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Deep-ShrimpNet fostered Lung Cancer Classification from CT Images

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Abstract: Lung cancer affects the majority of people, due to genetic changes in lung tissues. Several existing methods on lung cancer detection are utilized with machine learning, but it does not accurately classify the lung cancer and also it takes high computation time. To overwhelm these issues, Deep-ShrimpNet fostered Lung cancer classification from CT images (LCC-Deep-ShrimpNet) is proposed. Initially, the input lung CT images are taken from IQ-OTH/NCCD Lung Cancer Dataset. Then the input lung CT images are pre-processed using Kernel co-relation method. Then these pre-processed lung CT images are given to Bayesian fuzzy clustering for extracting lung nodule region. Then the extracted lung nodule region is given into Deep-ShrimpNet classifier for representing features and classifying the lung CT images as normal (Healthy), Benign, and Malignant. The proposed LCC-Deep-ShrimpNet method is activated in python. The performance of the proposed LCC-Deep-ShrimpNet method attains 26.26%, 16.9%, 12.67%, 21.52% and 24.05% high accuracy, 68.86%, 59.57%, 57%, 62.72% and 65.69% low error rate and 60.76%, 53.67%, 68.58%, 59% and 56.61% low computation time compared with the existing methods.

Index Terms: Lung cancer, Deep-ShrimpNet, Kernel co-relation method, Bayesian fuzzy clustering and CT images

1. Introduction

As reported by world health organization (WHO), lung cancer is a most common cancer that caused deaths [1,2]. Lung cancer causes almost1.69 million fatalities annually [3,4]. Cancer screening is crucial to preventative healthcare [5-7]. The study reveals that malignant lung nodules more frequently exhibit lobulation, spiculated contours, and inhomogeneous attenuation [8-10]. At present, chest x-rays may be easily obtained in rural locations [11]. Notwithstanding, CT image gives lesser quality imageries, therefore, a higher quality diagnosis is generally expected [12]. It investigates how a computer-aided diagnosis (CADx) system can employ a CT image to enhance lung cancer diagnostic performance [13].

The advent of dynamic machine learning and artificial intelligence techniques has offered a way to detect lung cancer accurately [14]. Lung cancer detection based on machine learning is fast, automated, inexpensive and suitable for rapid use [15,16]. Several existing methods on lung cancer detection are utilized with machine learning, but it does not accurately classify the lung cancer and also it takes high computation time. To overwhelm these drawbacks, some solutions require to be put forward. These drawbacks have incited to do this research work.

The major contributions of this manuscript are;

- A Deep-ShrimpNet fostered Lung cancer classification from CT images (LCC-Deep-ShrimpNet) is proposed for classifying normal (Healthy), Benign, and Malignant CT images.
- Initially, the input lung CT images are taken from IQ-OTH/NCCD Lung Cancer Dataset [17].
- Then the input lung CT images are pre-processed using Kernel co-relation method [18] for removing noise.

- Then these pre-processed lung CT images are given to Bayesian fuzzy clustering for extracting lung nodule region [19].
- Then the extracted lung nodule region is given into Deep-ShrimpNet classifier [20] for representing the features and classifying the lung CT images image as normal (Healthy), Benign, and Malignant.
- The proposed LCC-Deep-ShrimpNet method is implemented in python and the efficiency is estimated with the help of several performance metrics, such as f-measure, accuracy, sensitivity, specificity, precision, Error rate, Computation Time.
- Then the performance of the proposed LCC-Deep-ShrimpNet is compared to the existing methods, such as LCC-IDNN-HSOA-EC [21], LCC-DFD-Net [22], LCC-CNN-FPSOA [23], LCC-DL-AHHMM [24] and LCC-NB-DT-SDS [26] respectively.

Remaining manuscript is structured as: segment 2 portrays the literature survey, segment 3 describes the proposed method, segment 4 shows the results with discussion, segment 5 concludes this manuscript.

