International Journal of
INTELLIGENT SYSTEMS AND APPLICATIONS IN ENGINEERING
ISSN:2147-6799 www.ijisae.org Original Research Paper

Multi-constraint Deep Inception-V7 DenseNet 169Architecture for Liver Lesion Classification and Tumor Staging

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Submitted:10/03/2024 **Revised**: 25/04/2024 **Accepted**: 02/05/2024

Abstract: Liver Cancer is one of the deadliest cancer types which propagating around the world due to its increased morbidity and mortality. Complications associated with liver cancer is considered as fibrosis, cirrhosis, obesity, smoking, and hepatitis B and C. Liver cancer is high challenging to be diagnosed at an initial stage due to reduced primary symptoms and it initiate in the deep location of the body without leaving any symptoms. Machine learning models has been increasingly implemented for monitoring disease prognosis and for diagnosing initial disease. However, those models are time consuming and error prone due to critical features extraction on the segmented disease regions. Henceforth, new architecture for early identification of liver cancer becomes mandatory to identify the liver deteriorations and manage the disease from further liver deterioration. In order to manage those complications, a new deep learning prototype represented as Multi-constraint Deep Inception V3 DenseNet169 is designed for liver lesion classification and tumor staging. Initially acquired data is preprocessing using wiener filter as it produces the enhanced image quality with high contrast and sharpness for efficient segmentation of the tumor regions. Next, Yolov7 algorithm is applied to pre-processed images to segment the lesion and non legions region with efficient placement of boundaries effectively. Those segmented image has been applied further to feature extraction technique named as Non-linear discriminant analysis to extract the multiple lesion feature of the liver lesion segments. Extracted feature from lesion segments has been employed to the proposed deep learning model mentioned as multiparameter Inception V7 DenseNet169 Classifier of the produce the liver lesion classification and staging of disease on basis of its feature scores. DenseNet 169 layer architecture is considered as classifier which is composed of convolution layer for feature mapping of the extracted features, max pooling layer to extract the high level features map and fully connected layer utilizes the softmax function on employing naive bayes classifier to classify the feature map into liver lesion classes such as hepatocellular carcinoma, hemangioma and liver metastasis .Further current architecture is capable to reduce the challenges of the network and increases the computing efficiency using loss function named as cross entropy. Experimental outcomes of the current architecture is accessed using MATLAB software on using LiTs dataset which contains 1500 CT images. Performance analysis of the current architecture produces the liver disease classes such as cirrhosis, fibrosis, basal hepatocellular carcinoma, hemangioma and liver metastasis with 98.65% accuracy, 97.46 specificity and 98.84% sensitivity respectively on compared with state of art deep learning and machine learning classifiers

Keywords: *Liver Cancer, Deep Learning, Multi- Constraint Dense Inception V7 DenseNet 169 architecture ,Yolo v7 Segmentation, Non Linear Discriminant Analysis, CT images*

1. Introduction

Liver Cancer is a one of the world's largest deadly cancer diseases which causes due to hepatitis infection. Hepatitis infection in liver generates dues to variation in the mutation of DNA cells and it forms the malignant lesion with irregular structure, representation and boundaries [1]. Manual screening of the liver cancer disease is carried out using invasive approaches such as laboratory test and biopsy and further it uses the non invasive techniques such as imaging diagnosis. Imaging diagnosis includes the magnetic resonance imaging (MRI) scans, and computed tomography (CT) scans which acquires the cancer region and produces the test report in DICOM format.

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However, manual processing of the liver cancer classification of liver lesion is high challenging and cumbersome and it is complex due to heterogeneous structure, non uniform structure and lesion segments [2][3]. Machine learning architectures such K Nearest Neighbor [4], Random Forest [5], Artificial Neural Network [6] is implemented to classify the lesion diseases with respect to lesion appearance and its characteristics into multiple classes of the lesion malignancies. Further Machine learning architecture is insufficient in multiple disease stages of the malignant structures and those architectures are time consuming and it generates reduced scalability and accuracy. Furthermore, those model produces the less discriminative capability and less suitable to classify the lesion boundary variations on the multiple disease categories.

