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Design of novel convolution neural network model for lung cancer detection by using sensitivity maps

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ABSTRACT

Despite the existence of numerous models for detecting lung cancer, there is still room for achieving higher levels of accuracy. In this paper, a maximum sensitivity neural network (MSNN) has been proposed. As the name suggests, the model aims to achieve high sensitivity and offers a viable remedy to minimize the number of false positive in oder to improve the overall accuracy for lung cancer detection. The MSNN model is a promising model since it can efficiently interpret grayscale lung computed tomography (CT) scan images as inputs and can be trained using just a few images also. This model has surpassed previous deep learning models by obtaining a remarkable sensitivity of 94.6% and an accuracy of 96.9%. A sensitivity map is created, offering important insights into the critical regions for finding malignant nodules. This innovative method has shown outstanding performance in identifying lung cancer with a low false positive rate which can increase the accuracy of medical diagnoses.

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1. INTRODUCTION

Accurate diagnosis of disease is a challenge in medical research. Lung cancer among many types of cancer have been identified most dangerous and having negative effects [1]-[3]. According to India's National Cancer Registry Programme, cancer accounts for about 7,84,821 fatalities each year [4], [5]. Neoplasm, which are abnormal cell growths, can cause benign or malignant tumours or nodules to develop in lungs. The effectiveness of treatment can be greatly improved, and patient survival rates can be subsequently raised by early detection of lung or pulmonary nodules.The best diagnostic technique for detecting lung cancer is a computed tomography (CT) scan because more thorough study of the lungs and quicker detection of lung nodules are possible as it has high resolution, low distortion, and high contrast . However, noise in CT scan images can degrade image clarity and make it more difficult for radiologists to identify lung cancer in its early stages. Therefore, models based on deep neural networks have been developed to significantly detect the cancer with great accuracy. In recent years, the field of artificial intelligence (AI) has shown significant progress, particularly in image recognition, and speech recognition [6]-[8].In this paper, a deep convolution neural network called maximum sensitivity neural network (MSNN) has been proposed which finds and learns patterns in lung CT scan images to detect lung cancer. This model employs 512×512 grayscale images and can also be trained on a dataset with a small number of images. MSNN can extract

deep features of the image which later can be fed into the k-nearest neighbor (k-NN) classifier for classification. As a result, the proposed model has a high accuracy for lung cancer detection.

Another important feature of this model is use of pre-batch normalization (BN) and max pooling layers to reduce model complexity. Sensitivity maps has been plotted to visualize which part of image contributes more for the classification of image. It is essential to detect a lung nodule with high accuracy. This is a difficult task for radiologist and more enquiry time is required. Therefore, variety of deep neural networks have been developed for lung cancer detection and proved to be better than artificial neural network [9]–[11]. Some of them are studied and summarized. Zhang *et al.* [12] used deep neural network to extract shallow and deep features for ovarian cancer classification. Wu *et al.* [13] designed convolutional neural network (CNN) which is based on AlexNet architecture for categorization of ovarian cancer pathological images, and the model accuracy rate was 78.2%. Tajbakhsh and Suzuki [14] applied artificial neural networks and CNN for testing benign and malignant nodules in lung CT scan images. The experimental results showed that when it came to categorising lung lesions and tumours, CNN outperformed other artificial neural networks. Shen *et al.* [15] designed a convolutional network named multi crop CNN for classification of lung nodule malignancy by using learned deep features. Masood *et al.* [16] proposed deep fully convolution neural network (DFCNet) model which is a convolution neural network used for classification of lung nodule into four stages. This proposed network gave an accuracy of 84.58% indicating the effectiveness of proposed method. Govindarajan and Swaminathan [17] proposed a CNN model with optimized parameters to detect COVID-19 with sensitivity of 97.63% and F-measure of 97.1%. The model proved to be efficient in providing visual diagnostic solution. Shelhamer *et al.* [18] developed new model which is a CNN. In this model, fully convolutional layer is used in place of fully connected (FC) layer. This modification enabled the precise pixel-by-pixel prediction of the entire image in a single forward pass. Christ *et al.* [19] segmented the liver by cascading two fully connected networks (FCN), with the first FCN segmenting the liver as the region of interest for the second FCN segmenting the lesions in the liver. This method successfully segmented lesions in CT images with a dice score of 0.823 and magnetic resonance imaging (MRI) images with a dice score of 0.85. To limit the number of false positives (FP) brought on by the imbalanced ratio of background and foreground pixels in medical images, to apply the focal loss on the FCN [20]. In this structure, the intermediate segmentation results were generated using the FCN, and the FP were subsequently eliminated using the focal FCN. This paper is organised as follows: This paper is organised as follows: section 2 presents a literature review, section 3 discusses the proposed MSNN architecture, section 4 presents the experimental results and compared with other models. Finally, concluding remarks and future work to be carried out is discussed in section 5.