2. Literature Survey

Among the recent studies related to lung cancer detection using machine learning, a few recent studies are reviewed here,

In 2020, Shakeel et al [21] have suggested the Automatic lung cancer identification from CT image utilizing improved deep neural network with ensemble classifier. For recognizing lung cancer, CT images were examined by multiple level brightness-preserving methods for eliminating the noise, also enhancing the lung imagery quality. The affected region was segmented using improved deep neural networks from the noise-removed lung CT imagery, and then certain features were extracted. The effectual features were chosen by hybrid spiral optimization intelligent-generalized rough set model, those features were categorized by ensemble classifier. It provides best classification accuracy with lower F-score.

In 2021, Sori, W.J., [22] have presented a DFD-Net: lung cancer identification from denoised CT scan imagery utilizing deep learning. The input images were given to two path convolutional neural networks (DFD-Net), which handle the pre-processing process, the segmented process and feature extraction process and classification process for detecting lung cancer. It provides higher accuracy with lower sensitivity

In 2020, Asuntha, A., et.al, [23] have presented a Deep learning for lung Cancer detection and classification. The input imageries were fed to pre-processing for eliminating noise then the pre-processed images. The pre-processed imageries were fed to the feature extraction for extracting the texture, volumetric, geometric and intensity features. Then the extracted features were fed to the process of feature selection to select the importance feature set. Then the selected features were given to the classification process to detect the lung cancer. Fuzzy particle swarm optimization convolution neural network was presented for detecting the lung cancer. It provides high error rate with lower computation time.

In 2020, Yu, H., [24] have presented a Deep learning assisted predict of lung cancer on computed tomography images utilizing adaptive hierarchical heuristic mathematical model. The input images were fed to pre-processing for eliminating noise. The Adaptive Hierarchical Heuristic Mathematical Model was utilized for the lung cancer classification. It provides higher accuracy with high computation time.

In 2021, Heuvelmans, M.A., [25] have presented a Lung cancer prediction by Deep Learning to recognize benign lung nodules. The input images were fed to pre-processing for eliminating noise.Lung Cancer Prediction was done with the help of Convolutional Neural Network. It provides high F-Score with low accuracy.

In 2021, Shanthi, S., et.al, [26] have presented a Lung cancer prediction utilizing stochastic diffusion search based feature selection with machine learning methods. The input images were fed to pre-processing for eliminating noise, then the pre-processed image was fed to feature extraction with the help of stochastic diffusion search (SDS) for extracting the features of texture, shape and colour. Then the extracted features were fed to the process of feature selection for selecting the importance feature set. Then the selected features were given to the Naïve Bayes and decision tree classifier. It provides lower error rate with high computation time.

3. Proposed Methodology

In this section, Deep-ShrimpNet fostered Lung cancer classification from CT images (LCC-Deep-ShrimpNet) is discussed. The block diagram of the proposed Deep-ShrimpNet methodology is represented in Fig.1. It contains four stages, such as Data acquisition, pre-processing, segmentation, and classification. The detailed description about each stage is given below,

3.1 Data acquisition

In this, IQ-OTH/NCCD Lung Cancer Dataset is taken. It is collected from Iraq-Oncology Teaching Hospital/National Center for Cancer Diseases (IQ-OTH/NCCD) over a period of 3 months at 2019. The input CT image

contains noise. So noise removal is important for accurate classification. Therefore the input CT images are given to pre-processing phase.

