A Robust Approach for Segmentation and Classification of Lung Cancer using Marker Controlled Watershed Method and Deep Hybrid Learning

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Abstract

Lung cancer is identified by the appearance of pulmonary nodules. The use of computer-assisted diagnosis (CAD) and the categorization of such nodules in Computed Tomography(CT) images has improved lung cancer screening. The objective of the proposed model is to segment the nodules using marker controlled watershed algorithm. A novel hybridized feature extraction approach for lung nodule classification based on transfer learning technique. The deep features are extracted by identifying the optimal layers which improved the performance of the classifiers. After using deep learning to extract image features, the principal component analysis algorithm is used to achieve dimensionality reduction. The performance of various machine learning based classifiers were analyzed based on deep features. The statistical findings show that using a deep fused model and supervised classifier algorithm to evaluate lung CT images can be very beneficial. The proposed model achieves higher classification accuracy, precision, recall, and AUC values outperforming other state of art models with an overall accuracy of 94.21%.

***Keywords*: Marker controlled watershed algorithm;Vgg-16;ResNet-50;Principal component analysis.**

1. Introduction

The use of computer-assisted diagnosis (CAD) and the categorization of nodules in CT images has improved lung cancer screening. Lung cancer is the second most prevalent cause of cancer mortality making it one of the most serious threats to human health . Lung cancer is mostly evaluated using X-ray or Computer Tomography (CT) screening, which is a time-consuming and arduous task for a radiologist. The screening procedure demands a high level of focus and competence. The detection rates of less experienced radiologists are indeed inconsistent, which increases the false positive detection rate, especially in intricate instances where interpretation is heavily dependent on prior expertise [1].

With the advancement of information technology and medical imaging techniques, CT-image-based computer-aided detection systems have yielded specific study outcomes [2,3]. The application of the CAD system model for the automated detection and identification of lung nodules not only enhances efficiency significantly, but also improves precision and resiliency. The traditional CAD algorithm is divided into two steps: the first step is image pre-processing [4] (lung CT image improvement, lung medullary segmentation, ROI extraction, etc.), and the second step is feature point extraction (local feature descriptor features)[5], gray texture features [6], scale invariant features [7], and gradient orientation frequency distribution features [8], etc. after which traditional machine learning algorithms (K-nearest neighbours, support vectorial regression) are applied.

There are several types of spatial and frequency domain image enhancement filters [9] that may be utilized. Sobel filter is a gradient-based approach that searches for significant changes in an image's first derivative. The wiener filter eliminates noise with a low-pass filter and conducts deconvolution with a high-pass filter (Inverse filtering) on a lung CT image taken from the Lung Image Database Consortium [10]. Segmentation is the most difficult process in medical imaging for obtaining characteristics from a segmented tumor nodule area. There are a number of segmentation approaches [11], including Watershed transform edge-based segmentation, Region-based segmentation, and Thresholding. The global thresholding and morphological post-processing operations are performed to detect and segment the lung area nodule from the surrounding tumorous region.

Classification is the most significant criterion for determining the performance characteristics, i.e., precision, sensitivity, and specificity, of the model that aids in the process of lung cancer prediction performed by specialists. As part of the comparative classification study, approaches such as neural network, support vector machine, decision trees and convolutional neural network are considered. [12, 13].

Deep learning [14] is a promising field that improves performance in a variety of medical imaging applications [15, 16]. The fully connected convolutional neural network with a lattice connection of neurons includes activation function and backpropagation for weight modification [17, 18]. The current state-of-the-art performs better than the fully connected convolutional neural network in computer-assisted lung cancer imaging diagnosis.

Deep hybrid learning is a subfield where the various neural networks are used to auto unwrap the features which are further fed into conventional machine learning methods for categorization.

The main contributions of our work are highlighted as follows:

- Segmentation of lung nodules using marker controlled watershed segmentation.
- Deep feature extraction using Vgg-16 and ResNet-50 models
- Applying dimensionality reduction technique on fused extracted features.
- Performed a comprehensive performance evaluation of Random forest, Support vector machines, K-Nearest Neighbour and Decision tree classifiers based on reduced deep features set.

The remainder of this paper is organized as follows: Related work approaches are introduced in Section 2. The proposed model architecture with image pre-processing, segmentation, feature extraction and reduction methods are discussed in Section 3. Section 4 summarizes the experimental results with a comparative analysis of different supervised based classifiers to state-of-the-art models. Finally, in Section 5 conclusion with scope for future work is discussed.

2. Related Work

Gupta et al. [19] developed a conventional method for the automated diagnosis of lung disease in CT scans employing four types of image aspects, namely Gabor, Zernike, Tamura, and Haralick features. In addition, they proposed three evolutionary strategies for optimum feature selection to enhance classification accuracy. The classification task was performed using k-Nearest Neighbor (kNN), SVM, decision tree, and random forest classifier.

