RESEARCH ARTICLE

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Integrating Ant Colony Optimization with Deep Learning Models for Improved Lung Cancer Diagnosis and Prognosis

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Abstract

Objective: The goal of this study is to increase the accuracy and reliability in diagnosing lung cancer with a new approach that employs Ant Colony Optimization in an ensemble with deep learning models: DenseNet, ResNet 50, VGG 16, and Long Short-Term Memory networks. In this study, Ant Colony Optimization has been united with advanced deep learning models like DenseNet, ResNet 50, VGG 16, Long Short-Term Memory networks, for improved detection of lung cancer from CT images and medical records. ACO optimization in feature selection was performed, greatly enhancing the performance of models, which when tested showed high accuracy rates in AI-driven health care solutions.

DenseNet, combined with ACO and LSTM, achieved an accuracy of 97.9%. The study demonstrates the effectiveness of ACO in improving diagnostic precision, setting a foundation for future AI-driven healthcare solutions to improve lung cancer diagnosis and patient outcomes. **Methods**: This research integrates Ant Colony Optimization (ACO) with advanced deep learning models-DenseNet, ResNet 50, and VGG 16-and Long Short-Term Memory (LSTM) networks to improve lung disease diagnosis from CT scans and medical records. **Results:** This research enhances lung cancer diagnosis by integrating Ant Colony Optimization (ACO) with advanced deep learning models like DenseNet, ResNet 50, VGG 16, and LSTM networks. ACO optimizes feature selection, improving model accuracy. DenseNet with ACO and LSTM achieved the highest accuracy of 97.9%. ResNet 50 reached 96.2%, while VGG 16 had 92.3%. The study demonstrates the effectiveness of combining swarm intelligence with deep learning for improved medical diagnosis. **Conclusion:** The ACO approach effectively optimizes feature selection, significantly improving model performance. With DenseNet achieving an accuracy of 97.9%, this study highlights promising advancements in AI-driven healthcare solutions for more precise and reliable lung cancer diagnosis and prognosis.

Keywords: Ant Colony Optimization- Deep Learning- lung cancer- Feature Selection- CT Scans

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Introduction

Lung cancer, especially renal cell carcinoma (RCC), is a severe global health problem and contributes to high mortality from malignancy. As the prevalence of lung cancer continues to rise, better tools for diagnosing disease earlier and improving outcomes in patients are warranted. Existing diagnostic methods predominantly involve imaging modalities such as CT, MRI, and ultrasound, in addition to biopsy through histopathology [1-3]. However, this is not enough to guarantee high diagnostic performance in distinguishing between malignant and benign tumours, as well as to assess cancer stage/prognosis. Conventional imaging modalities often have low specificity and sensitivity, potentially resulting in overdiagnosis or detection at a later stage. Consequently, there is an urgent need for such innovative strategies that are suited and possible with state-of-the-art technologies to support correct diagnosis as well as earlier disease intervention [4-5].

Deep Learning, is a subset of artificial intelligence (AI), has made unprecedented transformations in medical imaging by providing tools for automated image analysis. One of the more popular deep learning architectures used for image classification and object detection is Convolutional Neural Networks (CNNs). CNNs are very useful for automatically learning hierarchical features from images, which makes them well-suited for medical imaging [6-8]. Given the numerous CNN models that exist, VGG 16, ResNet 50, and DenseNet are some of

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the most promising in detecting cancer. VGG 16 is a deeper model and is able to capture finer details quickly, but it may be computationally expensive. ResNet 50 uses well-known residual connections to address the vanishing gradient problem and improve the training of deeper networks, resulting in better performance on feature extraction and classification. Dense connectivity improves feature reuse and gradient flow, thus increasing image classification accuracy. All of them have demonstrated a remarkable ability to enhance the diagnostic performance for lung cancer, but many issues still need to be solved, and barriers that are related mainly to their overfitting or computational complexity must be overcome [9-10].