2. PROPOSED METHOD

2.1. Maximum sensitivity neural network architecture

A private database with thousands of lung CT scan images is used in this study. The goal of the research is to create a novel, effective convolution neural network architecture that detects lung cancer and outputs a two-dimensional vector for binary data (cancerous vs noncancerous). Therefore, MSNN has been designed for the diagnosis of lung cancer by using lung CT scan images. It is designed based on the pretrained deep neural network AlexNet [21]. Each input CT scan image is a member of a specific class, and a probability score is assigned to it as an output.

AlexNet is a deep convolution neural network which is well suited for image classification making it viable choice for lung cancer detection. Due to deep architecture, it uses large number of parameters and is more prone to overfitting, particularly when the dataset is small. The architecture consists of five convolution layers, three max pooling layer, three FC layers, and a soft max (SM) layer at the output. Hence, MSNN model has been proposed which is a modified version of AlexNet by utilizing global average pooling (GAP) layer in the architecture to tackle the problem of model overfitting caused by small dataset. Figure 1 presents MSNN architectural layout which shows that it is made up of five successive blocks [21]. Block1-block4 are made up of four layers namely convolution (conv), BN, rectified linear unit (ReLU) and max pooling layer. Wherein, block 5 is made up of convolution, BN, ReLU, and GAP layer followed by FC layer and softmax layer. To classify the test images, it learns and identify patterns from lung CT scan images. This network input layer accepts grayscale images with a 512×512 pixels.

Firstly, MSNN is trained to distinguish between malignant and noncancerous lesions in lung CT scan images. Secondly, the network extracted features from deep layers of lung CT scan images and then it is fed to KNN classifier for classification. Although CNN can perform image classification task very well but, medical applications require fine-grained classification, where the distinctions between classes are subtle. So, an additional KNN classifier has been utilized to refine the classification and to make more precise distinctions.

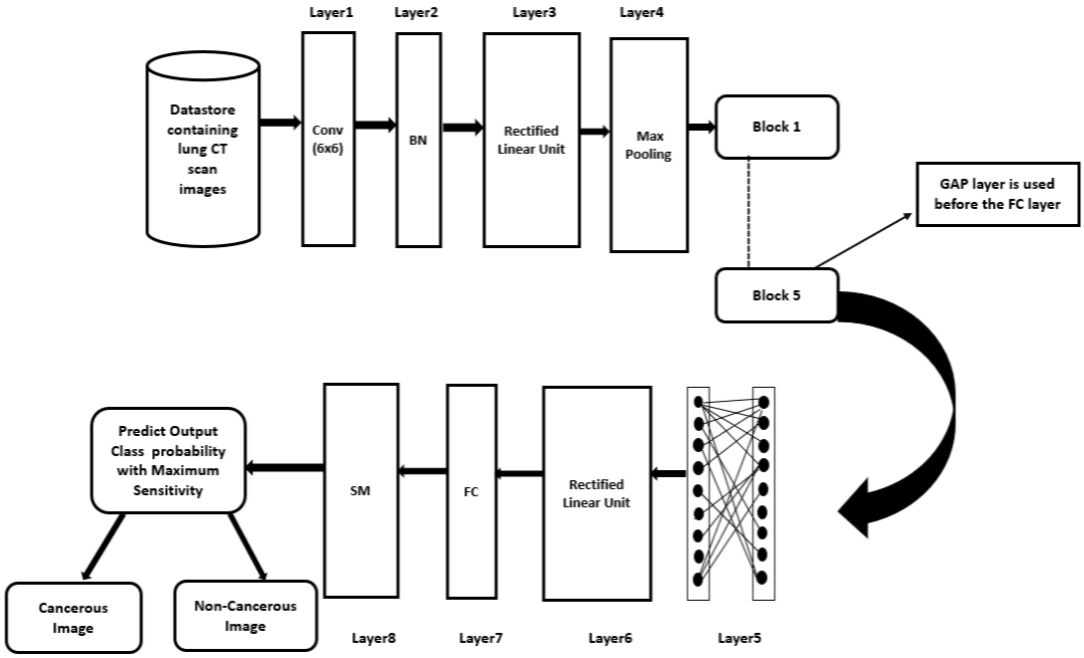

Figure 1. Internal architecture of MSNN model

The combined architecture of MSNN with a k-NN classifier has been designed carefully. Preprocessed grayscale CT scan image is passed through a series of convolutional layer, BN layer, ReLU, and max pooling layer multiple times through block1-block5. Each convolutional layer applies multiple filters to the input image and capture different feature maps like edges and patterns. The extracted features have been applied to the GAP layer which will then calculate the average value of all elements of each feature map, resulting in a single value. The output from GAP layer is a 1-dimensional vector which is further fed as an input to the FC layer. Each neuron in the FC layer takes this input vector, multiplies each input value by a corresponding weight, and adds a bias term and computes a weighted sum of the input values. Atlast, the weighted sum of input values from the FC layer is applied to the softmax layer to produce class probabilities. After the MSNN has performed its feature extraction, the features extracted from the FC layer can be used as inputs for the k-NN classifier. The k-NN algorithms works as follows:

- Firstly, take all features extracted from the FC layer as an input to knn clasifier, where each image has attributes and a corresponding class label.
- For a new, unlabeled test image, the algorithm calculates the distances between test image and all the images in the training dataset. The distance metric used is Euclidean distance.
- Identify the images with the shortest distances to the test image.
- Sort all the calculated distance metric in ascending order.
- The images near to test image are considered as k-NN.
- The algorithm looks at the class labels of these k neighbors and determines the majority class.
- At last, the test image is then assigned to this majority class.

