class1	Dense Inception v4 CNN – Proposed model	0.9978	0.9412	0.9989
	Probabilistic Neural Network-Existing Model	0.9851	0.9336	0.9853
Hemangioma-Class 2	Dense Inception v4 CNN – Proposed model	0.9965	0.9514	0.9971

	Probabilistic Neural Network-Existing Model	0.9842	0.9389	0.9889
liver metastasis-Class 3	Dense Inception v4 CNN – Proposed model l	0.9956	0.9615	0.9965
	Probabilistic Neural Network-Existing Model	0.9836	0.9399	0.9841

- **Dice similarity Coefficient**

It is estimated by distance variation between the classification result and ground truth data. Further it can be determined using true positive, false positive and false negative values of lesion classification results[18]. It is denoted as

$$\text{Dice Similarity Coefficient} = \frac{2TP}{2TP+FP+FN}$$

The Dice similarity Coefficient produces excellent results on evaluating with Liver cancer classification results containing the malignant lesion classes as basal hepatocellular carcinoma, hemangioma and liver metastasis with 96.75% accuracy respectively on comparing against conventional classifiers and it is represented in the figure.

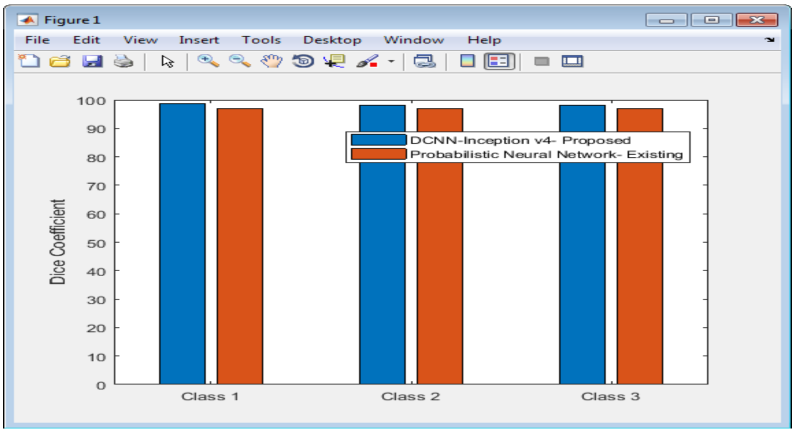


Figure 9: Performance Comparison of Liver Lesion Classification model in terms of Dice Coefficient

- **Sensitivity**

It is measure of percentage of True Positive which computes the cell correctly in terms of various lesion features of the cancer [19]. It is given by

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

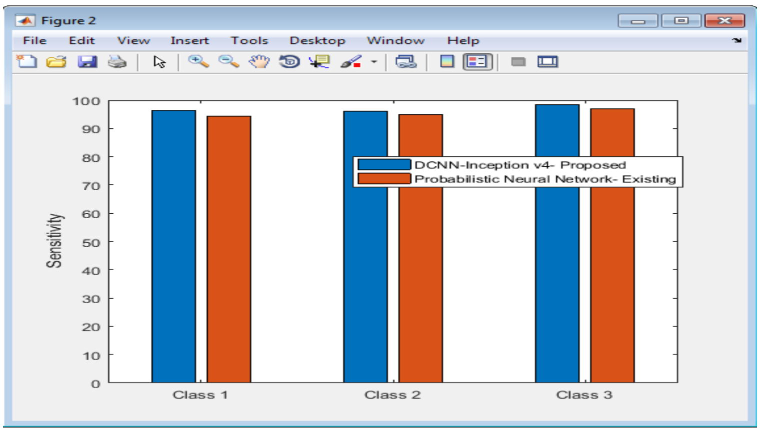


Figure 10: Performance Comparison of Liver Lesion Classification model in terms of Sensitivity

Performance analysis of the proposed architecture on sensitivity metric which yields 3 classes of the disease as basal hepatocellular carcinoma, hemangioma and liver metastasis with 98% sensitivity respectively on comparing against conventional classifiers. Figure 10 represents the performance of the liver lesion classifier on sensitivity.