Employing intensity, gradient, and geometrical characteristics, Narayanan et al. [20] suggested a conventional method for detecting and categorizing lung nodules in CT images with different slice thicknesses. Using the LUNA16 dataset, they also assessed the performance of feature selection strategies for SVM.

Utilizing eighteen intensity, seventeen gradient, and nine geometric variables, a clustering approach based on feature selection is presented for lung nodules in chest radiographs and CT scans by Narayanan et al[21]. For the performance assessment of their suggested approach, they leveraged the Japanese Society of Radiological Technology (JRST) dataset and the Lung Image Database Consortium image collection (LIDC-IDRI) dataset.

Residual U-Net (RUN) was proposed by Lan et al. [22] to conduct lung nodule identification without the selection of nodule candidates. The concept of a residual network was created to enhance the classic U-Net, therefore addressing the drawbacks of poor outcomes due to insufficient network depth.

Migration learning is a method of machine learning that reapplies a previously learned model to a different problem. In medical image analysis, the use of pretrained CNN models on ImageNet for migration learning has become widespread.

Van Ginneken et al. [23] used a linear support vector machine to extract 4096 off-the-shelf features from the first fully connected layer of a pretrained OverFeat model for lung nodule identification in CT images (SVM).

Integrating deep CNN with image features, Gao and Nie [24] devised a technique for distinguishing benign from malignant lung nodules. The key concept is as follows: partition the lung nodule area from CT scans and extract its imaging characteristics using conventional machine learning techniques. Then, train the 3D-Inception-ResNet model using the lung nodules that were intercepted, extract the CNN features learnt by the network, merge the two types of features, and utilize the Random Forest (RF) model to select features. Finally, a Support Vector Machine (SVM) was employed to differentiate benign-malignant lung nodules.

Fu et al. [25] created a computer-aided lung nodule recognition method that makes effective use of three-dimensional spatial data by employing a three-dimensional deep CNN. The technique consists mostly of two stages: lung nodule detection and categorization. Specifically, an 11-layer 3D fully CNN is employed for the first time in the detection phase to screen all lung nodules. Experimental results illustrate the efficacy of 3D deep CNNs for detecting lung nodules.

Abraham et al. [26] utilized three 2D-CNN (SilNet, VGG16, and AlexNet) to categorize lung nodules and developed a novel network model based on the acquired inference findings to remove the shortcomings of existing networks for early lung cancer prediction. According to the aforementioned study, 2D-CNN networks have the advantages of low network complexity and rapid computation, but they disregard certain spatial information. This is mostly owing to the fact that CT scans are 3D pictures, but the majority of existing CNN-based methods utilize a 2D model that cannot collect the spatial features between slices.

Zhu and Qin [27] suggested a robust U-Net convolutional neural network lesion detection algorithm that utilizes convolutional and pooling operations to retrieve high-level features, enables high-speed flow of derived features between input and output layers via DenseNet.

Lu et al. [28] employed a DenseNet for computer-assisted diagnosis of lung cancer, which employs a patch-based, spatial and spectral DenseNet to extract features and categorize them using four distinct integration approaches.

Furthermore, Zhang et al. [29] devised a classifier using information from unlabeled images in a semi supervised manner. A random forest technique with a framework for a hybrid random forest supported by clustering is presented in [30] in order to boost the ensemble classification advantage in lung nodule detection tasks. In the majority of datasets, the imbalance between the number of nodule and non-nodule candidates is evident.

Sui et al. [31] employed 2D features set such as circularity, elongation, homogeneity, and moment, as well as 3D features such as surface-area, capacity, texture, and centroid-offset, to recognize lung nodules. In general, classifiers are supervised learning techniques in the machine learning area, such as artificial neural networks, support vector machines (SVM), nearest neighbor (NN).