The efficacy of the k-NN classification technique hinges on the selected k value. In this work, the elbow method was employed to ascertain the ideal k value for the dataset. This involves plotting the sum of squared error (SSE) values against various k values and identifying the juncture on the graph where elevating the k value ceases to yield substantial changes. This inflection point, known as the "elbow," designates the optimal k value. The optimal k value for the k-NN classifier was determined to be 300.

2.2. Dataset and training options

Since classification of test images depends on several parameters, neural network training is quite crucial and needs to be carefully considered. The following setting has been done while training MSNN. ADAM optimization method has been chosen because it updates the learning cofficients in each iteration and maintains separate learning rates for each parameter. It also adapts the learning rates during training. It also requires less manual tuning of hyperparameters. A batch size of 20 and epoch value of 20 has been set to train MSNN. Optimum batch size and epoch value has been chosen with a trial method. Batch size

contributes to learning processes by balancing the convergence rate of the network as well as accurate estimation [22]. However, the size of batch size has not been considered high since this may be costly in terms of time consumption and memory usage. It is observed that the network will experience overfitting if the epoch value choosen is too high. Conversely, a low epoch value will cause the network to converge quickly and cause training to end early. The dataset is divided into training and validation set randomly for split1. 70% of images from datasets are used for training and the remaining images are used for testing. Split2, Split3, and Split4 imply that 75%, 80%, and 85% of the database images are used for training respectively, while the remaining images are used for testing. Therefore, the training process has been performed four times, each with a different split of the dataset to assess the model's performance across different training scenarios and to obtain a more robust estimate of the model's generalization capabilities.

In this work, lung CT scan images in DICOM format have been acquired from A. J. Hospital and Research Centre to test the performance of MSNN. The dataset consists of 434 lung CT scan images of patients, in which 249 lung CT scan images belong to patients with cancer and the remaining 185 lung CT scan images belong to patients with healthy lungs. Sample images from the dataset are displayed in Figure 2.

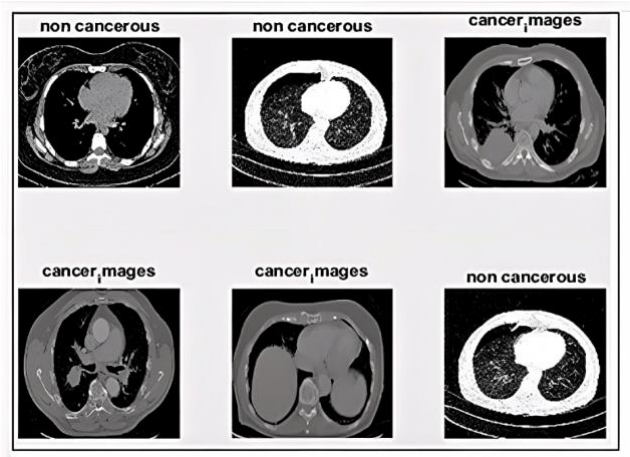

Figure 2. Samples of lung CT scan images

The performance of MSNN has been evaluated by obtaining confusion matrix which helps in calculating all the metrics related to performance of network. The following is a description of the different layers used in the architecture:

- Input layer: the MSNN architecture accepts grayscale CT scan images.
- Convolution layer: it performs convolution operation between the input image(f) and filter size(g) by using (1) [23].

$$f(x) * g(x) = \sum_{k=-\infty}^{\infty} f(k).g(x-k) \quad (1)$$

  where x and k are spatial variables. In general, a smaller filter size may lead to an overfitting issue, while a bigger filter size may increase the underfitting issue. Therefore, this layer uses 8 filters with a 6×6 ideal filter size.
- BN layer: the next successive layer is BN layer which expedites training speed and lessens network sensitivity. Therefore, performing normalization over a batch(v) of m instances for 'i' unit can be done using the following steps. Firstly, compute batch mean by using (2) [23] for 'i' unit. This is done by summing up the values of unit 'i' from all instances (ranging from 1 to m) in the batch and then dividing it by the total number of instances(m) in the batch.

$$\mu_i = \sum_{r=1}^{m} v_i^r / m \quad (2)$$

Where r ranges from 1 to m.

