

LUNG CANCER CLASSIFICATION USING DENSENET MULTI MODEL OPTIMIZATION TECHNIQUES

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ABSTRACT

Unchecked cell growth in lung tissue is indicative of lung cancer. Early identification of cancerous cells in the lungs is essential for functions including the body's carbon dioxide and oxygen elimination. The potential influence on patient diagnosis and treatment has led to a great deal of interest in the application of deep learning to identify lymph node invasion in CT scan and histology pictures. This approach consists of three stages: preprocessing, feature extraction, and classification. In order to identify lung cancer, we suggest using DenseNet's capability to continually propagate learnt characteristics backward via each layer. Pre-processing methods like contrast enhancement and filtering can be used to reduce undesired noise in the incoming image. Next, optimization techniques like Otsu thresholding are used to achieve the required picture segmentation. Among the suggested classifiers is the DenseNet classifier. Structure, hyperparameter optimization, etc. are used in DenseNet's multi-process optimization. We use performance matrices like accuracy, precision, recall, specificity, sensitivity, and F_Measure to execute the suggested technique in MATLAB.

1. INTRODUCTION

The term "cancer" is wide. suggests a condition where uncontrollable cell growth and division are brought on by alterations in the cells. The majority of bodily cells have set lifespans and specialized roles. Apoptosis, however, is a component of the natural phenomena known as apoptosis. The body instructs cells to die so that fresh, more functional cells can take their place. The machinery needed to teach cancer cells to cease proliferating and die is absent. As a result, they often develop inside the body, feeding other cells with nutrition and oxygen. Tumors, immune system impairment, and other anomalies that impair normal bodily functions can all be brought on by cancer cells. [1] Unchecked cell growth in lung tissue is a hallmark of lung cancer, a malignant lung tumor. [2] The most common cause of death from cancer is lung cancer.

The primary goal of this study is to identify the existence of lung cancer cells using data and symptoms from humans. This study investigates if lung cancer may be identified from a person's body using artificial neural network models. The following are the study's objectives:

- Human lung CT image identification is accomplished using the method proposed in this study to construct DenseNet for lung cancer prediction.
- The suggested technique comprises four processes: preprocessing, feature selection, segmentation, and classification.

- The ineffectiveness of classification is attributed to the unwanted noise seen in the CT images gathered here. One may use preprocessing techniques such as filtering and contrast enhancement to eliminate unwanted noise from the input image.
- After that, the image is segmented using Otsu thresholding and other optimization techniques.
- The categorization process then takes place.

2. LITERATURE REVIEW

In this field of study, Nasser, Ibrahim M., and associates developed several neural network-based models for categorization, prediction, and diagnosis. Neural networks were suggested for many purposes such as predicting the category of movies to watch [3], predicting the price range of mobile phones predicting the category of animals [4], diagnosing tumors [5], and diagnosing autism [6]. Abu Nasser together with others. Artificial neural networks serve as the foundation for several categorization methods [7].

In their work, Jock et al. (2023) [8] suggested a neuro-heuristic method to deal with the minute alterations in lung tissue structure that arise in cases of pneumonia, sarcoidosis, or cancer as well as certain potential side effects of treatment. The outcomes of the method's testing showed how promising the recently suggested approach was. The approach also has a minimal computing load and is adaptable.

It was discovered by Rakshit S. et al. (2023) [9] that chest research is necessary to comprehend what he is discussing. After that, DenseNet is used for categorization. Here, we go over how the suggested model, the ResNet18 network, performs comparably to earlier tested models and requires less parameters to train.

The usage of convolutional neural networks and machine learning techniques in medical image processing are discussed by Justin Cole et al. (2022) [10]. In this section, we go over the significance of deep learning in identifying specific medical disorders. The clinical and deep learning components will be the main focus.

3. METHODOLOGY

In order to diagnose lung cancer, we first provide a dataset in this part that includes pictures from chest CT scans and images from histology. Next, we'll go over the specifics about feature selection, partitioning, and preprocessing in this post. Lastly, this part concludes with information regarding the DenseNet architecture.

3.1. Dataset Description

15,000 JPEG-formatted histopathology photos, each measuring 768 by 768 pixels, are included in the collection. These photos adhere to HIPAA regulations, and the veracity of their sources has been confirmed. At first, there were 750 lung tissue photographs in the collection; these were split equally into three categories: 250 images of positive lung tissue, 250 images of lung adenocarcinoma, and 250 images of lung squamous cell carcinoma.

- Lung benign tissue;
- Lung adenocarcinoma;
- Lung squamous cell carcinoma.

Figure 1 presents samples associated with these three classes.