To handle those complications, deep learning approaches has been explored as it is produces better result

discrimination with high accuracy [7]. In this article, a novel multi-constraint deep inception v7 DenseNet169 architecture for liver cancer classification and tumor stages on processing the CT images is designed 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 along Image preprocessing, segmentation and feature extraction approaches for noise removal, Image enhancement and region of the interest extraction with coarse appearance and lesion boundary.

The remaining of the article has been sectioned as follows; section 2 represents the related works using machine learning and deep learning for liver lesion classification. In Section 3, the proposed multi constraint deep Inception V7 DenseNet169 architecture for liver cancer classification on processing the lesion features into cancer types and cancer stages has been designed. Experimental analysis of the current methodology is evaluated using Liver cancer dataset and its performance is evaluated in the section 4 using accuracy, recall and precision measures. Finally section 5 concludes the article

2. Related work

In this part, numerous conventional models have been implemented using deep learning and machine learning for Liver cancer identification and classification on processing the MRI and CT mages has been detailed as follows.

2.1. **Liver Lesion Classification using Deep learning Architectures**

Convolution Neural Network, Recurrent Neural Network and Artificial Neural Network are effective deep learning architecture employed for identifying and characterizing the liver lesion classification especially fibrosis , cirrhosis and Hepatocellular carcinoma (HCC) in the liver. The process of the identifying the lesion uses the segmentation and classification process together [9]. Various layers of the model with linear rectified unit used as activation function discriminate the lesion classes accurately.

2.2. Liver Lesion Classification using Machine learning Architectures

Machine learning architecture such as Support Vector Machine , K- Nearest Neighbor, Random forest , Naive bayes classifier has been employed to the preprocessed

3.3 Feature Extraction – Non Linear Discriminant Analysis

Non Linear Discriminant Analysis is employed for extract the feature which is highly discriminating images and feature extracted images to classify the liver lesion features. Those architecture identifies and characterizes the liver cancer classification especially on the regions of fibrosis , cirrhosis and Hepatocellular carcinoma (HCC) in the liver segments.

3. Proposed model

In this section, a new deep learning architecture named multi-constrained Deep Inception V 7 DenseNet 169 architecture has been designed to classify and stage the liver lesion disease is carried out on basis of its appearance. This architecture is designed to detect and classifies the complication of disease liver lesion into basal hepatocellular carcinoma, hemangioma and liver metastasis. It is been classified and staged on basis of the lesion features

3.1. Image Pre-processing - Noise Removal

Preprocessing of the image is employed to eliminate the noise and enhance contrast of the image through wiener filter to the CT images which is taken for classification. The noise elimination is achieved using filter conditions on CT images containing noise in the selected windows. Weiner filter computes the average intensity of the selected window in image and associate with the changing characteristic among the other windows of the train image. Those selected image will associates with center to generate the similar characteristics on the complete train images[10].

3.2. Image Segmentation – Yolov7 Technique

In this segmentation, distinct pixel of the liver region is computed initially and these pixels are grouped together until it reaches the entire image. A segmentation rule on the Yolov7 layers[11] gathers the pixel with similar intensity. Lesion region pixel has different value, hence it is considered as constraint. Pixel related to constraints is grouped together and formed as segment. A rule verifies the homogeneity of the feature regions after each grouping process.

Homogeneity verification of pixel in the group is as follows

If (pixel intensity is close to the mean value $|I(j,d) - M(i)| <= T(i))$...Eq.1

Threshold T varies with respect to the region R_n and the intensity of the pixel I(j,d)....Eq.2

The lesion segment of the CT image obtained using segmentation uses homogeneity verification.

features among features on the segmented region using Yolov7. NLDA evaluate the pixel elements in the segmented region to calculates the features and its changes to represent the features on processing the

scatter matrix. Each feature extracted will be mentioned with largest amount of variance through variance. Variance for obtained feature X in a image is calculated as follows

$$\text{Standard Deviation (y)} = \frac{\sum_{i=1}^{n} b(yi - y)\,(yi - y)}{n-1} \text{...Eq.3}$$

Scatter matrix derives the mean and standard deviation on the features is calculated for the large regions which changes on calculation of mean to each segment is mentioned as

$$\text{Mean}(x,y) = \frac{\sum_{i=1}^{n} a(yi - y)\,(xi - x)}{n-1} \text{..Eq.4}$$

In this calculation, feature vector of F_{ij} is a feature composed of significant feature for classification of the liver lesion features.