The second step is to compute batch variance for the 'i' unit by using (3) [23]. This involves calculating the squared difference between each value of 'i' unit in the batch and the batch mean (μ_i). The squared differences are then summed up and divided by the total number of instance(m) in the batch.

$$\sigma_i^2 = \sum_{r=1}^{m}(v_i^r - \mu_i)^2/m \quad (3)$$

The third step is to normalize each instance's value (v_n^r) in the batch using the calculated batch mean (μ_i) and batch variance (σ_i) by using (4) [23]. For each instance 'r', the value of unit 'i' is subtracted by the batch mean (μ_i) and then dividing by the batch variance (μ_i).

$$v_n^r = v_i^r - \mu_i/\sigma_i \quad (4)$$

Lastly, scale with learnable parameters by using (5) [23]. The normalized batch instances (v_n^r) are scaled using learnable parameters, γ_i, and β_i. These parameters allow the network to learn the appropriate scale and shift for each unit 'i' in the batch normalization process.

$$a_i^r = \gamma_i * v_n^r + \beta_i \quad (5)$$

After applying batch normalization to each unit 'i' in the batch, the network can continue with further layers and activations.

- ReLU layer: it is an activation function used to add nonlinearity to the network by adding a rectifier function which is computing linear operations during convolution. The function works by using (6) [24]. The ReLU function keeps the positive values unchanged (identity function) and sets negative values to zero. This non-linear activation helps the network to learn complex relationships in the data and makes the network capable of learning more complex functions.

$$f(x) = 0, x < 0$$
$$f(x) = x, x > 0 \quad (6)$$

- Max pooling layer: it helps to decrease the size of the convolved feature map to reduce computational costs.
- GAP layer: applying this layer to the feature maps summarizes the spatial information within each channel by taking the average value across all spatial locations. This operation retains the channel-wise information while discarding the spatial dimensions, resulting in a compressed representation of the feature maps.
- FC layer: it helps in classifying the images.
- SM layer: it converts the output of the last layer into a probability distribution.

2.2.1. Accuracy

This parameter defines true positive (TP) and true negative (TN) or correct cases over total number of cases which includes false cases too. In (7) can be used for accuracy calculation. TP are the number of lung cancer cases correctly predicted by the model (71 in this case). TN are the number of non-lung cancer cases correctly predicted by the model (55 in this case). Wherein FP are the number of non-lung cancer cases incorrectly classified as lung cancer cases (0 in this case). False negatives (FN) are the number of lung cancer cases incorrectly classified as non-lung cancer cases (4 in this case). A high accuracy value indicates that the model is making correct predictions for a large proportion of lung cancer cases and non-lung cancer cases [25].

$$Accuracy = \frac{TN+TP}{TN+TP+FN+FP} \quad (7)$$

2.2.2. Precision

This parameter determines TP cases over TP and TN cases. In (8) can be used for precision calculation. This is essential to calculate in medical applications because it helps assess the model's ability to minimize FP. A high precision value indicates that the model has a low rate of FP, meaning it correctly identifies most positive cases. Conversely, a low precision value indicates that the model incorrectly classifies non-lung cancer cases as positive, leading to a higher rate of FP [26].

$$Precision = \frac{TP}{TP+FP} \quad (8)$$

2.2.3. Recall/sensitivity

This parameter measures TP rate and is also known as sensitivity. It evaluates the model's ability to correctly identify positive cases (lung cancer cases) out of all instances that belong to the positive class. A value close to 100% means its test result is positive and patient has disease. Conversely, a low recall value

suggests that the model is missing many positive cases, leading to a higher rate of FN. In (9) can be used for recall calculation [26].

$$Recall = \frac{TP}{TP+FN} \quad (9)$$

2.2.4. F-score

It is a metric that combines both precision and recall providing a single score that balances their trade-off. This parameter determines how many cases are classified correctly. A high F1 score indicates that the model has achieved a good balance between precision and recall, making it effective at correctly identifying positive cases (lung cancer) while keeping FP and FN in check. In (10) can be used for calculating this parameter [26].

$$F\text{-}Score = \frac{2*(Precision*Recall)}{Precision+Recall} \quad (10)$$

2.2.4. Specificity

Specificity is also known as a TN rate. This parameter determines how many cases are correctly classified as negative. It is essential to calculate in medical related applications because it evaluates the model's ability to minimize FP specifically for the negative class. A high specificity value means that the model is correctly identifying most of the non-lung cancer cases, reducing the rate of FP for patients who do not have the disease. Wherein a low specificity value indicates that the model is misclassifying many negative cases as positive, leading to a higher rate of FP. In (11) can be used for calculating this parameter [26].

$$Specificity = \frac{TN}{TN+FP} \quad (11)$$

3. RESULTS AND DISCUSSION

Performance comparison of proposed MSNN with other existing deep learning models has been shown in Table 1. The confusion matrix is shown for four different splits of the dataset in Figure 3. Table 2 compares performance metrics across split1, split2, split3, and split4. It's evident that split 1 exhibits the highest accuracy, precision, recall, specificity, and F-score attributes particularly significant in medical contexts. Notably, the false positive rate (FPR) is at 0% in split 1, indicating the model's adeptness in distinguishing between positive and negative cases, reducing the misclassification of negatives as positives.