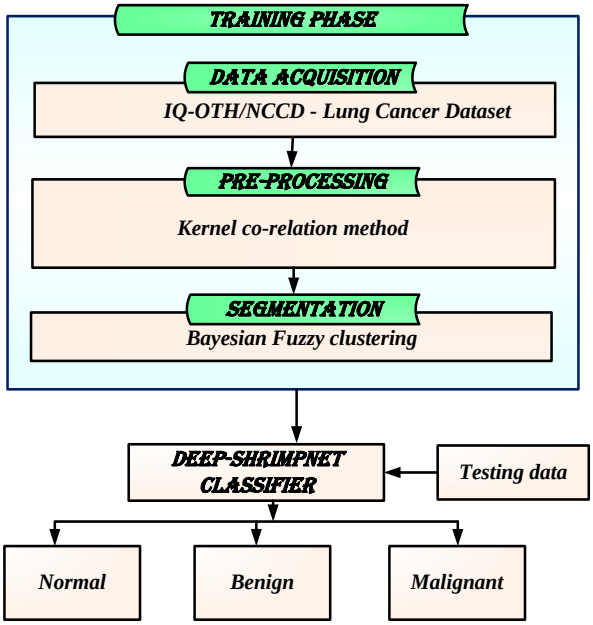

Fig. 1. Block diagram of the proposed Deep-ShrimpNet methodology

3.2 Pre-processing using Kernel co-relation method

In this segment, noise removal is done with the help of proposed Kernel co-relation method. Here, consider the noise removal as an important concern in CT lung images. Initially correlation filter is scaled by equation (1),

$$Correlation\ \ filter = \frac{\sum_{d}\left(Input\ \ \mathrm{Im}age \odot Filter^{*}\right)_{d} \odot Filter_{d}^{*}}{\sum_{d} Filter_{d} \odot Filter_{d}^{*}} \tag{1}$$

where $\odot$ denotes for multiplication process, $*$ denotes multifaceted conjugation. The kernel correlation filter contains crumple deterioration of episodically shifted samples and uses the fast logarithmic Fourier transform in the place of matrix algebra for performing fast operation. For kernel correlation filter, the noise removal is minimized using equation (2),

$$\min_{\psi} \sum_{d}\left(f\left(input\ \ image\ \ sample_{d}\right) - removal_{d}\right)^{2} + \lambda \left\|\psi\right\|^{2} \tag{2}$$

where $\lambda \left\|\psi\right\|^{2}$ denotes the regularization expression. Then, the pre-processed input CT image is fed as input for segmentation.

3.3 Segmentation using Bayesian fuzzy clustering

In this section, lungs nodules are segmented with the help of Bayesian fuzzy clustering. It affords the fragments for mining lungs nodules aspects. The collective likelihood of information points along aspects are labeled as Bayesian model. The Bayesian Fuzzy clustering is assessed utilizing equation (3)

$$p\left(I_{pre}^{j}, C^{*}, B^{*}\right) = p\left(I_{pre}^{j} / C^{*}, B^{*}\right) p\left(B_{*}\right) \overline{p}\left(C_{*} \mid B_{*}\right) = lung\ \ nodule \tag{3}$$

where $p\left(B^{*}\right)$ is represented as the Gaussian prior distribution (GPD), $\overline{p}\left(C_{*} \mid B_{*}\right)$ is represented as the fuzzy cluster prior (FCP), $p\left(I_{pre}^{j} / C^{*}, B^{*}\right)$ is represented as fuzzy data likelihood (FDL). Based on FDL, the Bayesian Fuzzy clustering model is assessed by equation (4),

$$p\left(I_{pre}^{j} / C^{*}, B^{*}\right) = \prod_{a=1}^{z} FDL\left(i_{a} \mid b_{a}, B\right) \tag{4}$$

where I_{pre}^{j} specifies pre-processed CT image, C^{*} specifies fuzzy relationship, B^{*} is represented as the cluster prototypes, z is represented as the measure of the segmented data points in cluster B, i_a is represented as the number of segmented lung nodules data points. The outlook of data is associated with the development of B^{*} and normal likelihoods are fuzzy data likelihood. The gatherings are prepared as well as shared mean ethics are clustered and it is called the cluster models. The cluster models are given in the equation (5)

$$p\left(I_{pre}^{j}/C^{*},B^{*}\right)=\prod_{a=1}^{z}\frac{1}{V\left(b_a,n,B\right)}\prod_{l=1}^{q}N\left(i_a\mid\mu=g_l,x=b_{al}I\right) \tag{5}$$