- **Specificity**

It is measure of percentage of True Negative which computes the malignant lesion in terms of features of the lesion segments [20]. Figure 11 represents the performance evaluation of the specificity.

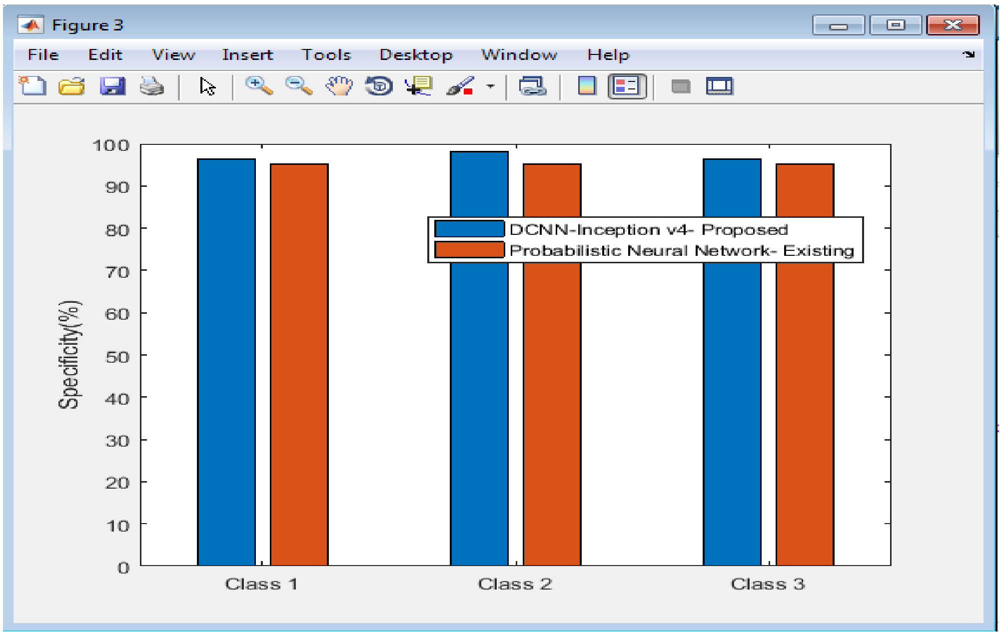


Figure 11: Performance Comparison of Skin Lesion classification model in terms of Specificity

Specificity = $\frac{\text{TP}}{TP+FN}$

Performance analysis of the proposed model 3 classes of the disease as basal hepatocellular carcinoma, hemangioma and liver metastasis with 98.46% specificity respectively on comparing against conventional classifiers. Figure 11 represents the performance of the skin lesion classifier on specificity.

Performance analysis validates the proposed model efficiency and accuracy on skin lesion classification on cross fold validation using confusion matrix. Deep learning methods shows excellent performance compared to conventional methods for disease analysis. The proposed model provides the improved performance with gradient descent optimization as parameter tuning. The performance is produces nearest results on validating with ground truth data.

Conclusion

In this paper, dense Inception V4 convolution neutral network for Liver cancer classification and staging of the disease to the CT images has been designed and implemented using various preprocessing mechanism such as median filter for noise removal, CLAHE technique for image enhancement and normalization, region growing algorithm for segmenting the liver region and PCA for extracting the feature on segmented liver region. Feature vector generated on preprocessing steps has been employed to Inception V4 classifier which incorporates the convolution 7*7 layer, max pooling layer with strides, fully connected layer with ReLu activation function to generate the effective disease classes. Proposed model has been validated on LiTs dataset with classification results containing three classes of malignant tumor classes such as basal hepatocellular carcinoma, hemangioma and liver metastasis. Further it has shown better performance than existing conventional method with 97.75% accuracy, 96.46 specificity and 98% sensitivity respectively on comparing against conventional classifiers.

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