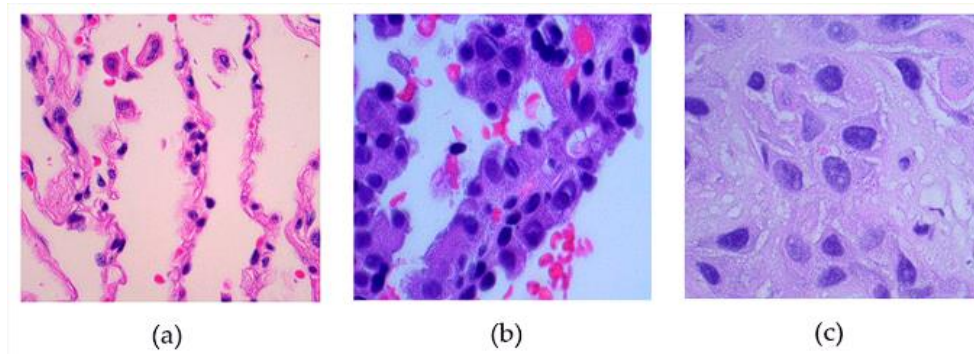


Figure 1. Histopathological images for lung cancer detection: (a) lung benign tissue, (b) adenocarcinoma, (c) squamous cell carcinoma.

We take into account one normal level and three cancerous levels for chest CT scan pictures. Adenocarcinoma, large cell carcinoma, and squamous cell carcinoma are the three forms of cancer. For teaching and assessment, 340 photos overall per class (including the general class) are utilized. Sample photos for these classes are displayed in Figure 2.

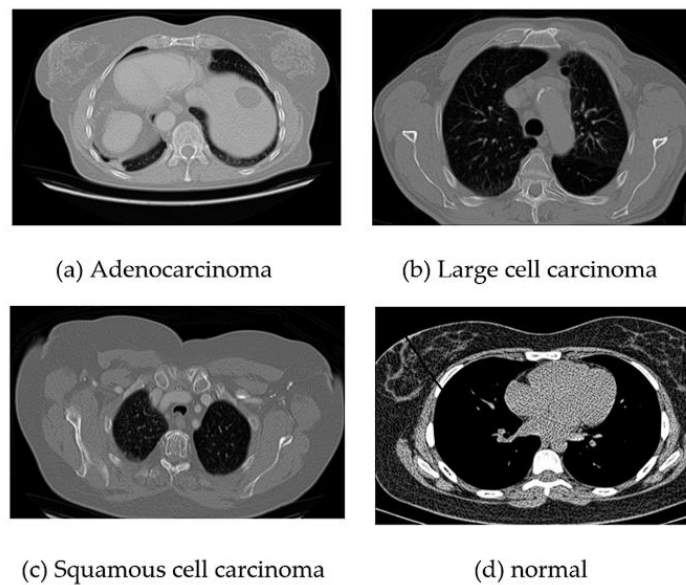


Figure 2. CT scans for lung cancer detection: (a) adenocarcinoma, (b) large-cell carcinoma, (c) squamous cell carcinoma, (d) normal.

3.2. Pre-processing

Our strategy involves the use of wavelet threshold to suggest several picture resolutions for the adaptive bilateral method. Its primary outcome is:

3.3. Adaptive bilateral Filter

To adjust different changes in picture resolution, the spatial domain ($\{d\}$) and intensity domain ($\{\Phi r\}$) parameters are employed on both sides. In order to investigate the best parameter values through experimentation, it is necessary to alter the noise variance in picture denoising applications. correlation between the parameters d , r , and n for the standard deviation. Using the parameters d and r , we test the multivariate picture resolution and use the bilateral approach to minimize the noise in the input image. Record the MSE and PSNR readings and repeat for effective noise dispersion.

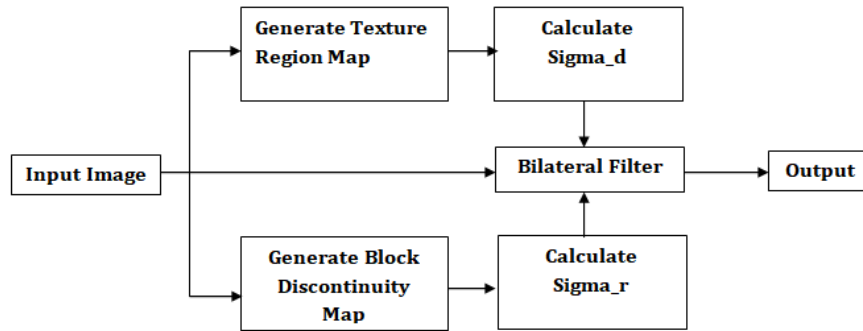


Figure 3: Architecture diagram of Adaptive bilateral method

Parameter d has a value range of 1.5 to 2.0, and the value of r varies dramatically as the standard deviation n value varies. Figure 1. One of the best strategies to minimize noise is to alter the analysis of various picture resolutions. It may raise the degree of picture resolution and sequentially separate images from noise. Wavelet thresholding in conjunction with the adaptive bifacial approach at different picture resolutions. Sub-bands are subjected to an adaptive bidirectional technique to minimize low-frequency noise components.