The ant colony optimisation method is a metaheuristic algorithm with which the foraging behaviour of ants has been simulated. Feature selection in machine learning is a type of optimisation problem where ACO has been successfully applied. To reduce data dimensionality, improve model performance, and minimise computational expenses, feature selection is one of the significant steps. The ACO aims to mimic how ants search for the shortest path between food sources and their nests while automating which features are most important in a dataset [11-13]. This feature selection algorithm works in the best way when one weights and rates features appropriately, then ants also converge on a better subset of pheromones considering such feature factorisation. Several previous studies have shown the utility of ACO in improving machine learning models in different applications, including some related to medical diagnostics. ACO is proposed to optimise the selection of features in lung cancer and, thereby, could have a potential impact on enhancing feature selection approaches for more accurate classification models with high performance [14-15].

Combining ACO and deep learning models provides a promising path toward improving model performance, more specifically in medical diagnostics. Some earlier researchers have investigated the synergy of ACO and deep learning frameworks since they can provide better outcomes than using a single approach. ACO improves the selection of features through which the relevant attributes from complex data sets are selected, and these are sent to deep learning models for training as well as prediction. By integrating dotted lesions into the dataset(label), these networks increase accuracy in detecting subtle patterns of abnormality through medical images. The features of the] image are optimised by ACO in VGG 16, ResNet50 and DenseNet at the feature level to improve their performance on lung cancer detection, for example. Many studies have shown that improving diagnostic accuracy and reducing the risk of overfitting this approach was beneficial by improving model generalization capabilities[16-17].

LSTM (Long Short-Term Memory) networks are a class of RNNs designed to recognize sequential data or temporal patterns. Since LSTMs can capture dependencies across time and have a powerful ability to predict sequence outcomes, they are helpful in the modelling of medical records (exceptionally patient history datasets). LSTMs are a valuable addition to deep learning models, providing another perspective when interpreting temporal data such as patient symptoms, treatment history and therapy response in the context of lung cancer diagnosis [18-20]. Combining CNN models with LSTMs allows a holistic analysis of the convolutional features learned from medical imaging and clinical temporal patterns in large-scale electronic health records. This combination of data sources significantly improves diagnostic accuracy globally and provides a complete image of the patient's health perspective. There has been much research on the efficiency of using LSTMs for medical applications, including cancer detection, which has been shown to increase prediction and classification performances.

Although new techniques of integrating ACO, deep learning and LSTM networks for cancer diagnosis have been beneficial in yielding better results, the current state-of-the-art research leaves several gaps. Although integrating these techniques has shown more excellent diagnostic as well as methodologic accuracy, challenges remain with respect to how best they can be applied [21- 22]. Failures related to problems such as feature selection, model complexity balancing and the integration of different data sources should be systematically analyzed. Furthermore, more inclusive studies to investigate integrated approaches for different types and stages of lung cancer are also required. Frequent research in this area will help to fill these gaps, and the results can provide potential pathways for integrating swarm intelligence with deep learning for more qualitative medical diagnostics. Avoiding the vanishing-gradient, enhancing feature propagation, reusing features and lowering the number of training parameters are some of the benefits as compared with other models. This is the reason why highest accuracy is achieved as compared with other models. The major strength of this work is that it deals with forecasting the possibilities of lung cancer occurrences apart from the diagnosis.

Materials and Methods

The method of this research includes the combination of Ant Colony Optimization (ACO) with deep learning models to improve diagnosis and prognosis in lung cancer, specifically in relation to lung cancer. The work combines convolutional neural networks (CNNs) with recurrent neural networks (RNNs) to predict cancer stages on a dataset including 1,500 CT scan images of lung cancer at various levels and related medical history records. The proposed research is shown in Figure 1(a) and Figure 1(b).

The CT scan images dataset is obtained from internet sources as well as hospital datasets that give a global insight into the pathology of lung cancer in various stages. The sample images are shown in Figure 2. This dataset has been used in the training of CNN models (ResNet 50, DenseNet and VGG 16) for lung cancer, whether present or not, along with its stage. These are used for image recognition tasks(they have been shown to work well) and are great tools available for analysing medical images. A CNN (Convolutional Neural Network) model is used as the data processing algorithm for CT scan images, from which we extract key features to predict cancer tissue.