3.4. Deep Inception V7 DenseNet 169 architecture

The extracted features from non linear discriminant analysis is applied to the Multi constraint Inception v7 densenet169 Architecture. It processes the feature vector to produce the cancer class and cancer stages as fibrosis , cirrhosis, basal hepatocellular carcinoma, hemangioma and liver metastasis. Inception v7 architecture [12] is to generate a feature map using the convolution layer and max pooling layer. Fully connected layer process the ep inception v7 densenet169 architecture.

- **Convolution layer**

In this convolution layer with kernel size of 9*9 is set to process the features. It generate the feature map from the feature vectors. Figure 1 represents the architecture of the DenseNet 169 composed of various layers.

- **Max pooling layer -Dense Block**

In this layer, feature vector in form feature map is down-sampled to generate the high level features on computing the feature associations and produces the pooling index which eliminate the over fitting issues. Max pooled feature is parsed in dense block of the model.

- **Activation function - Transition Layer and Fully Connected Layer**

Rectified linear units (ReLU) is applied as activation function to training of fully connected layer and transition layer to reduces the non-linearity among the max pooled feature vector. Figure 2 mentions the current architecture of the multi constraint deep inception v7 densenet169 architecture.

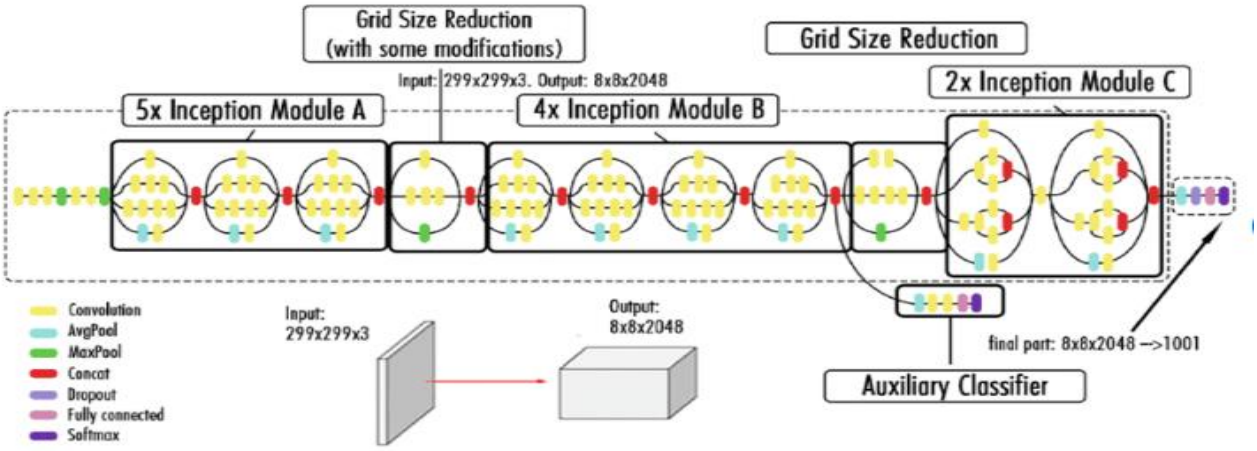


Fig 2: Multi constraint Deep Inception V7 DenseNet 169 architecture

- **Fully Connected layer**

Fully connected layer is composed of softmax and loss function . Softmax uses naive bayes classifier to processes the feature map obtained previous layers to feature map to classify the cancer features using activation and softmax function. Finally loss function is used to reduce the classification error.

generate the class and stages of the disease features. Softmax layer is capable of obtaining the most discriminative features of the feature map to construct a class. Current architecture is represented in the figure 3