From the results it can be observed that MSNN achieved an accuracy of 96.9% and sensitivity of 94.6. Therefore, it can be concluded that MSNN worked well in the identification of lung cancer because the accuracy reported in [27]–[29] is 80.1%, 84%, and 88.1%, respectively. It was found that all three methods used to compare the results of our proposed MSNN are popular object detection neural network algorithms. To ensure the fair comparison similar datasets are utilized in [27]–[29] which are acquired from private hospitals consisting of lung CT scan images of size 512×512.

Generally, medical data will be so large that overfitting is a constant issue for deep neural networks. To overcome this problem, an average pooling layer is used which reduces network complexity. Accuracy and loss plots clearly indicate that the proposed model does not overfit the data and therefore exhibits good efficacy. Sensitivity maps [30] have been used in this work to determine which area of the lung CT scan image contributes the most to the proposed model classification. It is clear from these maps that the classification decision is based on a deep neural network image feature. Sensitivity maps use a mask, which is a grey square, to cover different portions of the input image to calculate the change in probability score for a specific test image. Figure 4 shows lung CT scan image with a probability score and sensitivity maps overlaid on it. Red area in sensitivity maps shows highest contribution in classification decision wherein blue area in maps represents less or no contributions in classification decision.

Table 1. Performance comparison of MSNN with other existing deep learning models

Deep learning models	Performance metrics				
	Accuracy (%)	Sensitivity (%)	Precision (%)	F-score (%)	Specificity (%)
Faster R-CNN [27]	80.1	-	-	-	-
Cascade R-CNN [28]	84	-	-	-	-
SC-dynamic R-CNN [29]	88.1	-	-	-	-
MSNN (proposed method)	96.9	94.6	100	97.22	100

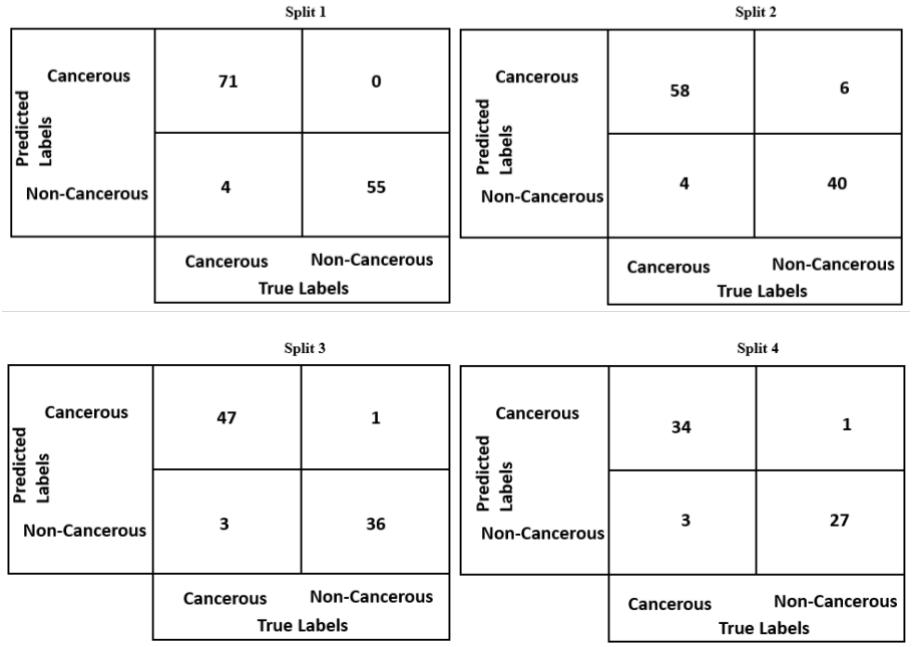

Figure 3. Confusion matrices obtained for different dataset splits

Table 2. Calculation of performance parameters for different splits

Splits	Accuracy (%)	Precision (%)	Recall (%)	FPR (%)	Specificity (%)	F-score (%)
Split1	96	100	94	0	100	97
Split2	90	90	93	13	86	91
Split3	95	97	94	2	97	95
Split4	93	97	91	3	96	94