A grayscale picture is created from the original. Non-linear bidirectional filters maintain picture edges while lowering noise. Replace the intensity of each pixel with the weighted average of its surrounding pixels. a pixel value weighted average derived from a Gaussian blur. This is described as:

$$BF[I]_p = \frac{1}{W_p} \sum_{q \in S} G_{\sigma_s}(|p - q|) G_{\sigma_r}(I_p - I_q) I_q$$

Where W_p is normalization factor:

$$W_p = \sum_{q \in S} G_{\sigma_s}(|p - q|) G_{\sigma_r}(I_p - I_q)$$

Where,

σ_s and σ_r - compute quantity of filtering input image

G_{σ_s} – To decrease distant pixels

G_{σ_r} – If decrease a gaussian the influence of pixels q with intensity value different from I_p .

To smooth bigger features and get the filter closer to a Gaussian blur, raise the parameter σ_s and adjust the parameter σ_r to make the range more Gaussian-flat.

3.4. Feature selection

The suggested ITEO algorithm for choosing predicted genes from cancer microarray gene expression profiles is presented in this section. The algorithm uses the ITEO method, a packaged gene selection technique that selects informative and relevant genes in advance using the DenseNet classifier. The goal is to pick more informative genes in order to increase the DenseNet classifier's accuracy performance. The suggested algorithm's solution representation is shown. It is clear that characteristics are chosen for our suggested approach from tiny data sets that include relevant genes. When compared to the original method that chooses genes based just on the initial microarray data set, this enhances the optimization process.

3.5. Improved Thermal Exchange Optimization Algorithm

Thermal exchange is started by grouping objects together, and item temperatures are expressed at each location in Thermal Exchange Optimization (TEO). Consequently, the revised location is represented by the new temperature.

A few flaws in the fundamental heat exchange optimization technique are early convergence problems and stability problems. To address these issues as much as feasible, we created a modified version of the TEO algorithm in this instance.

Using L'evy Flying (LF) as the appropriate mechanic is the first solution. To overcome the drawbacks of early convergence, metaheuristic algorithms frequently employ this method. This technique may be mathematically described as follows. It adjusts the local search suitably by using a random work strategy.

$$Le(x) \approx \frac{1}{x^{1+\tau}}$$

$$x = \frac{A}{|B|^{\frac{1}{\tau}}}$$

$$\sigma^2 = \left\{ \frac{\Gamma(1+\tau)}{\tau \Gamma\left(\frac{1+\tau}{2}\right)} \times \frac{\sin\left(\frac{\pi\tau}{2}\right)}{2^{1+\frac{\tau}{2}}} \right\}^{\frac{2}{\tau}}$$

where $A \sim N(0, \sigma^2)$, $B \sim N(0, \sigma^2)$, τ signifies the L'evy index which is located in the range $[0, 2]$ (here, $\tau = 1.5$ [25]), $\Gamma(\cdot)$ represents Gamma function, and w defines the step size. By assuming the above equations, the updating formulation for the TEO algorithm is as follows:

$$T_{i,j}^{new} = T_j^{min} + Le(T_j^{max} - T_j^{min}) \exp(-\gamma t)$$

Using the chaotic mechanism to accelerate the system's convergence is the second change. Here, chaos correction is achieved by Singer characteristics [13]. This process in mind, rnd may be updated in the following manner:

$$rnd_{i+1} = 1.07(7.9 \times rnd_i - 23.3 \times rnd_i^2 + 28.7 \times rnd_i^3 - 13.3 \times rnd_i^4)_x$$

where $rnd_0 \in [0, 1]$.