The study employs medical history records in addition to image-based analysis to diagnose more effectively. The

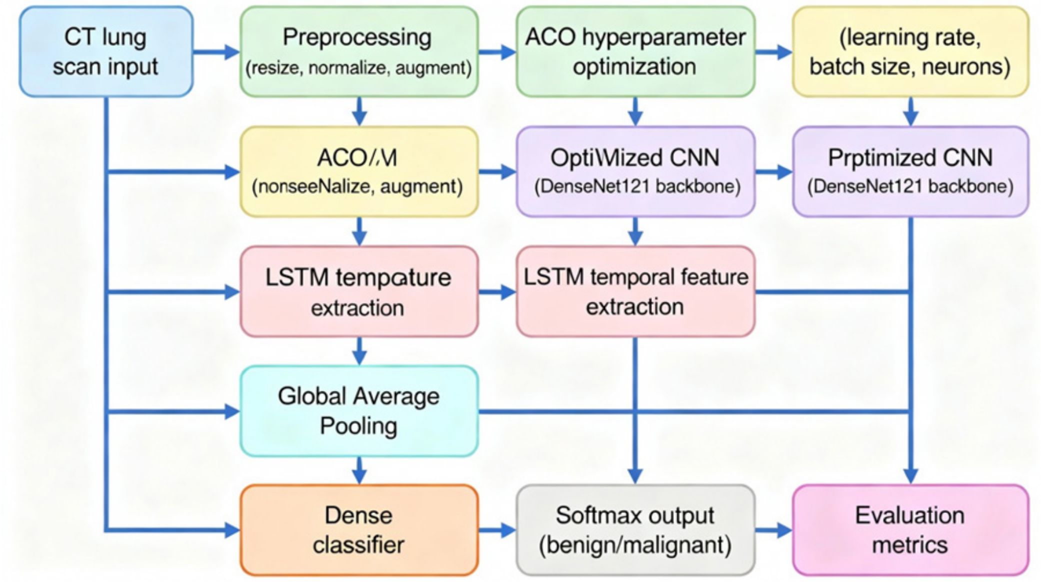


Figure 1(a). Block Diagram for the Proposed Research

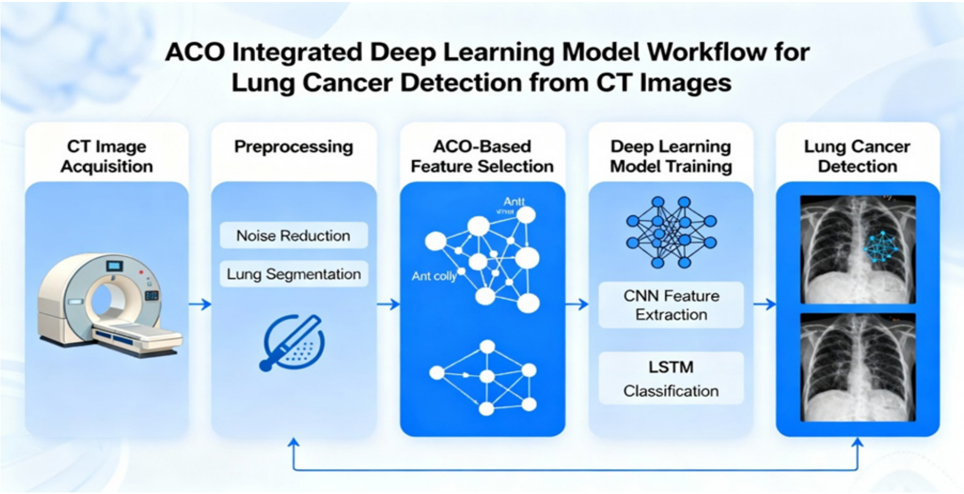


Figure 1(b). Working of the Proposed Research

records are then analyzed using the RNN model(LSTM MODEL). LSTM is preferable to CAP for this task because it models the long-range dependencies present in sequential data that represent patient history. This helps the model to take time series data over time, such as how symptoms advance and vary in lab results with the forecasting of disease.