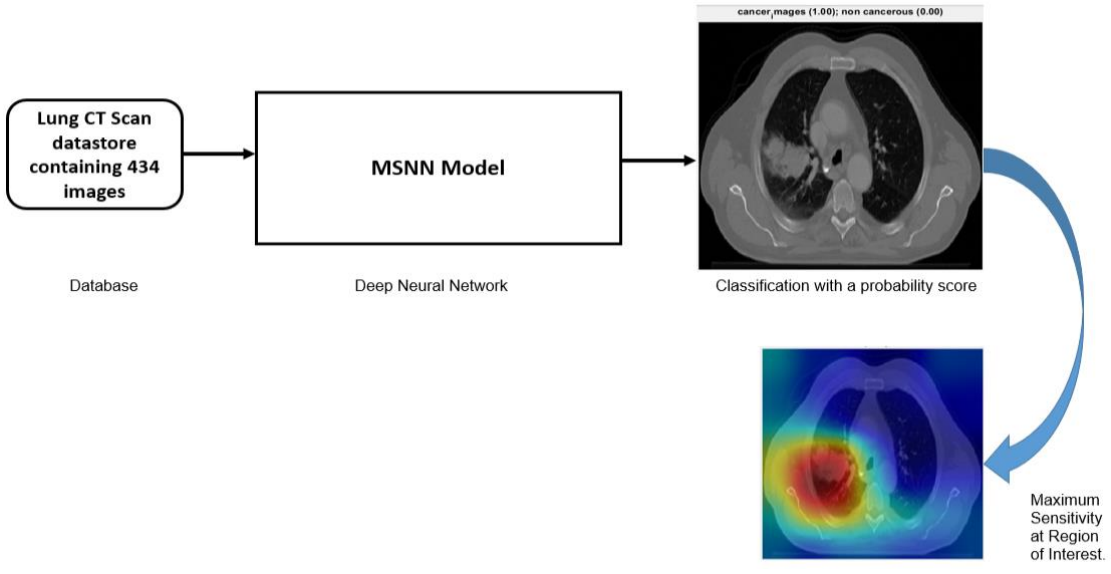

Figure 4. MSNN Model classifying lung cancer with a probability score and ploting of sensitivity map

In this research work, the proposed model extracted deep layer features. These features contain a lot of distinguished information about the image. Therefore, by using lung CT scan image, features of different convolution layers have been extracted which is shown in Figure 5. Convolution layers can extract features from various angles and therefore, the first convolution layer extracts fundamental information which

contains spots and edges. Results showed that deep layers extracted high level and abstracted features by merging earlier features. Hence, features retrieved from the deeper layers are more suited for classification [31]. The extracted features are then fed as an input to KNN classifier. While using classifier different parameters need to be set manually.