Where $V\left(b_a,n,B\right)$ is represented as the normalization constants, B is represented as the cluster, q is represented as the overall count of clusters, l indicates cluster number, n indicates fuzzifier. Depending on Bayesian model, the fuzzy cluster prior is exploited to mock fuzzy C-means (FCM) performance. It is determined by equation (6-7),

$$\bar{p}\left(C_{*}\mid B_{*}\right)=\prod_{a=1}^{z}FCP\left(b_a\mid B^{*}\right) \tag{6}$$

Where FCP comprise three aspects, such as $V\left(b_a,n,B\right)$, $\prod_{l=1}^{q}\left(h_{al}^{\frac{nq}{2}}\right)$ and Dirichlet$\left(b_a\mid\mu\right)$

$$\bar{p}\left(C_{*}\mid B_{*}\right)=\prod_{a=1}^{z}V\left(b_a,n,B\right)\prod_{l=1}^{q}\left(h_{al}^{\frac{nq}{2}}\right)Dirichlet\left(b_a\mid\mu\right) \tag{7}$$

Where h_{al} denotes data point membership on group l, mean factor specifies μ. The initial factor castoffs the fuzzy data likelihood equilibrium persistent. The subsequent inspiration to offer higher member-ship reverences. Enthusiasm implies third factor. It distributes additional manipulability and expertise for clustering practice. The Gaussian prior distribution is scaled with the help of equation (8),

$$p\left(B^{*}\right)=\prod_{l=1}^{q}N\left(\mathrm{g}_l\mid\mu_g,\sum_{g}\right) \tag{8}$$

where μ_g is represented as the mean of the dataset and it is determined with the help of equation (9)

$$\mu_g=\frac{1}{\mathrm{z}}\sum_{a=1}^{z}i_a \tag{9}$$

where $\sum_{g}$ is represented as the data covariance and it is determined with the help of equation (10)

$$\sum_{x}=\frac{\chi}{\mathrm{z}}\sum_{a=1}^{z}\left(i_a-\mu_g\right)*\left(i_a-\mu_g\right)^{T} \tag{10}$$

where χ is represented as the user recognized constriction which interrupts the strong point. The combined probability of the data including parameters is created utilizing these factors. Then the extracted lung nodule segmented region is given as the input of Feature representation and Classification phase.

3.4 Feature representation and Classification using Deep-ShrimpNet classifier

In this, Deep-ShrimpNet is utilized for extracting features and classifying the lung cancer. Generally, Deep-ShrimpNet classifier is an innovative form of Alexnet, VGGNet, GoogleNet and DenseNet, which is deemed as local feature self-learning mode from lower to higher level layers. Deep-ShrimpNet is the improved Alexnet architecture, which provide efficient outcome for classification. The proposed Deep-ShrimpNet structure overcame the over-fitting problem of traditional AlexNet on the shrimp dataset. Moreover, Deep-ShrimpNet could simplify the network structure and improve the validation accuracy, laying the foundation for efficient shrimp classification.