3. Proposed Model

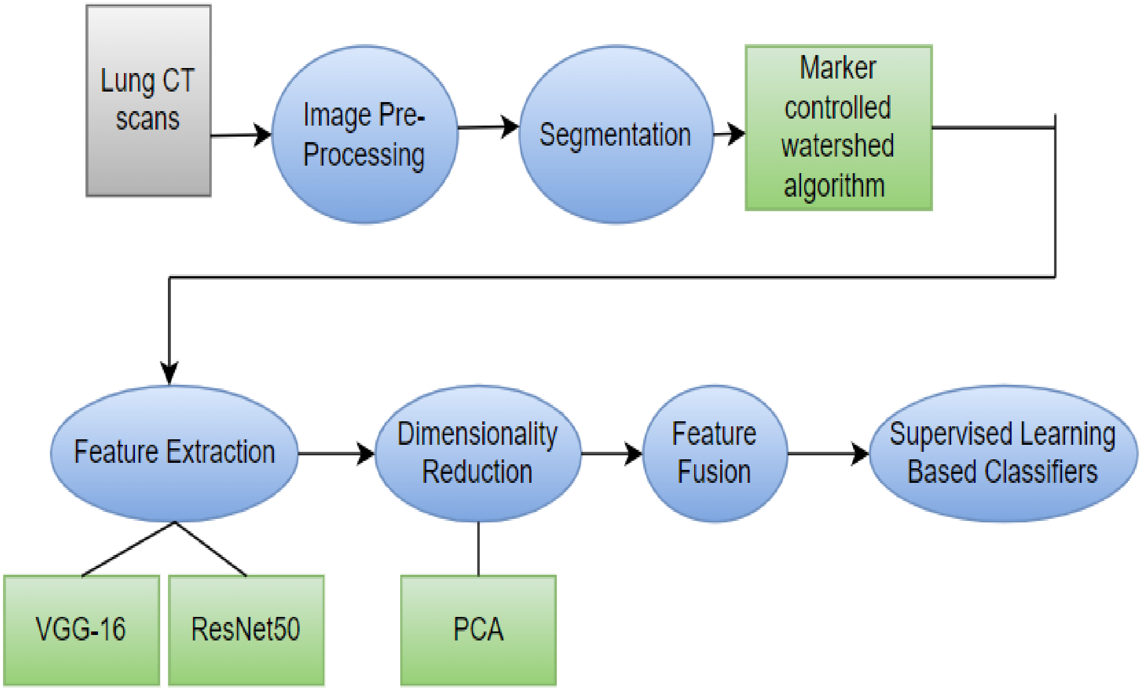

Fig.1. Proposed Methodology

The proposed deep hybrid learning model for lung cancer classification using CT images is presented in this section. Figure 1 illustrates the architecture of the proposed framework. First, pre-processing of the CT images is done followed by image enhancement. At each pixel point, the gradient of the image is computed using sobel filters. Marker controlled watershed algorithm is applied for segmentation. The segmented images are passed to the fine-tuned deep networks Vgg-16 and ResNet-50 for training purposes. Principal Component Analysis is employed to lower the dimensions of features in order to retain features that are more concise and to simplify the required amount of processing. The reduced features of Vgg-16 and ResNet-50 are fused. Finally various supervised learning based classifiers are applied for classification of images as benign or malignant. The techniques will be discussed in depth in the subsections that follow.

3.1 Image Pre-processing

Image pre-processing is considered an important phase in clinical research application of neuroimaging for improving the quality. Image enhancement is achieved by applying a Sobel filter for discernment of edges as shown in figure 2.

The magnitude of the edge along the x and y axis is calculated as in equation

$$\sqrt{{M_x}^2 + {M_y}^2} \tag{1}$$

The gradient direction is calculated as in equation

$$\theta = atan\left(G_y/G_x\right) \tag{2}$$

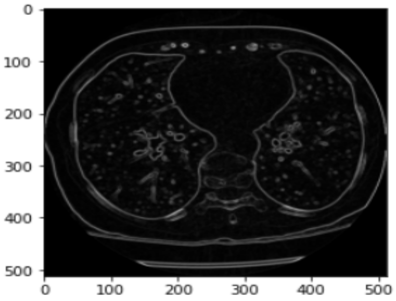

Fig.2.Sobel filtered image

3.2. *Segmentation*

A digital image's segmentation is the process of dividing it into a number of disjoint areas such that the pixels in each region have comparable visual qualities. The idea is to simplify or modify the representation of a picture so that it may be analysed further. This is one of the most important tasks in pattern recognition and classification [32], visualization [33] image compression based on objects of interest [34] etc.

A watershed method is one of the most frequent segmentation algorithms used in the processing of medical [35] and material science images [36]. It is built on the depiction of a grayscale image as a flooded topographic relief, with watersheds delineating regions of water from various basins [37]. The traditional watershed [38] is designed around flood modelling. Practical implementation of the watershed segmentation method by flooding from regional minimums or ultimate eroded points usually results in over segmentation due to noise and other local gradient anomalies.

Too much over segmentation will render the watershed algorithm's output unusable. There are two techniques that can help to solve this problem. One technique is to integrate adjacent regions based on specified criteria following the use of a watershed. This strategy, however, is time expensive, and merging criteria is extremely hard to construct. The alternative method is to use a watershed that is controlled by markers. One is internal marker on region of interest i,e lung tissue and other external marker outside the region of interest as shown. External marker is created by morphological dilation of the internal marker, by iterating twice and subtracting the results. The watershed marker is created by superimposing both the markers. The internal, external and watershed markers are shown in figure 4, 5 and 6 respectively. The Sobel operator accentuates regions of high spatial frequency that correspond to edges by performing a 2D spatial gradient measurement on an image. The black top hat morphological operation is used as structuring element for the filter. The watershed image and segmented lung is shown in figure 7.