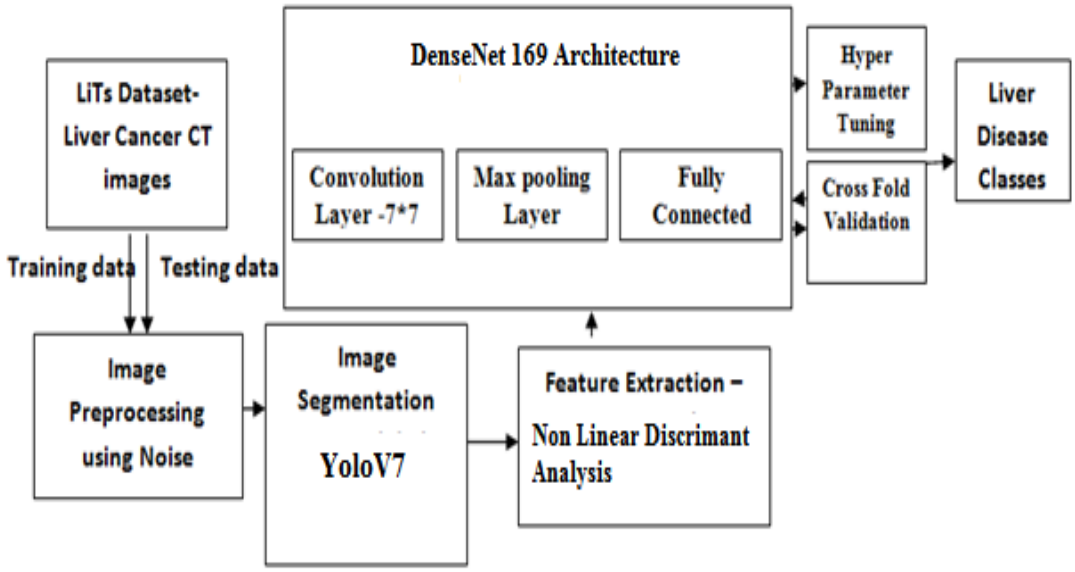


Fig 3: Current Architecture

Algorithm 1: Multi-Constraint Deep Inception V7 DenseNet 169

Input: Feature Vector V ={v1,v2,…VN**}**
Output: Disease Class Label D={C1,C2..CN}
Process
Convolution layer ()
Set Kernel 9*9
Obtain the Low level feature
Compute Feature Map using Stride value and ReLu function
Dense Layer()
Fix Two Kernel 3*3 and 5*5
Generate Tensor for Each kernel
Concatenate the Tensor
Transition Layer()
Reduce the feature size on the strides of 6,12,18,24
Max pooling layer ()
Apply ReLu() on feature vector
Generate high level feature and feature map
Fully Connected layer()
Classification= Naive Bayes_Softmax(Feature map)
Compute Probability Mean and Standard Deviation for each feature vector
Class= { Cirrhosis, Fibrosis, basal hepatocellular carcinoma, hemangioma and liver metastasis }
Stages = { Stage 1, Stage 2, Stage 3}