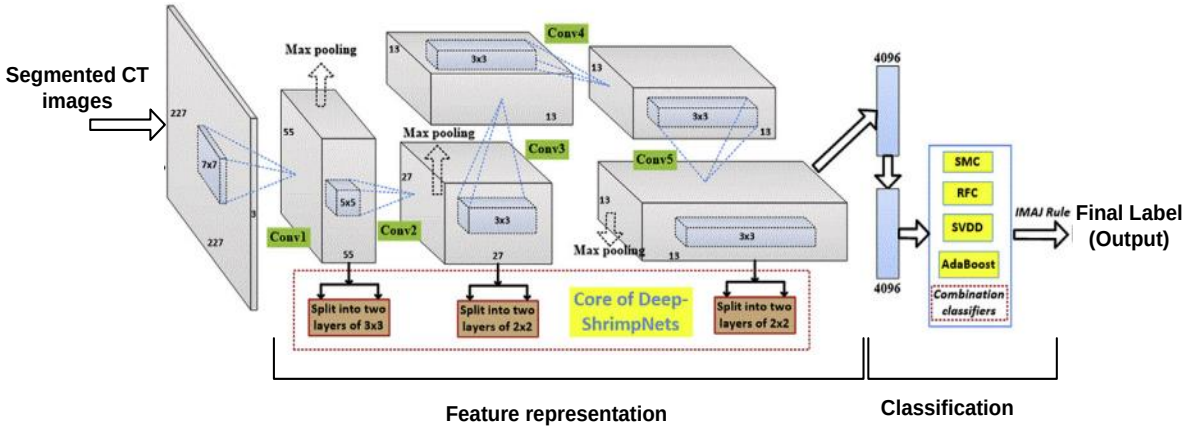

Fig. 2. Structure of proposed Deep-ShrimpNet approach

Fig. 2 shows that the structure of proposed Deep-ShrimpNet model. In Deep-ShrimpNet, 8 main convolutional layers are utilized, out of which 3 special layers are divided into 2 sub-layers. Through higher layers, more complexity with huge data is learned whereas; fundamental features are learned through lower layers. Inserted with max pooling guidance, deformable and inflexible features are apprehended via affine conversion. The last 2 fully connected layers can apprehension multifaceted co-occurrence data, which drop spatial location semantics. To the classification of lung CT image, the final classification layer agrees preceding comprehensive feature representation.

Feature representation using Deep-ShrimpNet classifier

In this, Feature representation using Deep-ShrimpNet classifier is discussed. The Local Receptive Field (LRF) is a filter, which accomplish convolutional operation. So it is called as convolutional kernel. Numerous local features of CT lung nodule features through dissimilar representations and functions are derived through adopting dissimilar convolution kernel types. Therefore, convolutional kernel size are converted 11×11 to 7×7 in first convolutional layer for learning subtle feature representations and make reinforce the capacity for discerning subtle morphological features of CT lung nodule features.

Then the second, third, fifth convolutional layers of DeepShrimpNet have been divided as 2 layers. By this, the computation burden along time-consume could not rise, whilst changes the network depth. This is employed to identify CT lung nodule including deep imminent without higher necessities at running time. Then the DeepShrimpNet classifier acts as an AlexNet, in which all Local Response Normalization (LRN) functions are removed, and then the group manipulations in 2 blocks of Graphics Processing Units (GPUs) are deleted. Because, Local Response Normalization does not increases the capability of network's normalization.

Classification using Deep-ShrimpNet classifier

Here, the Classification using Deep-ShrimpNet classifier is discussed. DeepShrimpNet classifier is a combinational classifier, which included Soft-Max Classifier, Random Forest Classifier, Support Vector Data Description (SVDD) and Adaptive Boosting Classifier. The last label decision done through DeepShrimpNet classifier acted in line along the "majority" of these created processed labels. The aspect of DeepShrimpNet classifier is that final label decision is taken by "elite votes" rather than "all votes". By utilizing the DeepShrimpNet classifier, a certain positive votes are selected that contributes to the final accuracy; other negative votes that reduced the final accuracy are eradicated. By this, accurate detection of lung cancer can be detected.

The DeepShrimpNet classifier is performed in real-time, also attain a fast renewal speed through agreeing newly samples. So, this is desired to speedup the model training as well as recollects a performance of higher level. The accuracy including time-consume of these new created models are examined through shrinks the depth (total count of layers) as well as width (filters at every layer). The count of LRFs is tuned to each convolutional layer to determine ideal network architecture. For instance, DeepShrimpNet classifier depths changed from 8 to 11 layers, then the total count of LRFs including classification layer's grading style are varied. Furthermore, several hyper-parameters in DeepShrimpNet classifier are maximized, like size of LRF, convolutional strides, grading styles, count of LRFs in every layer.