Pseudocode for marker-controlled watershed segmentation algorithm

```
1.Read the original image I
2. Morphological reconstruction of the I
3. To detect the minimum, compute the complement of image obtained by the morphological reconstruction, the result image notes $I_c$.
4. For markers of the original image, subtract from the original image I, the image $I_c$:
→ $M_r$= difference=I-$I_c$ or $M_r$ – 1-h
5. Extended and imposed minimum, we obtained the markers.
6. Compute the watershed transforms of the markers.
7. Show the watershed segmented image
```

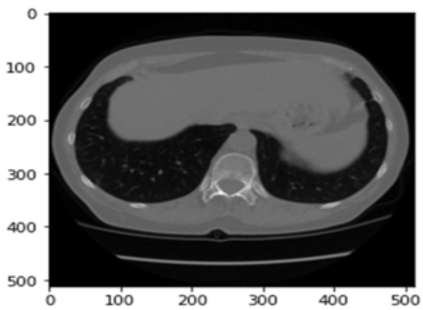

Fig.3. Original image

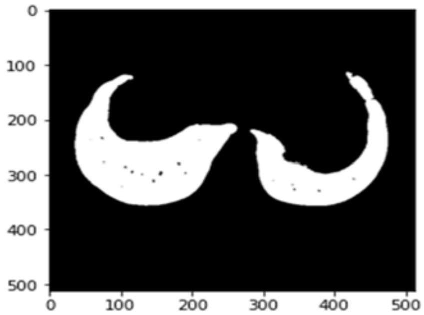

Fig.4. Internal marker

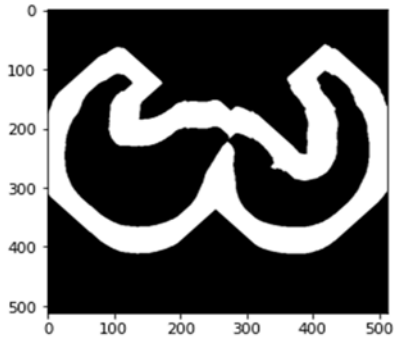

Fig.5. External marker

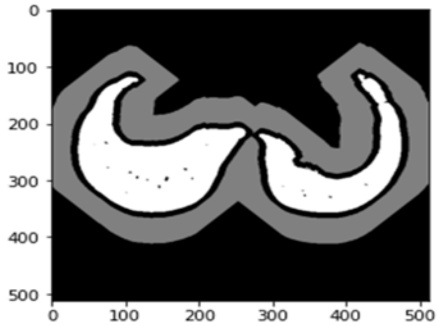

Fig.6. Watershed marker

Fig.7. Watershed Image

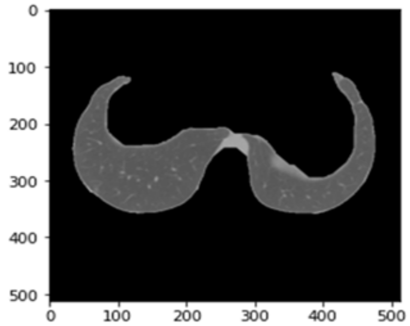

Fig.8. Segmented lung

3.3. Feature extraction and Reduction

3.3.1 Vgg16 model

It has 5 max-pooling layers, 3 fully-connected and softmax in the final layer . There are five feature extraction units for each convolutional layer in these models. For each successive filter group, the number of filters rises by a factor of two, all the way up to 512 in the final feature extraction unit. All convolutional layers have stride and padding set to 1. After convolutional layers in each group, a 2x2 pixel window with stride 2 is used for max-pooling.The dense and fully connected layers are removed to extract the features from last max pooling layer to generate the 7*7*512 feature map as shown in figure 9.