Here, X represents the current person, j is the location of the nearby individual, N is the number of neighboring individuals, and d is the separation of the individual.

$$A_i = \frac{\sum_{n=1}^N Vel_n}{N}$$

In (2), A_i represents the i th individual's alignment, while Vel_n denotes the n th surrounding individual's velocity.

$$Coh_i = \frac{\sum_{n=1}^N X_n}{N} - X$$

Coh_i in (3) refers to the unity of the i -th person. The equation that follows illustrates a dragonfly's attraction to a source.

$$Food_i = X^+ - X$$

In (4), X^+ denotes the source location (classification accuracy), X stands for the current individual location, and $Food_i$ is the source of the sixth person. The following is the computation for distributing unnecessary features:

$$Ene_i = X^- + X$$

The locations of unnecessary features in (5) are designated by X^- and Ene_i , respectively. Step size (Δx) and location (X) are the two vectors that must be taken into account in order to update the artificial dragonfly's position in the search space and replicate the motion. The alignment mark's movement direction is denoted by Δx , which is determined in the following manner.

$$\Delta X_{t+1} = (dD_i + aA_i + cCoh_i f Food_i + eEne_i + w\Delta X_t)$$

The separation weight, food factor, alignment weight, enemy factor, cohesion weight, inertia weight, and repetition counter are represented by the letters d , f , a , and t in equation (6). Compute the position vector as follows after determining the step vector:

$$X_{t+1} = X_t + \Delta X_{t+1}$$

The goal of a dragonfly's motions is to form a dynamic group. The dragonfly moves quite slowly in a static position, yet it has great strength when facing up against adversaries. Consequently, the array coefficients are high and the harmonic coefficients are low during the discovery phase, and the opposite is true during the extraction phase when the array coefficients are small and the harmonic coefficients are big.

To enhance artificial dragonfly discovery in the absence of neighbor solutions, we incorporate stochastic solutions using LFM. Consequently, the alignment mark's location is updated as follows.

$$X_{t+1} = x_t + Levy(d) \times X_t$$

In (8), d represents the size of the position vector.

$$Levy(x) = 0.01 \times \frac{r_1 \times \sigma}{|r_2|^{\frac{1}{\beta}}}$$

In (9), r_1 and r_2 are random numbers which is ranges from 0 to 1 and β is the constant value. σ is calculated as,

$$\sigma = \left(\frac{\Gamma(1 + \beta) \times \sin\left(\frac{\pi\beta}{2}\right)}{\Gamma\left(\frac{1+\beta}{2}\right) \times \beta \times 2^{\beta-\frac{1}{2}}}\right)$$

In (10), $\Gamma(x) = (x - 1)!\dots$

3.6. Segmentation

3.6.1. OTSU Thresholding

This strategy's goal is to identify pixels in a picture that belong to a certain comparable category and then determine how close together neighboring pixels are in order to create a focussed image object. It is challenging to extract background and subregions from medical pictures. There is a greater "blurring" or "recognizing" of the contextual material of the prior item using the OTSU segmentation method. This is the binary process with an adjustable threshold that OTSU presented in 1979. The threshold classification rule (11) states that the biggest within-class variation between context and target is used in this method. The features of gray value are used to divide the picture into a foreground and a context image. The greatest distance exists between the two zones when the thinnest threshold is crossed. Typically, the Otsu algorithm takes use of the highest within-class variation. The disparity between the two regions is higher the larger the variance value. This is due to the fact that variance may be used to determine a grayscale distribution that is uniform. The distance between two areas is too short if certain contexts are improperly separated into areas, or if some areas are erroneously divided into contexts. Therefore, the likelihood of misdiagnosis resulting to cohesive splitting decreases with increasing diversity across groups.

The fundamental ideas of OTSU-based threshold segmentation are as follows. Let n_x be the number of pixels and g be the gray value. following that

$$P = \sum_{x=0}^{L-1} n_x = n_0 + n_1 + n_2 + \dots + n_{L-1} \dots$$

Here, the number of pixels is represented by $g=0, 1, \dots, L-1$, and P . Assume there are two kinds of pixels, C_1 and C_2 . C_1 's pixel range is $[0, x]$, while C_2 's pixel range is $[x+1, L-1]$.

$$\sigma_{Gv}^2 = \sum_g^{L-1} (g - m_{Gv})^2$$

$$\sigma_{Bv}^2 = P_1(m_1 - m_{Gv})^2 + P_2(m_2 - m_{Gv})^2$$

The below-mentioned calculations are used to compute the mean intensities.

$$m_1 = \frac{1}{P} \sum_{g=0}^x g \cdot P_g$$

$$m_2 = \frac{1}{P} \sum_{g=x+1}^{L-1} g \cdot P_g$$

$$m_{Gv} = \sum_{g=0}^{L-1} g \cdot P_g$$

where m_{Gv} is the overall average intensity and m_1 and m_2 are the average intensities of C1 and C2 pixels. Lastly, the optimal threshold is found using the ratio τ shown below.