Let BS , ch_{in} , $height_{in}$, $weight_{in}$ are the input parameters and BS , ch_{out} , $height_{out}$, $weight_{out}$ are the output parameters. Here, BS represents the batch size, ch represents the count of channels, $height$ represents the height in CT lung image pixels, $weight$ represents the width in CT lung image pixels. The equation (11) and (12) explains the calculation method of output image size after convolution.

$$height_{out} = \frac{height_{in} + 2 \times padding[0] - dil[0] \times (\ker nel\ size[0] - 1) - 1}{stride[0]} + 1 \tag{11}$$

$$width_{out} = \frac{width_{in} + 2 \times padding[1] - dil[1] \times (\ker nel\ size[1] - 1) - 1}{stride[1]} + 1 \tag{12}$$

here $padding[0]$, $padding[1]$ symbolize x and y-coordinates padding count of implicit zero-paddings on both sides for padding count of points in every dimension, dil represents dilation and it controls the pixel points of image spacing and the dilation of the x-coordinate and y-coordinate are denoted as $dil[0] and\ dil[1]$. In this work, 128 batch size is preferred for training the Deep ShrimpNet classifier, $\ker nel\ size$ is represented as kernel size in every convolutional layer and the LRF size of the x-coordinate and y-coordinate are denoted as $\ker nel\ size[0]$ *and* $\ker nel\ size[1]$. The output size of every CT lung image is deemed. Finally, the proposed Deep-ShrimpNet classifier classifies the lung CT image into normal (Healthy), Benign, and Malignant CT images.

4. Result with Discussion

The experimental result of proposed LCC-Deep-ShrimpNet method is discussed in this section. The simulations are carried out in PC along Intel Core i5, 2.50 GHz CPU, 8GB RAM, Windows 7. The proposed approach is simulated utilizing Python. The performance metrics are analyzed to analyze the performance of the proposed method. The obtained results of the proposed LCC-Deep-ShrimpNet are compared with the existing methods, such as Automatic lung cancer detection from CT image utilizing improved deep neural network with ensemble classifier (LCC-IDNN-HSOA-EC) [21], DFD-Net: lung cancer detection from denoised CT scan image utilizing deep learning (LCC-DFD-Net) [22], Deep learning for lung Cancer identification with classification (LCC-CNN-FPSOA) [23], Deep learning assisted predict of lung cancer on computed tomography images utilizing adaptive hierarchical heuristic mathematical model (LCC-DL-AHHMM) [24] and Lung cancer prediction depending on stochastic diffusion search (SDS) based feature selection with machine learning method (LCC-NB-DT-SDS) [26].Output result of proposed LCC-Deep-Shrimp Net method is shown in Fig.3.

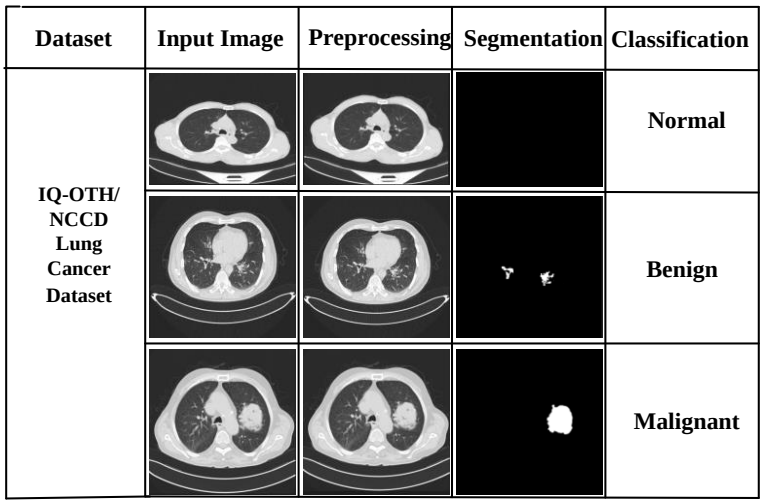

Fig. 3. Output result of proposed LCC-Deep-Shrimp Net method

4.1 Dataset description

To validate the performance of the proposed method, IQ-OTH/NCCD - Lung Cancer Dataset is taken. It is gathered via Iraq-Oncology Teaching Hospital/National Center for Cancer Diseases (IQ-OTH/NCCD) over 3 months period at 2019. It involves CT scans of patients diagnosed with lung cancer at dissimilar stages with healthy subjects. IQ-OTH/NCCD contains 1295 images. Out of 1295 CT images, 50% CT imageries for training phase, 50% CT images for testing phase.