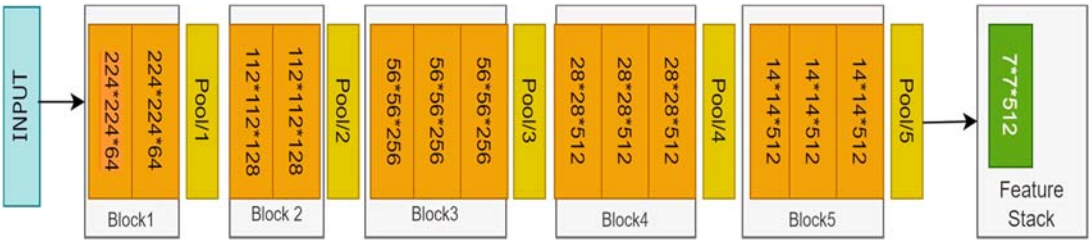

Fig. 9. Fine-tuned Vgg-16 architecture

3.3.2 ResNet-50

The ReLu activation function and multiple convolution layers (1*1-64, 3*3-64, 1*1- 256) are shown in this building block of a residual network [47]. With the skip connection, residual network addresses the issue of diminishing gradients by intermittently allowing some input to the layer to incorporate the flow of information and minimize its loss. Averaging the models is one way to reduce noise while still maintaining a reasonable level of generalizability. The most efficient technique used to raise accuracy and an approximated degree of the traversal is to increase the number of labeled data points.Faster training of deep neural networks and better accuracy on huge training datasets are the activations of the last convolution layer, resulting in the most detailed and distinctive features.The feature map of 7*7*2048 is obtained at the end of block 5 convolution as shown in figure 10. One advantage of global average pooling over the fully connected layers is that it is more native to the convolution structure defined by enforcing correspondences between feature maps and categories. Thus the feature maps can be easily interpreted as categories confidence maps.

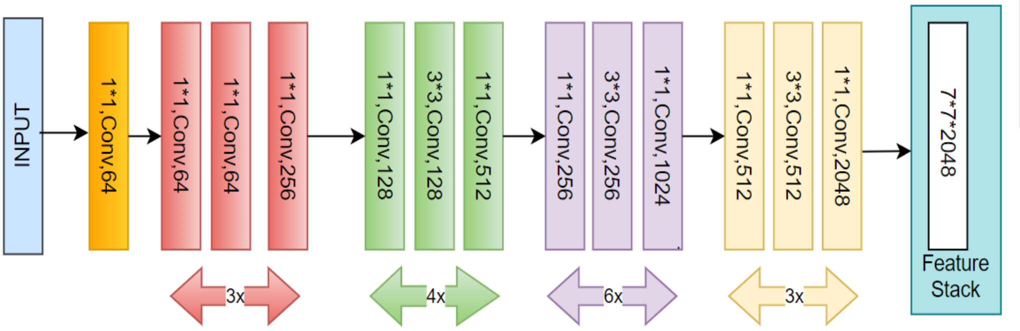

Fig. 10. Fine-tuned ResNet-50 architecture

3.3.3 Principal Component analysis

Principal component Analysis(PCA) is a method that employs orthogonal transformation techniques on numerical datasets. It converts an observation into a series of variables, which are then plotted beside a set of variables identified as Principal Components(PCs). PCA is especially useful for handling the noisy data sets since it is considerably simpler if the inconsistency is restricted to a subset of the components rather than the complete set. As the signal-to-noise ratio of the initial components increases, there is a relative reduction in the noise impact. PCs are determined using the eigenvalue decomposition of the data covariance /correlation matrix.Typically, once the data for each feature have been mean-centered. When the variances of variables are substantially greater than their correlation, a covariance matrix is recommended. When the variables are of distinct forms, it is best to apply type correlation for some components.

```
Algorithm: PCA
Input: Dataset matrix [Z]
Output: Features reduction
Step 1: Generate A x b dataset matrix (one row vector per data point $z_n$)
Step 2: subtract the mean from every vector row $z_n$ in Z.
Step 3: calculation covariance of matrix Z.
Step 4: find eigenvalues and vectors of a covariance matrix.
Step 5: Principal Components the mean eigenvectors with the greatest eigenvalues.
Step 6: Output
```

After identifying the best subset of features with the least error rate and optimum precision, these features were fused. The next section describes the feature fusion approach.

3.3.4 Feature Fusion

After sampling, the superficial and deep layer characteristics are mixed to the same degree in order to manage the flaws of low dimensionality in the deep layer and the inadequate appearance of small particles In the suggested model, we employ the approach of late feature fusion. After extracting features from the Vgg-16 and ResNet-50 models, we used a PCA-based faeture selection strategy . By extracting the finest subset of features using PCA, we combined these features further.

3.4. Supervised learning based classifiers

These fused features are fed to several classifiers, including Support Vector Classifier(SVC), K-Nearest Neighbor, Random Forest, and Decision Tree classifiers. The most accurate classifier was chosen as the optimal option.

3.4.1 SVC with Radial basis function kernel

Radial Basis Function(RBF) is the most popular kernel option for support vector machines. The math is intricate, but it translates to the kernel that can generate the most elaborate boundaries. RBFs are also responsible for kernel smoothing and, by inference, kernel density estimation. The RBF kernel function of linear SVC is calculated as in equation (3).

$$k(a.b) = \exp[-\frac{1}{2\sigma^2}\ ||m-n||^2 \qquad (3)$$

Here σ controls the width of kernel. $||m-n||^2$ is the Euclidean distance between two points m and n.