$$\tau = \frac{\sigma_{Bv}^2}{\sigma_{Gv}^2}$$

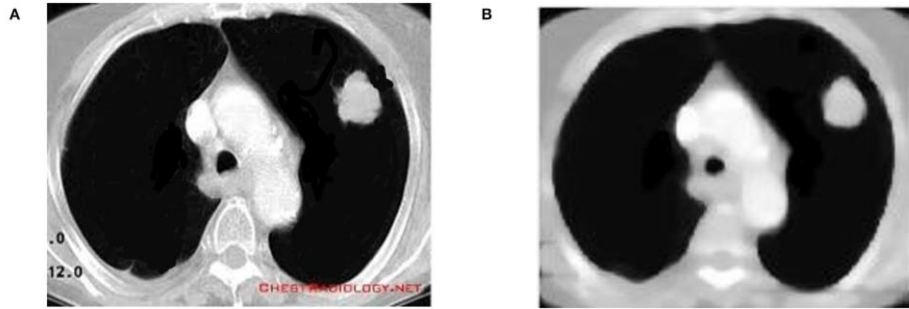


Fig 3: (A) Input CT image (B) Filtered output

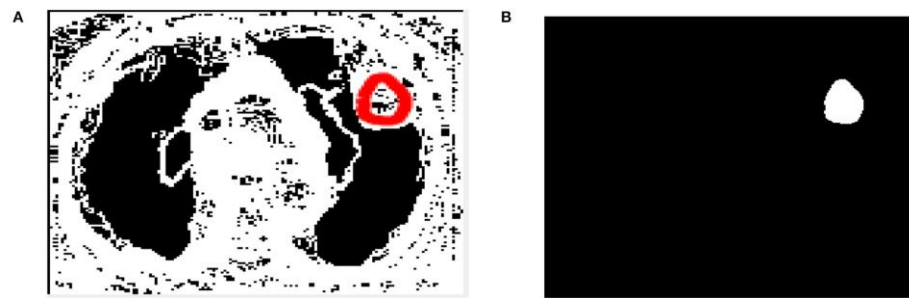


Fig 3: (B) Extracted output (B) Segmented output

3.7. Classification

Important issues that are frequently encountered in deep learning models, such as disappearing gradients and wasteful parameter consumption, are resolved by DenseNet [12]. The use of dense connections, which guarantee that every layer is directly and feed-forward coupled to every other layer, is a unique characteristic. This topology enhances learning stability and efficiency by facilitating the easy exchange of information throughout the network. DenseNet's fundamental building block is a small block made up of several layers, each of which transmits relevant feature maps and receives input from all levels before it. These patterns of dense connections encourage useful functional reuse across the network, efficiently using and combining representations acquired at various depths. Furthermore, by addressing the vanishing gradient issue, DenseNet adds shortcut connections that provide simpler gradient flow during training, enhancing the effectiveness and performance of model training.

DenseNet incorporates transformation layers between compact blocks to control computational cost and model complexity. In order to lower the number of channels and downsample the spatial dimension, these transition layers usually include pooling and convolution techniques[13]. A hyperparameter called growth rate controls how many more channels are added to each layer of

dense block, which has an impact on the network's capacity for feature learning and representation.

DenseNet frequently makes use of bottleneck layers within each dense block in addition to dense connections. To increase computational efficiency, 1×1 and 3×3 convolutions make up these bottleneck layers. Typically, the design is completed by a global average pooling layer that lowers the spatial dimension to a 1×1 grid and a final classification layer.

The best thing about DenseNet is that, in comparison to other designs, it uses parameters more effectively to build models with less parameters. Accuracy and training efficiency are increased when these effective parameters are used in conjunction with dense connections. DenseNet has been widely used in the field of computer vision since it has shown to be very successful for picture classification tasks. DenseNet may be represented simply as follows:

Dense block: Let's say that l -th layer output, X_l , is the input of the Dense block, and H_l is a collection of convolution operations[14]. A function connecting the input to the output of H_l is then required. Layer L 's output is the result of concatenating the outputs of every preceding layer and the H_l task.

Transformation layer: input, l th dense block's output (X_l). "C" stands for "lower-than-max-channel" compression factor. We next do the average pooling and convolution operations. The transition layer's output may be stated as follows:

$$X_{l+1} = \text{Conv}(\text{AvgPool}(X_l)\theta_l)$$

To improve parameter efficiency, the transition layer reduces the number of channels and spatial dimensions.

Overall DenseNet Structure: Considering X_0 as the input picture, with $H_1, H_2, \dots, H_L$ as dense blocks, and $\theta_1, \theta_2, \dots, \theta_L$ as compression factors for every transition layer. B is the growth rate, or the quantity of new channels that each layer adds.