4. Experimental Results

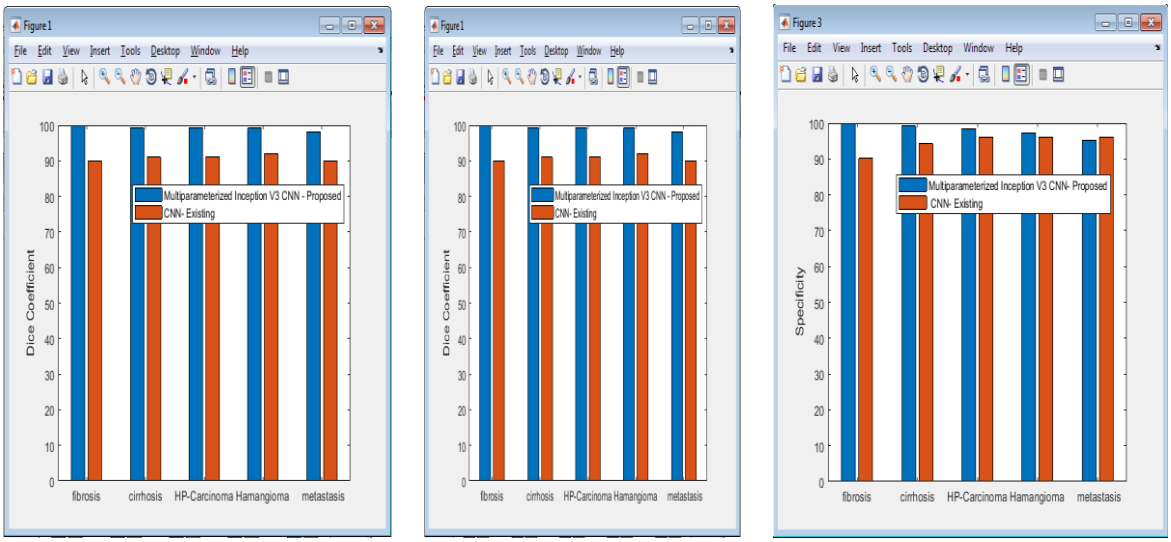
Experimental outcomes of the current model has evaluated in the MATLAB software on using LiTs dataset which contains 2886 CT images in DICOM format [17]. In this 10 fold validation has been employed to increase the performance of the classification and staging of the liver lesion with high scalability and accuracy. The performance of the architecture 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	Multi Constrain Deep Inception V7 DenseNet 169– Proposed model	0.9898	0.9612	0.9899
	Deep Inception V4 Convolution Neural Network- Existing Model	0.9751	0.9636	0.9853
Hemangioma-Class 2	Multi Constrain Deep Inception V7 DenseNet 169– Proposed model	0.9885	0.9614	0.9881
	Deep Inception V4 Convolution Neural Network - Existing Model	0.9752	0.9589	0.9789

liver metastasis-Class 3	Multi Constrain Deep Inception V7 DenseNet 169– Proposed model l	0.9896	0.9715	0.9875
	Deep Inception V4 Convolution Neural Network - Existing Model	0.9736	0.9499	0.9741
Cirrhosis	Multi Constrain Deep Inception V7 DenseNet 169– Proposed model	0.9899	0.9715	0.9865
	Deep Inception V4 Convolution Neural Network - Existing Model	0.9716	0.9519	0.9631
Fibrosis	Multi Constrain Deep Inception V7 DenseNet 169– Proposed model	0.9786	0.9615	0.9875
	Deep Inception V4 Convolution Neural Network - Existing Model	0.9746	0.9549	0.9731

The confusion matrix is applied to validation data to compute true positive, false positive and false negative values to evaluate the efficiency of the model on basis of Dice similarity Coefficient, Specificity and sensitivity. Current mode produces excellent results in generating cancer classes and stages as Cirrhosis, Fibrosis, basal hepatocellular carcinoma, hemangioma and liver metastasis with Dice similarity Coefficient as 98.75%, sensitivity as 98.79% and specificity as 98.89of sensitivity respectively on comparing against conventional classifiers is represented in the figure 3.



(a) (b) (c)

Fig 4: Performance Analysis

The performance is produces nearest results on validating with ground truth data. Finally on basis of feature value , stages of the lesion is determined as stage 1, stage 2 and stage 3.

5.Conclusion

In this paper, multi constraint Deep Inception V7 DenseNet 169 architecture for Liver cancer classification and caner staging is carried out using CT images is designed and implemented using various image processing steps such as wiener filter for noise removal, Yolov7 technique for segmenting the liver region and non liner discriminant analysis for extracting the feature on segmented liver region. Feature vector is applied to Multi Constrained Inception V7 DenseNet 169 classifier which incorporates the convolution layer, dense layer, Transition Layer, max pooling layer, fully connected layer with Softmax function using naive bayes classifier, activation function using ReLu and loss function using cross entropy computes the liver lesion classes with high accuracy. Current architecture is validated on LiTs dataset and it exhibits better performance with 98.75% accuracy, 97.46 specificity and 98.89% sensitivity on comparing against traditional machine learning and deep learning classifiers.

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