3.4.2 Decision tree classifier

In general, decision tree classifiers are easier to train than other algorithms like neural networks. Their complexity results from the characteristics and dimensions of the data. It is a non-parametric technique, which means does not reliant on conditional probability assumptions. This classifier is a equipped to handle high-dimensional data with a great degree of precision. The significance of each feature is calculated as defined in (4).

$$fe_b = \frac{\sum_{a: node\ a\ splits\ on\ feature\ b} nb_a}{\sum_{k \in all\ nodes} nb_k} \qquad (4)$$

where nb_a is the importance of node a, fe_b is the importance of feature b
The normalized feature value is computed as stated in equation (5).

$$norm\ fe_b = \frac{fe_b}{\sum_{a \in all\ features} fe_a} \qquad (5)$$

where fe_b is the importance of feature b, fe_a is the importance of feature a and norm fe_b normalized importance of feature b

3.4.3 K-Nearest Neighbor classifier

The k-nearest neighbors algorithm is a distribution free test, supervised training classifier that employs locality to create predictions or classifications involving the categorization of a single data point. Although it may be used for both regression and classification applications, it is commonly employed as a classification technique, based on the premise that comparable points are typically located in close proximity. The minkowski distance is calculated as follows in equation (6).

$$\sum_{x=1}^{y} |c_i - {d_i}^z|^{\frac{1}{z}} \qquad (6)$$

where c and d are points, z as distance value.

3.4.4 Random forest classifier

A random forest is a stochastic predictor that use averaging to improve predicted accuracy and minimize over-fitting by fitting a number of decision tree classifiers to diverse subsamples of the dataset. The equation for random forest feature importance is defined in equation (7).

$$RFfe_b = \frac{\sum_{b \in all\ trees} normfe_{ab}}{T} \qquad (7)$$

$RFfe_b$ is the importance of feature b calculated from all trees in the Random Forest model, $normfe_{ab}$ the normalized feature importance for a in b

4. Experimental Results

4.1 Dataset Description

The benchmark data utilized in this paper has 1211 CT scans taken from standard LIDC-IDRI dataset with two categories as normal and benign. Out of 1211 CT images, 632 are malignant scans and 579 are benign. The training data consisted of 968 images and testing data of 243 scans. The quantitative and comparative analysis is discussed in detail in next section.

4.2 Results and Analysis

In this study, several hyperparameter tunings were evaluated in order to achieve optimal tuning and high accuracy. The Vgg16 model is then loaded with the imagenet dataset's pretrained models weight .Image size of 224*224 is fed into model. To unwrap the features the output of last max pooling layer is used. Stochastic gradient descent optimizer with learning rate as 0.001, decay value of 1e^{-6}, loss value equals to binary cross entropy is applied. It is trained for 200 epochs with batch size set to 32.The features are extracted from block5_pool layer. The scores of most features can be retained PCA based dimensionality reduction. The model accuracy obtained for Vgg-16 is around 96.21% as shown in figure 11. The model loss of the Vgg-16 model is depicted in figure 12.