A densely linked network is formed by a sequence of dense blocks joined by transition layers that make up the overall structure. Figure 4 illustrates the DenseNet architecture for lung cancer detection utilizing pictures from histology and chest CT scans.

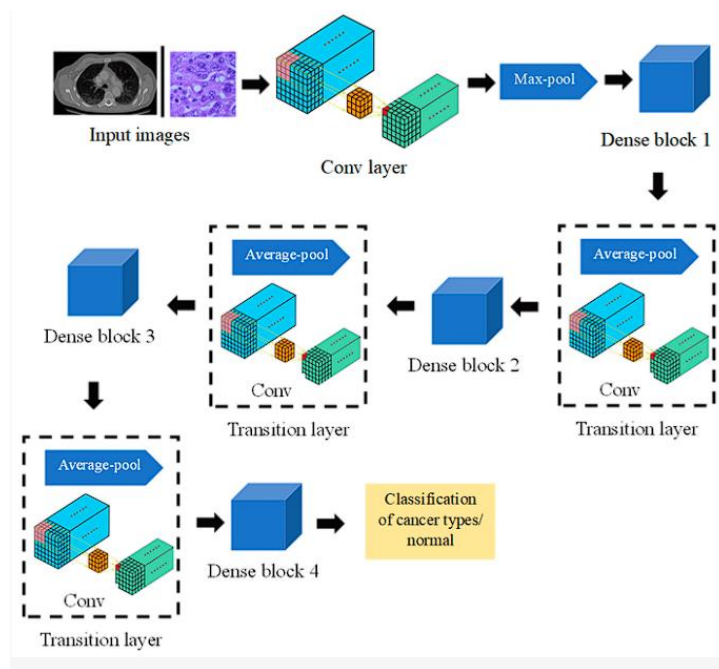


Figure 4. DenseNet architecture for lung cancer classification.

Physician Code explains how to use a specialized computer application to analyze medical video of lung cancer step-by-step. The picture must be systematically prepared as the initial stage. After that, it automatically extracts each image's key elements by going through several layers. As a result, the most important traits are given extra attention via unique attention processes, which increases their prominence throughout the decision-making process. Ultimately, the software ascertains if the picture exhibits any indications of lung cancer. Verify the process's effectiveness by examining the decisions' dependability and correctness.

1. Input: CT Scan and Histopathological Images;
2. Preprocessing: Normalize images to the same scale;
3. For each image in the dataset:
 - a. Pass image through DenseNet layers:
 - Convolutional layers: Extract features from the image;
 - Pooling layers: Reduce spatial dimensions of the feature maps;
- Dense blocks:
 - Enhance feature extraction through densely connected layers;
 - b. Integrate Attention Mechanism:
 - Compute attention scores for feature maps generated by DenseNet;
 - Multiply attention scores with corresponding DenseNet feature maps;
 - c. Classification Layer:
 - Flatten the attended feature maps;b
 - Pass through fully connected layers to obtain the final classification;
4. Output: Lung cancer diagnosis (Cancerous or Non-Cancerous);
5. Evaluation:
 - Use metrics such as accuracy, precision, recall, and the F1-Score to evaluate model.

4. RESULTS AND DISCUSSION

We then evaluated the performance of the best pipeline, consisting of a FIFB network, for nodule growth detection. A forecast is considered accurate if the diameter difference between the expected and actual nodules has the same sign[15]. Consequently, we obtained an F1 score of 0.90, a recall of 0.92, and an accuracy of 0.88 out of 36 properly classified instances. The confusion matrix is seen in the picture.

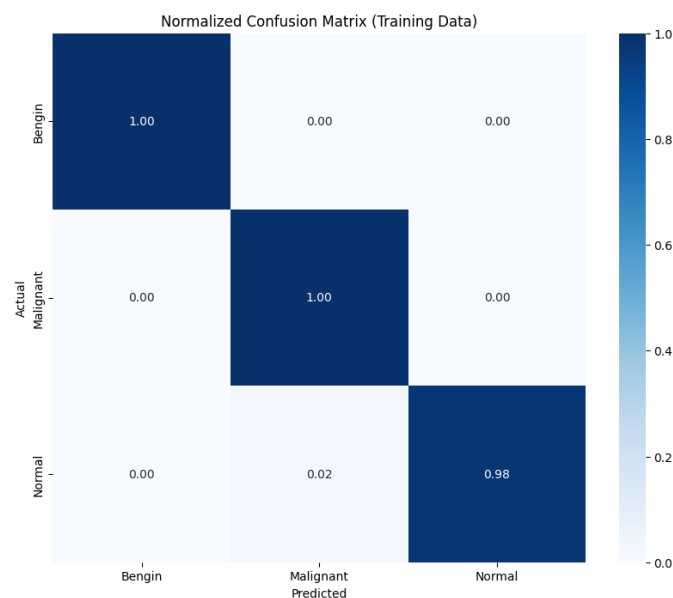


Figure 4. Confusion matrix for validation data (histopathological images): (a) DenseNet, (b) AlexNet, (c) SqueezeNet.