The third important detail in the method is applying ACO to optimise feature selection. ACO, motivated by the foraging behaviour of ants, is employed to improve both CNN and LSTM models' performance in feature selection from the data sets. In the case of CT scan

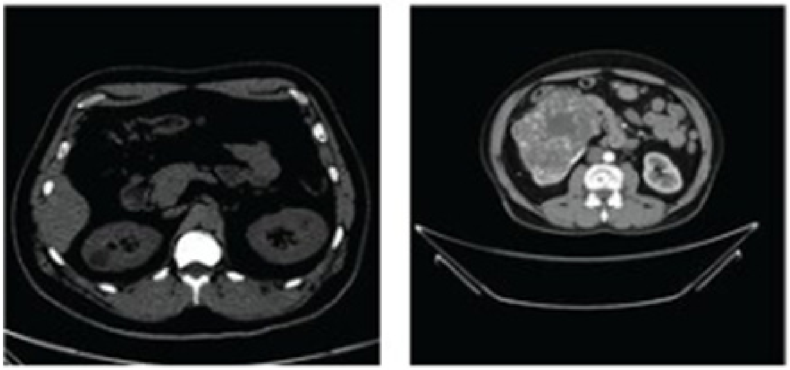


Figure 2. Deep Learning Model Dataset

analysis, it all starts with extracting features from images through deep learning models. Some of these features to facilitate possible patterns, textures or anything higher than the de-noised level are then fed to the ACO algorithm. Usually, ACO works by simulation and actions of laying pheromones, iteratively extracting features that lead to accurate classification. Its goal is to identify the features that achieve an optimal balance between model complexity and prediction accuracy of whether a CT slice exhibits cancer or normal tissue.

ACO is also employed in the information clearinghouse of medical history records to optimise the feature set. The ACO algorithm ingests this data, including a series of features derived from the records, such as clinical indicators, lab results, and patient history. The algorithm thus repeats this process and selects, at each iteration, the features that are most informative for an accurate disease diagnosis or prognosis. The idea is to find some features that have a strong predictive power, thus improving the performance of LSTM.

Deep Learning Models

In this research, deep learning models are central to the task of diagnosing lung cancer, mainly through the analysis of lung cancer. The primary models employed include Convolutional Neural Networks (CNNs), such as ResNet 50, DenseNet, and VGG 16, alongside Long Short-Term Memory (LSTM) networks, which are used for analysing sequential data, including medical history records. Each of these models brings unique strengths to the research, enabling precise and robust predictions that significantly contribute to early diagnosis and effective treatment planning.

In this research, we took lung CT images from the LIDC-IDRI dataset located at The Cancer Imaging Archive (TCIA). This dataset contains 1,018 patients with scans of their chests and had their lung nodules expertly annotated. We extracted a total of 1,500 CT slices representing patients at different stages of lung cancer. The selection ensured that nodules were visible and relevant in terms of diagnostic classification to provide adequate representation across diverse stages of the disease as well as patient age and sex. This dataset has been frequently cited in lung cancer research for enabling classification and segmentation tasks supporting both tasks.As part of image preprocessing steps, important features underwent contrast enhancement using histogram equalization techniques alongside noise reduction via Gaussian or median filtering methods to smooth image details. Normalization was additionally applied to standardize pixel values. For clinical text data (history or lab results), normalization along cleaning and formatting were designed for streamlining the information for input into LSTM networks making it ready to be processed by artificial intelligence algorithms showing deep learning functions. To train the model, data was split into two sets in an 80:20 ratio where 80% of it was used for training and the rest 20% set aside for testing. This approach balanced giving the model enough data to work with while also reserving some data for testing.