4.2 Performance measures

This is a significant task for best classifier selection. To examine the performance, the performance metrics, like accuracy, precision, recall, F-score, specificity, error rate, computational time are examined. To scale the performance

metrics, the confusion matrix is deemed. To scale the confusion matrix, the values of True Positive, True Negative, False Positive, and False Negative are needed.

- True Positive (TP): Count of samples where the predicted class label implies positive then the real class label is exact.
- True Negative (TN): Count of samples where the predicted class label implies negative then the real class label is exact.
- False Positive (FP): Count of samples where the predicted class label implies positive then the real class label is inexact.
- False Negative (FN): Count of samples where the predicted class label implies negative then the real class label is inexact.

4.2.1 Accuracy

This is computed by equation (13),

$$Accuracy = \frac{(TP + TN)}{(TP + FP + TN + FN)} \tag{13}$$

4.2.2 Precision

This is scaled by equation (14),

$$\Pr ecision = \frac{TP}{(TP + FP)} \tag{14}$$

4.2.3 Specificity

This is computed by equation (15),

$$Specificity = \frac{(TN)}{(FP + TN)} \tag{15}$$

4.2.4 Recall or Sensitivity

This is computed by equation (16),

$$\mathrm{Re}call = \frac{TP}{(TP + FN)} \tag{16}$$

4.2.5 F1 Score

This is determined by equation (17),

$$F1Score = \frac{TP}{\left(TP + \frac{1}{2}[FP + FN]\right)} \tag{17}$$

4.2.6 Error rate

This is calculated utilizing equation (18),

$$Error\ \ Rate = 100 - Accuracy \tag{18}$$

4.3 Simulation analysis

In this section, the simulation performance of the proposed method is compared with existing methods like LCC-IDNN-HSOA-EC, LCC-DFD-Net, LCC-CNN-FPSOA, LCC-DL-AHHMM and LCC-NB-DT-SDS respectively. Here, the performance metrics like accuracy, precision, sensitivity, specificity, error rate, and computation time for the classification types as normal, benign, malignant by the proposed method is analyzed.

Table 1. Performance analysis of lung cancer classification

Performance metrics		Lung cancer classification Methods					
		LCC-IDNN-HSOA-EC	**LCC-DFD-Net**	**LCC-CNN-FPSOA**	**LCC-DL-AHHMM**	**LCC-NB-DT-SDS**	**LCC-Deep-ShrimpNet (Proposed)**
Accuracy	Normal	75.38	86.71	88.61	79.39	82.75	99.16
	Malignant	75.78	83.54	89.26	84.54	81.45	99.27
	Benign	85.46	84.54	86.46	81.26	76.16	99.35
F-Score	Normal	75.06	84.9	77.85	81.78	75.68	99.03
	Malignant	85.76	83.49	76.65	79.37	83.57	99.36
	Benign	86.54	74.95	75.43	74.86	76.23	99.24
Precision	Normal	76.33	70.56	71.67	79.45	83.78	99.44
	Malignant	74.26	71.87	78.84	75.36	84.47	99.57
	Benign	77.23	73.82	73.97	63.52	86.24	99.16
Sensitivity	Normal	69.75	73.66	74.79	78.34	77.87	99.23
	Malignant	73.82	77.67	63.57	73.87	76.34	99.47
	Benign	78.66	73.86	69.71	84.12	78.54	99.34
Specificity	Normal	75.34	63.67	77.89	70.81	76.56	99.87
	Malignant	74.68	78.48	67.89	75.45	77.56	99.67
	Benign	87.33	67.77	64.99	72.67	79.13	99.45
Error rate	Normal	24.62	13.29	11.39	20.61	17.25	0.84
	Malignant	24.22	16.46	10.74	15.46	18.55	0.73
	Benign	14.54	15.46	13.54	18.74	23.84	0.65
Computation time		209	177	261	200	189	82