4.1. Preprocessing

Sometimes the device takes pictures with low contrast and brightness, which might have an impact on the surrounding area because of issues with the imaging structure and lighting. At this stage, we produce pictures that more accurately depict the characteristics by applying image upscaling algorithms. In order to do this, we sharpen the edges, boost contrast, and apply noise filtering to the image. The comparative photographs' initial and enhanced iterations are displayed in the table, accordingly.

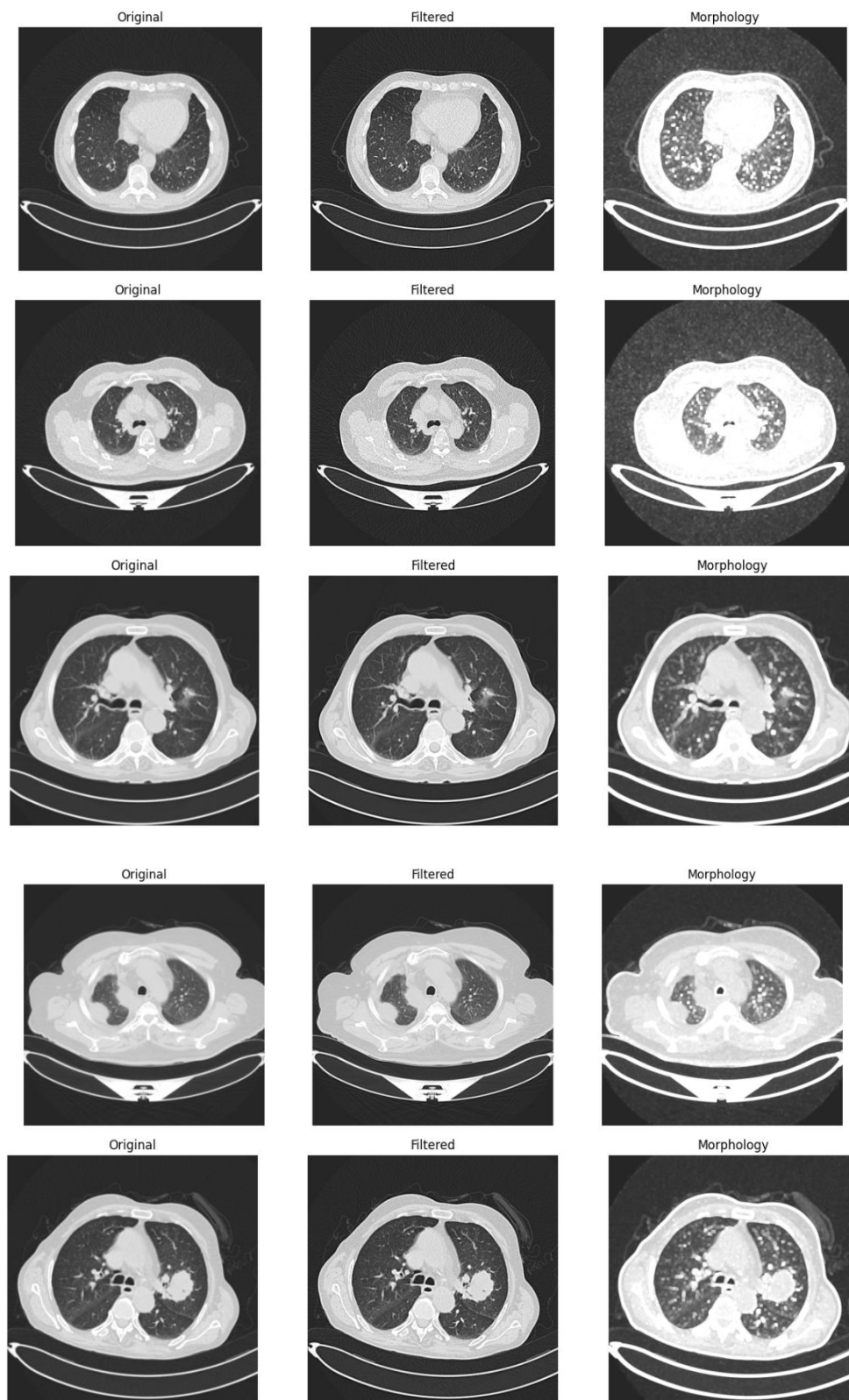


Figure 5: Pre-Processing Output

Upon reviewing the outcomes of several training trials, we discovered that the following combinations of parameters yield the greatest results: 20 filters, 5 x 5 filter size, learning rate of 0.01; momentum of 0.9; full size of 2; and stride of 2 x 2. The convolutional layer has a maximum Epoch. 30 and a completely linked layer with armed and unarmed categories for output size. These are going to be utilized in other research. The training accuracy against epochs and training loss vs epochs graphs are displayed in the appendix in Figure 6. For each to produce results, around 5/8 epoch are needed.