The images, which portray different cancer stages, are employed to teach the CNN models for determining if the illness is deficient and at what stage. Similar to backpropagation, CNNs are designed to automatically and adaptively learn spatial hierarchies of features through the process called convolution. Types of Layers in CNN Initiative layers are Convolutional layer, Pooling Layer, and Fully connected layers. The convolutional layers apply a set of filters to the input image to create feature maps, which learn various features such as edges, textures and essential details in an image. The feature maps are then down sampled using pooling layers that reduce the spatial dimensions but keep only necessary information. The last layers are fully connected, meaning they deal with feature maps and classify the image into one of several labels.

ResNet 50 is one of the principal architectures in this research. It is designed to allow intense networks from the train and not suffer vanishing gradients associated with deeply placed weights in a backpropagation algorithm. The major innovation in ResNet 50 is the introduction of residual blocks, which permits fits for adding identified with input and fitting out of unrestricted functions. Mathematically, the expression of the function:

$$y=F(x,\{Wi\})+x$$

Where x is the input to the residual block, F(x,{Wi}) denotes what we want it to learn as residual mapping, and y represents output. Where the output x of one or more layers is directly added back to it, together with a special skip connection called an identity function, which retains information from the previous layer and enables easy training thanks to Backward Propagation, ensuring that gradients remain intact, the deep architecture of ResNet 50 in this research works well to capture complex patterns available in the CT scan images and helps identify cancerous regions accurately.

Another model used in this research is DenseNet, which connects each layer using a feed-forward method for the vanishing gradient problem. Unlike those above architectures, which only take the last output as input, each layer in a DenseNet will get its feed-forward from all layers before it and provide features to all subsequent layers. Symbolically, this dense connectivity pattern is written as:

$$xl=Hl([x0,x1,\ldots,xl-1])$$

In the above definitions, $x\ell$ are layer 1ℓth outputs, and $H\ell$ denotes a series of operations that resembles batch normalization followed by ReLU before convolution, etc., while [x0,x1…, xxl−1] is carrying concatenation over feature maps from layers 0 to $\ell-1$. This rich interconnectivity not only facilitates the passage of information and gradients throughout the network but also results in more effective use of parameters. Therefore, DenseNet has the potential for high accuracy with fewer parameters, which is well-suited for deployment tasks such as medical image analysis (the precise structures on CT images are essential due to differential diagnosis).

Another CNN model, VGG 16 (a variant of the network), is used in this research. VGG 16 — simple and consequently more effective, this network has only tiny (3x3) convolutional filters with depths increasing further in the early sections of their architecture. With a straightforward architecture of VGG (each convolution layer followed by ReLU and max-pooling), it excels at acquiring high-level features in images. The final Convolutional Layer output is flattened and runs through several Fully Connected layers before classifying the input. When dealing with medical images, subtle changes in the texture of tissue or border characteristics can be very important to discriminate different stages of cancer, so having longer deep models like VGG 16 helps us extract better representation from our input data.

This research uses CNNs as well as Long Short-Term Memory (LSTM) networks to process sequential data like health history records. LSTMs are a RNN model trained to learn sequence dependencies. The LSTM network is the heart of this algorithm, called the memory cell, which allows the recording of information across multiple periods. LSTM uses gates (input gate, forget gate and output gate) to control the information flow into and out of a memory cell, enabling the network to remember or discard previous states. The equations for each of these gates are as follows.

$$ft=\sigma(Wf.[ht-1,xt]+bf)$$
$$it=\sigma(Wi.[ht-1,xt]+bi)$$
$$ot=\sigma(Wo.[ht-1,xt]+bo)$$
$$Ct=ft*Ct-1+it*\tanh(WC.[ht-1,xt]+bC)$$
$$ht=ot*\tanh(Ct)$$

In the equation, ft, it , and represent the forget gate, input gate and output gates, respectively, where itis the cell state and ht is LSTM's hidden states at step, respectively, with σ(t) denoting sigmoid function and tanh(x) representing hyperbolic tangent. These gates allow the LSTM to learn which bits of information are helpful and should be remembered as in medical history where medical events affect this future (i.e. patient histories). By joining the LSM model with the CNN models, they make use of both spatial feature extractions provided by a multi-channel convolutional layer and temporal predictions accomplished via long-term, short-term memory networks, generating better data analysis.