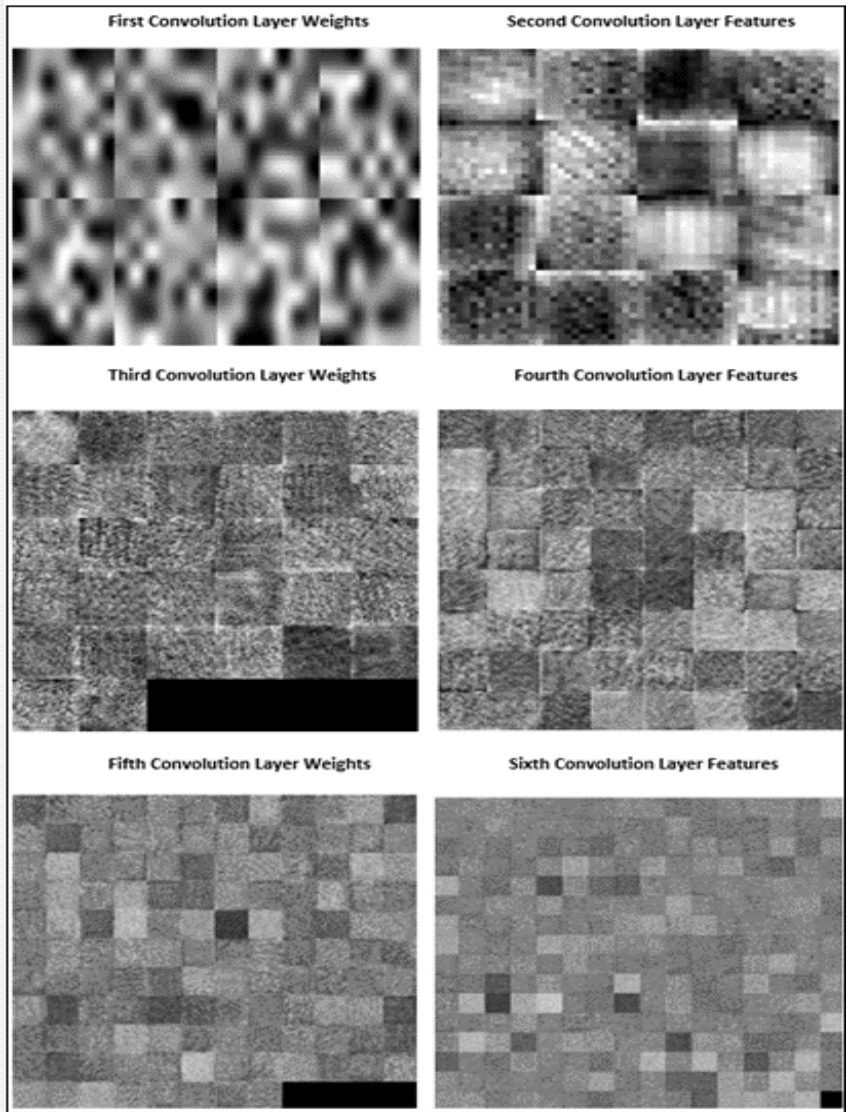

Figure 5. Features extracted from different convolution layer of MSNN

4. CONCLUSION

When building a deep learning model for lung cancer diagnosis, great accuracy is essential. As a result, MSNN model with rigorous design has been proposed which gives impressive levels of efficiency. In comparison to previous methods, the proposed model outperformed them with accuracy of 96.9% and sensitivity of 94.6%. The suggested model considerably aids in the classification process by successfully extracting features from multiple convolution layers. On the input lung CT scan image, a sensitivity map has been created, showing the nodule area in red. This map makes it easier to distinguish between cancerous and non-cancerous areas of the image. Certain factors typically need manual adjusting to attain high accuracy using a classifier, which can take time. Therefore, fixing this issue could be the main goal of future effort. Utilising Bayesian optimisation, a tool for automatically choosing the best parameters, is one possible strategy. This strategy would simplify the parameter selection procedure and increase the classifier's effectiveness.

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REFERENCES

[1] R. L. Siegel, K. D. Miller, H. E. Fuchs, and A. Jemal, "Cancer statistics, 2022," *CA: A Cancer Journal for Clinicians*, vol. 72, no. 1, pp. 7–33, Jan. 2022, doi: 10.3322/caac.21708.

[2] National Lung Screening Trial Research Team, "Reduced lung-cancer mortality with low-dose computed tomographic screening," *New England Journal of Medicine*, vol. 365, no. 5, pp. 395–409, Aug. 2011, doi: 10.1056/NEJMoa1102873.

[3] F. Bray, J. Ferlay, I. Soerjomataram, R. L. Siegel, L. A. Torre, and A. Jemal, "Global cancer statistics 2018: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries," *CA: A Cancer Journal for Clinicians*, vol. 68, no. 6, pp. 394–424, Nov. 2018, doi: 10.3322/caac.21492.

[4] P. Mathur *et al.*, "Cancer statistics, 2020: report from National Cancer Registry Programme, India," *JCO Global Oncology*, no. 6, pp. 1063–1075, Nov. 2020, doi: 10.1200/GO.20.00122.

[5] D. Ravi *et al.*, "Deep learning for health informatics," *IEEE Journal of Biomedical and Health Informatics*, vol. 21, no. 1, pp. 4–21, Jan. 2017, doi: 10.1109/JBHI.2016.2636665.

[6] D. Singh, V. Kumar, V. Yadav, and M. Kaur, "Deep neural network-based screening model for covid-19-infected patients using chest x-ray images," *International Journal of Pattern Recognition and Artificial Intelligence*, vol. 35, no. 3, Mar. 2021, doi: 10.1142/S0218001421510046.

[7] E. Montagnon *et al.*, "Deep learning workflow in radiology: a primer," *Insights Into Imaging*, vol. 11, no. 1, pp. 1–15, Dec. 2020, doi: 10.1186/s13244-019-0832-5.

[8] G. Chartrand *et al.*, "Deep learning: a primer for radiologists," *Radio Graphics*, vol. 37, no. 7, pp. 2113–2131, Nov. 2017, doi: 10.1148/rg.2017170077.

[9] M. Savic, Y. Ma, G. Ramponi, W. Du, and Y. Peng, "Lung nodule segmentation with a region-based fast marching method," *Sensors*, vol. 21, no. 5, Mar. 2021, doi: 10.3390/s21051908.

[10] M. F. Abdullah *et al.*, "A comparative study of image segmentation technique applied for lung cancer detection," in *2019 9th IEEE International Conference on Control System, Computing and Engineering (ICCSCE)*, Nov. 2019, pp. 72–77, doi: 10.1109/ICCSCE47578.2019.9068574.

[11] M. Vas and A. Dessai, "Lung cancer detection system using lung CT image processing," in *2017 International Conference on Computing, Communication, Control and Automation (ICCUBEA)*, Aug. 2017, pp. 1–5, doi: 10.1109/ICCUBEA.2017.8463851.

[12] L. Zhang, J. Huang, and L. Liu, "Improved deep learning network based in combination with cost-sensitive learning for early detection of ovarian cancer in color ultrasound detecting system," *Journal of Medical Systems*, vol. 43, no. 8, Aug. 2019, doi: 10.1007/s10916-019-1356-8.

[13] Z. Wu *et al.*, "DeepLRHE: a deep convolutional neural network framework to evaluate the risk of lung cancer recurrence and metastasis from histopathology images," *Frontiers in Genetics*, vol. 11, Aug. 2020, doi: 10.3389/fgene.2020.00768.

[14] N. Tajbakhsh and K. Suzuki, "Comparing two classes of end-to-end machine-learning models in lung nodule detection and classification: MTANNs vs. CNNs," *Pattern Recognition*, vol. 63, pp. 476–486, Mar. 2017, doi: 10.1016/j.patcog.2016.09.029.