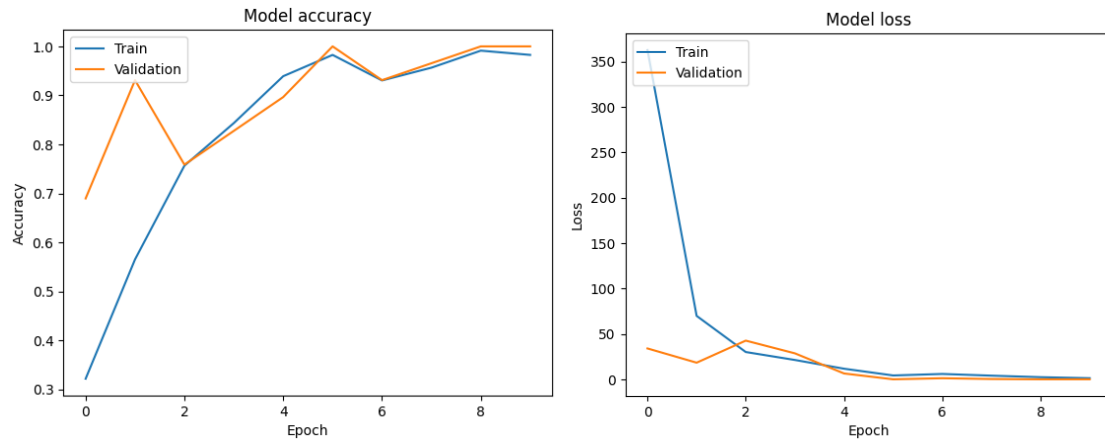


Figure 6: Model Accuracy and Loss

A performance of DenseNet is shown in Figure 7. Recall, accuracy, precision, and F1-score are the performance indicators that are taken into consideration.

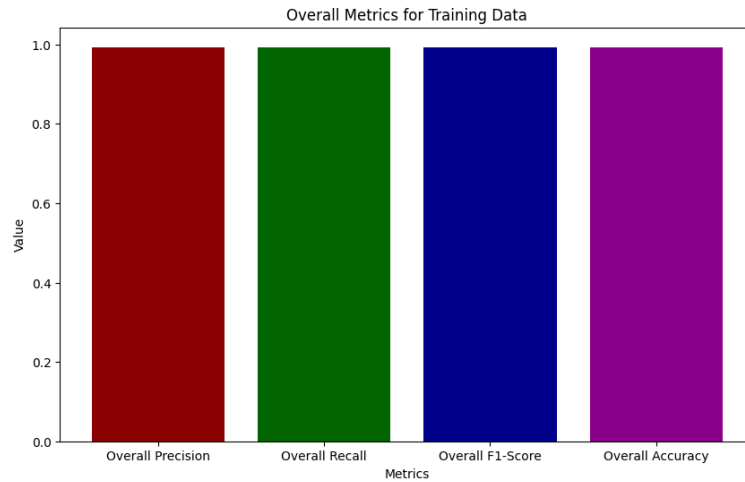


Figure 7: Overall Metrics

Overall Metrics for Training Data:
 Overall Precision: 0.9932002314814814
 Overall Recall: 0.9930555555555556
 Overall F1-Score: 0.9930563091577742
 Overall Accuracy: 0.9930555555555556

5. CONCLUSION

In this work, we propose to predict and categorize lung cancer by segmenting and interpreting human lung CT images using DenseNet generation. To eliminate extraneous noise from the input image, preprocessing methods like contrast enhancement and filtering may be taken into consideration. After that, it is divided up using optimization methods like Otsu Thres holding. The suggested classifier and DenseNet have been combined. In this work, we utilize the suggested approach to identify lung cancer in CT scans of humans in order to construct the DenseNet lung cancer prediction model. We utilize performance matrices like F_Measure, Specificity, Sensitivity, Precision, Recall, and Recall in order to execute the suggested method in MATLAB. This method's results were 99.5, 93.5, 95.5, 95.5, and 93.5 for accuracy, sensitivity, specificity, and recall, respectively.

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