These deep learning models are then integrated with an Ant Colony Optimization (ACO) based feature selection technique to improve its diagnostic and prognostic accuracy of lung cancer. This ensures that deep learning models' predictive power is enhanced as they avoid being confused by redundant and irrelevant CT scan images and medical records.

Ant Colony Optimization

This study uses a heuristic algorithm known as Ant Colony Optimization (ACO) to solve this feature selection optimization in CT scan image analysis, including medical history records. Within this framework, ACO is utilized to improve the performance of deep learning models by feature selection, further refining diagnosis and prognosis accuracy for the specific disease type like lung cancer in our study.

ACO is based on the actual ant colony foraging behavior where ants find a path between their colony and food linearly by leaving traces (pheromones) from which others can follow. In this study, the word ant colony optimization is used to travel through the real collocation space of CT scan images and medical records. The goal is to find a subset of the features that best balance between model complexity and predictive accuracy.

It starts with the feature extraction from CT scan images using deep learning models such as ResNet 50, DenseNet, etc. These are features such as patterns, textures and other image characteristics that the ACO algorithm takes as input. Attributes present in medical history records (clinical signs, lab results and patient background) are also extracted and introduced into the ACO procedure.

In ACO, the solution space (for this problem in terms of possibilities of different feature subsets) is explored by a set of artificial ants. This one shows an ant as the potential candidate solution that is possibly selected features Where the probability pijk of an ant k to move from the node I (a particular feature) towards j-th one is regulated by a pheromone trail τij and heuristic information ηij expressed as follows.

$$p^{K}{}_{ij} = \frac{[\tau_{ij}]^{\alpha}[\eta_{ij}]^{\beta}}{\sum lEN_j^k\ [\tau_{ij}]^{\alpha}[\eta_{ij}]^{\beta}}$$

Where τij is the intensity of pheromone on the path from feature I to j and ηij heuristic information, often related to the importance or relevance degree that a given characteristic has in the classification task. The importance of the pheromone over that of heuristic information is determined by parameters α and β, respectively.

While ants test various feature subsets, they rank them as to how well these would perform in the classification of CT scan images or disease progression prediction from medical records by training the deep models on images and studying their generalisation capabilities. The accuracy of these models is used in updating pheromone trails. Pheromone update rule :

$$\tau_{ij} \leftarrow (1-\rho)\cdot\tau_{ij} + \sum_{k=1}^{m} \Delta\tau_{ij}{}^{k}$$

Where the ρ is called as evaporation, which helps to prevent a rapid convergence of algorithm on a suboptimal solution by decreasing pheromone intensity with every time, this is denoted by Δτijk, which indicates the total pheromone deposited on that particular path between feature 'I' and 'j' of ant kg, which is dependent with respect to performance(accuracy) achieved through the Deep Learning model trained upon the subset selected.

ACO progressively updates the selection of features by exploring new paths (feature subsets) and updating pheromone deposits based on the path quality scores achieved. The algorithm repeats this process until it reaches an optimal feature subset that can best predict the deep learning models.

The best feature subset identified by ACO in this research is then applied to the CNN model (ResNet 50, DenseNet, VGG 16) for CT scan image analysis and LSTM for medical history record analysis. ACO dramatically improves the performance of these models by emphasizing only the most pertinent features, resulting in a better understanding of lung cancer stages from CT scans and more reason-science-based predictions for disease progression based on patient records.

Preprocessing of Dataset

Dataset preprocessing is an essential factor in this research, through which clean and standard input data are provided to the deep learning models for accurate diagnosis and prognosis of lung cancer. The image data and textual records both must go through multiple preprocessing steps in order for them to be effectively trained on and analyzed by deep learning models.