[15] W. Shen *et al.*, "Multi-crop convolutional neural networks for lung nodule malignancy suspiciousness classification," *Pattern Recognition*, vol. 61, pp. 663–673, Jan. 2017, doi: 10.1016/j.patcog.2016.05.029.

[16] A. Masood *et al.*, "Computer-assisted decision support system in pulmonary cancer detection and stage classification on CT images," *Journal of Biomedical Informatics*, vol. 79, pp. 117–128, Mar. 2018, doi: 10.1016/j.jbi.2018.01.005.

[17] S. Govindarajan and R. Swaminathan, "Differentiation of COVID-19 conditions in planar chest radiographs using optimized convolutional neural networks," *Applied Intelligence*, vol. 51, no. 5, pp. 2764–2775, May 2021, doi: 10.1007/s10489-020-01941-8.

[18] E. Shelhamer, J. Long, and T. Darrell, "Fully convolutional networks for semantic segmentation," *IEEE Transactions on Pattern Analysis and Machine Intelligence*, vol. 39, no. 4, pp. 640–651, Apr. 2017, doi: 10.1109/TPAMI.2016.2572683.

[19] P. F. Christ *et al.*, "Automatic liver and lesion segmentation in CT using cascaded fully convolutional neural networks and 3D conditional random fields," in *International Conference on Medical Image Computing and Computer-Assisted Intervention*, 2016, pp. 415–423, doi: 10.1007/978-3-319-46723-8_48.

[20] X.-Y. Zhou, M. Shen, C. Riga, G.-Z. Yang, and S.-L. Lee, "Focal FCN: towards small object segmentation with limited training data," *arXiv-Computer Science*, pp. 1-17, 2017.

[21] M. Toğaçar, B. Ergen, and Z. Cömert, "Detection of lung cancer on chest CT images using minimum redundancy maximum relevance feature selection method with convolutional neural networks," *Biocybernetics and Biomedical Engineering*, vol. 40, no. 1, pp. 23–39, Jan. 2020, doi: 10.1016/j.bbe.2019.11.004.

[22] T. Hinz, N. N. -Guerrero, S. Magg, and S. Wermter, "Speeding up the hyperparameter optimization of deep convolutional neural networks," *International Journal of Computational Intelligence and Applications*, vol. 17, no. 2, Jun. 2018, doi: 10.1142/S1469026818500086.

[23] C. Garbin, X. Zhu, and O. Marques, "Dropout vs. batch normalization: an empirical study of their impact to deep learning," *Multimedia Tools and Applications*, vol. 79, no. 19–20, pp. 12777–12815, May 2020, doi: 10.1007/s11042-019-08453-9.

[24] H. Ide and T. Kurita, "Improvement of learning for CNN with ReLU activation by sparse regularization," in *2017 International Joint Conference on Neural Networks (IJCNN)*, May 2017, pp. 2684–2691, doi: 10.1109/IJCNN.2017.7966185.

[25] D. L. M. and P. M., "Performance evaluation of convolutional neural network for lung cancer detection," in *2022 International Conference on Electronic Systems and Intelligent Computing (ICESIC)*, Apr. 2022, pp. 293–298, doi: 10.1109/ICESIC53714.2022.9783533.

[26] L. Wang, "Deep learning techniques to diagnose lung cancer," *Cancers*, vol. 14, no. 22, Nov. 2022, doi: 10.3390/cancers14225569.

[27] S. Ren, K. He, R. Girshick, and J. Sun, "Faster R-CNN: towards real-time object detection with region proposal networks," *IEEE Transactions on Pattern Analysis and Machine Intelligence*, vol. 39, no. 6, pp. 1137–1149, Jun. 2017, doi: 10.1109/TPAMI.2016.2577031.

[28] Z. Cai and N. Vasconcelos, "Cascade R-CNN: delving into high quality object detection," in *2018 IEEE/CVF Conference on Computer Vision and Pattern Recognition*, Jun. 2018, pp. 6154–6162, doi: 10.1109/CVPR.2018.00644.
[29] X. Wang, L. Wang, and P. Zheng, "SC-Dynamic R-CNN: a self-calibrated dynamic R-CNN model for lung cancer lesion detection," *Computational and Mathematical Methods in Medicine*, vol. 2022, pp. 1–9, Mar. 2022, doi: 10.1155/2022/9452157.
[30] N. S. Nadkarni and S. Borkar, "Detection of lung cancer in CT images using image processing," in *2019 3rd International Conference on Trends in Electronics and Informatics (ICOEI)*, Apr. 2019, pp. 863–866, doi: 10.1109/ICOEI.2019.8862577.
[31] A. I. Khan, J. L. Shah, and M. M. Bhat, "CoroNet: a deep neural network for detection and diagnosis of COVID-19 from chest x-ray images," *Computer Methods and Programs in Biomedicine*, vol. 196, Nov. 2020, doi: 10.1016/j.cmpb.2020.105581.

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