Table 1 tabulates the performance Analysis for Lung Cancer classification of the existing methods and proposed LCC-Deep-Shrimp Net method. The proposed LCC-Deep-ShrimpNet method attains higher accuracy, higher F-Score, higher precision, higher sensitivity, higher specificity than the existing methods such as LCC-IDNN-HSOA-EC, LCC-DFD-Net, LCC-CNN-FPSOA, LCC-DL-AHHMM and LCC-NB-DT-SDS respectively. Also, the proposed LCC-Deep-Shrimp Net method attains lower error rate and lower computation time compared with the existing methods such as LCC-IDNN-HSOA-EC, LCC-DFD-Net, LCC-CNN-FPSOA, LCC-DL-AHHMM and LCC-NB-DT-SDS respectively. The comparative outcomes shows that the efficacy of the proposed LCC-Deep-ShrimpNet method for for Lung Cancer classification.

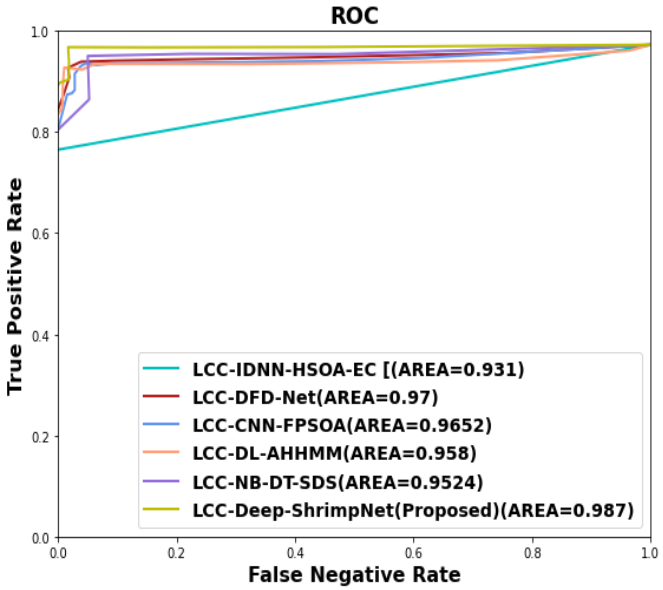

Fig. 4. ROC curve analysis

Fig.4 shows the ROC analysis of the existing methods and proposed LCC-Deep-Shrimp Net method. The proposed LCC-Deep-Shrimp Net method attains 6.015%, 1.75%, 2.25%, 3.02% and 3.63% higher AUC compared to the existing LCC-IDNN-HSOA-EC, LCC-DFD-Net, LCC-CNN-FPSOA, LCC-DL-AHHMM and LCC-NB-DT-SDS methods respectively.

5. Conclusion

A Deep-ShrimpNet fostered Lung cancer classification from CT images (LCC-Deep-ShrimpNet) was successfully implemented in this manuscript for classifying normal (Healthy), Benign, and Malignant CT images. The proposed LCC-Deep-ShrimpNet method is implemented in python and the efficiency is estimated with the help of several performance metrics, such as f-measure, accuracy, sensitivity, specificity, precision, Error rate, Computation Time. Then the performance of the proposed LCC-Deep-ShrimpNet attains 20.8%, 22.68%, 29.46%, 26.28% and 26.64% high F-Score, 32.92%, 32.9%, 41.42%, 33.88% and 24.8% high sensitivity, 26.54%, 41.27%, 42.63%, 32.02% and 27.77% high specificity, 26.85%, 36.55%, 32.66%, 36.49% and 20.45% high precision compared with the existing LCC-IDNN-HSOA-EC, LCC-DFD-Net, LCC-DL-AHHMM and LCC-NB-DT-SDS methods respectively.

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