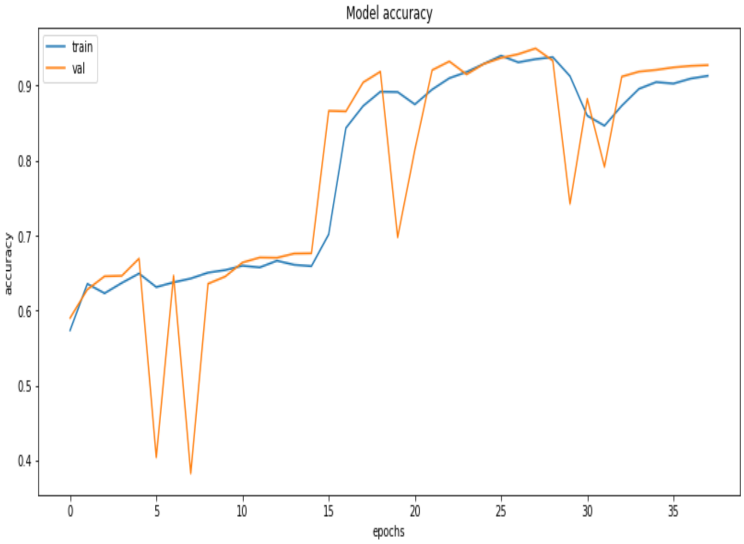

Fig.11. Vgg-16 model accuracy

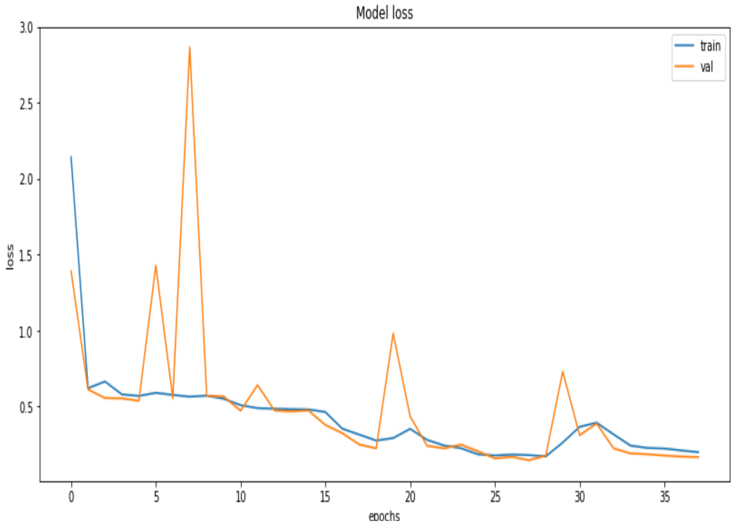

Fig.12.Vgg-16 model loss

Similarly the ResNet-50 is fed with 224*224. Adam optimizer with learning rate of 0.001 and sigmoid activation function is used. A dropout value is set to 0.7 and a global average pooling layer is added. Again the PCA is applied for minimizing the massive features obtained from con_5 block_3 layer.

The model accuracy obtained for ResNet-50 is around 98.01% as shown in figure 13. The model loss of the ResNet-50 model is depicted in figure 14.

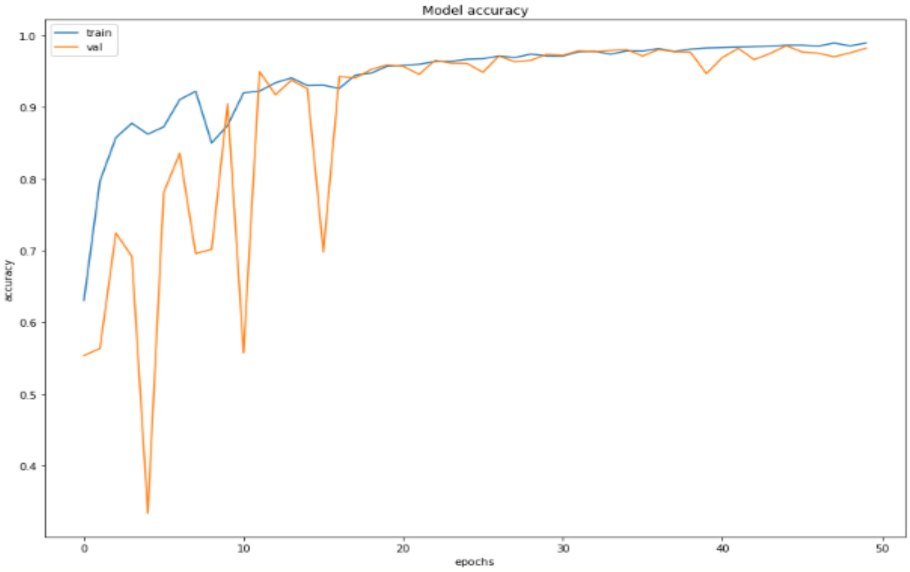

Fig.13. ResNet-50 model accuracy

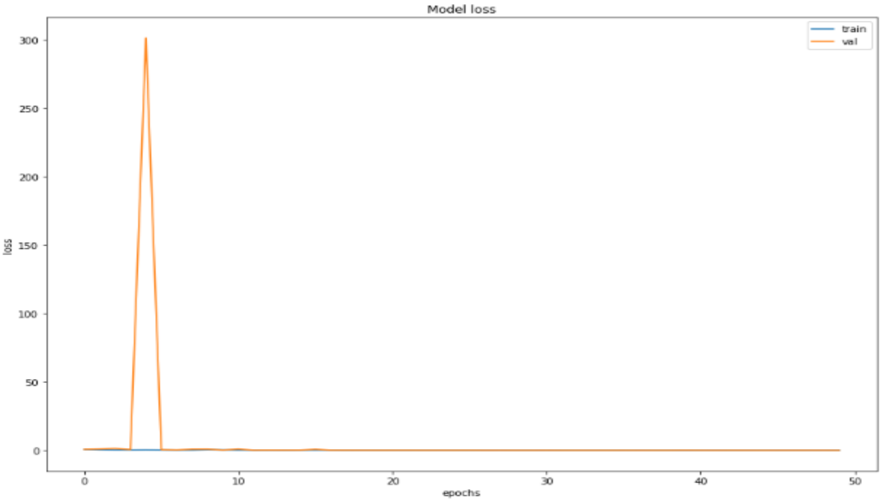

Fig.14. ResNet-50 model loss

The late feature fusion is applied on reduced feature set. These features are input to standard machine learning classifiers namely SVC with radial basis kernel function, Decision trees, Random forest classifiers and KNN. The results of experimented hybrid models along with accuracy is shown in table 1.

Hybrid Methods	Accuracy
Vgg-16+PCA+Random forest	93.04%
Vgg-16+PCA+Decision Tree classifier	91.13%
Vgg-16+PCA+K-Nearest Neighbour classifier	92.09%
Vgg-16+PCA+Support Vector Classifier	83.57%
ResNet-50+PCA+Random forest	94.21%
ResNet-50+PCA+Decision Tree classifier	92%
ResNet-50+PCA+K-Nearest Neighbour classifier	90.19%
ResNet50+PCA+Support Vector Classifier	80%

Table 1. Accuracy of hybrid methods proposed in the model

The best accuracy of 94.21% is achieved using ResNet-50 and Random forest classifier for classifying images as malignant or benign. The quantitative analysis of hybrid methods experimented is shown in figure 15.

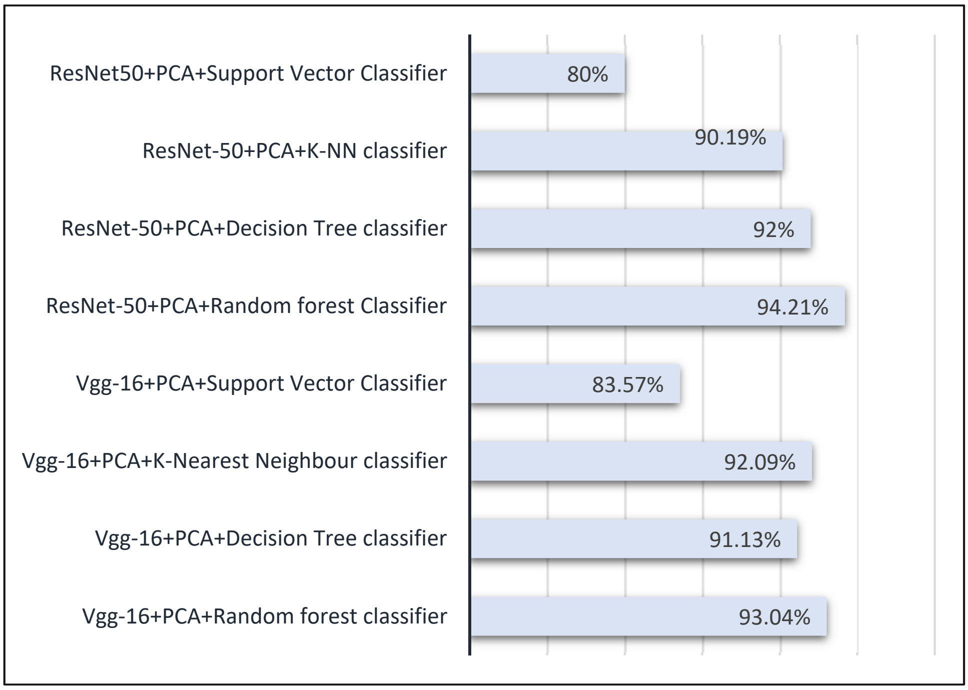

Fig.15. Comparative analysis of hybrid methods

The comparative analysis of the proposed deep hybrid model with other state-of-art models are discussed in table 2.

Authors	**Methodology**	**Accuracy**
Nibali et al[39]	Residual network (ResNet)—deep residual network	89.90%
Manikandan et al[40]	SVM kernels	94%
Yashaswini et al[41]	CNN and SVM	81%
Proposed Model	ResNet-50+PCA+Random forest	94.21%

Table 2.Comparative analysis of proposed model with existing models

5. Conclusion

This article instigated a robust approach on deep hybrid learning for lung cancer classification. The study shows that ResNet-50 with optimal hypertuning parmeters outperforms with accuracy rate of 94.21%. This deep hybrid model which is an integration of convolutional neural network based architectures Vgg-16 and ResNet-50 and standard machine learning classifiers highlights the efficacy and potential for clinical use in comparison with existing algorithms.The experiment have shown that a combination of ResNet-50 architecture based feature extraction followed by prinicipal component analysis feature reduction method fed to Random forest classifier has outperformed when compared to other traditional methods discussed.

In future,metaheuristic methods such as evolutionary algorithms, bio inspired algorithms or swarm based intelligence techniques can be applied to further optimize and improve the performance of the model.

6. Conflicts of Interest

The authors declare no conflict of interest

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