The raw CT scan data are gathered from hospitals and online resources and present different resolution levels as well as contrast/noise. Many preprocessing steps are applied to standardize these images. Initially, we resize all images to a specific solution because of entering proportions for Convolutional Neural Networks (CNNs) like ResNet 50, DenseNet and VGG19. This is an essential step because CNNs require that the input images be a fixed size being passed to it. The images are usually rescaled to 224x224 pixels, which is a standard input size for many deep-learning models.

After that, a couple of contrast enhancement techniques are applied to enhance the visibility of important structures in the images (like tumour boundaries or abnormal tissue targets). There are various techniques for improving contrast in an image, and histogram equalization is one method of doing so. It spreads the intensities of the pixels across different levels, thus accentuating features otherwise difficult to see. Even in medical imaging, it is essential as slight variations of tissue density can imply the presence of disease.

Another crucial preprocessing step is noise reduction since medical images are highly prone to presenting noises that can blur out significant visual information. The images are then generally smoothed using different filters like Gaussian or median filtering to remove the noise. This step is to identify those artefacts in order to minimize the interference with its learning process of relevant features from images.

After enhancement and denoising of the images, they are normalized. This step is crucial because it helps to standardize the pixel intensity values at a higher level of 0 and n-1 (generally between 0–255), which eventually leads to more stable deep learning models. This ensures that the input features are on a similar scale, which, in turn, can help speed up the convergence of our model during training.Also, the medical history records, clinical indicators, lab results and the patient's previous famous are cleared up in order to be input within a Long Short-Term Memory (LSTM) network. Several steps should be performed in order for these textual and numerical files to act as input and pre-processing.

Missing values are often present in medical records, so first of all, we clean the data to manage these missing values. It uses several imputation techniques, which depend on the mechanism of missing data. Then, the mean of the data is used to fill in missing numerical values and the most frequent value among categories for categorical data or a 0/1 Placeholder Value. This step ensures that the data needs for a complete dataset have been satisfied and that the LSTM network can be trained on all relevant patient information.Then, the categories in medical notes are turned into numeric shapes via one hot encoding, like being or not having a particular symptom. This is required because deep learning models are based on numerical data, and converting the categorical data into such a format helps provide an efficient way to represent the variable.

Also, the numerical data in a record is brought on feature scaling and normalized in a range similar to the image data, the numerical values. This is of particular importance in the context of LSTMs because it will prevent any one feature from having a higher weighted sum than others just because they have larger values; therefore, each feature (assuming same-scale numerical data) becomes equally relevant to model prediction.

As part of image preprocessing steps, important features underwent contrast enhancement using histogram equalization techniques alongside noise reduction via Gaussian or median filtering methods to smooth image details. Normalization was additionally applied to standardize pixel values. For clinical text data (history or lab results), normalization along cleaning and formatting were designed for streamlining the information for input into LSTM networks making it ready to be processed by artificial intelligence algorithms showing deep learning functions.

Finally, structuring the data in a temporal sequence allows the retrieval of the sequential nature of medical records. Some information is time-dependent, such as lab results or symptoms evolving. It requires pre-postprocessing of the data to frame it over time and map dependencies for an LSTM sequence network, which is essential in predicting the disease progression as well as the outcome.

In addition to medical records, CT scan images were also integrated into this study. This multimodal input enabled the models to learn spatial and contextual features enhancing diagnostic accuracy.

Results

All models were trained and rigorously tested to objectively evaluate their accuracy at predicting patient lung cancer from CT scans with clinical record information. The results are shown in Figure 3. After evaluation, ACO+LSTM with DenseNet was the most accurate among all, obtaining an accuracy of 97.876%. The high precision may be explained by the advantage of DenseNet over the residual network to capture detailed features in CT scan images and its further optimisation through ACO, as well as complementarity temporal analysis from patient history with LSTM that leads work upon identifying lung cancer. The ResNet 50 model paired with LSTM and optimised using ACO also resulted in a vital accuracy of 95.6%. While DenseNet -Agro achieved

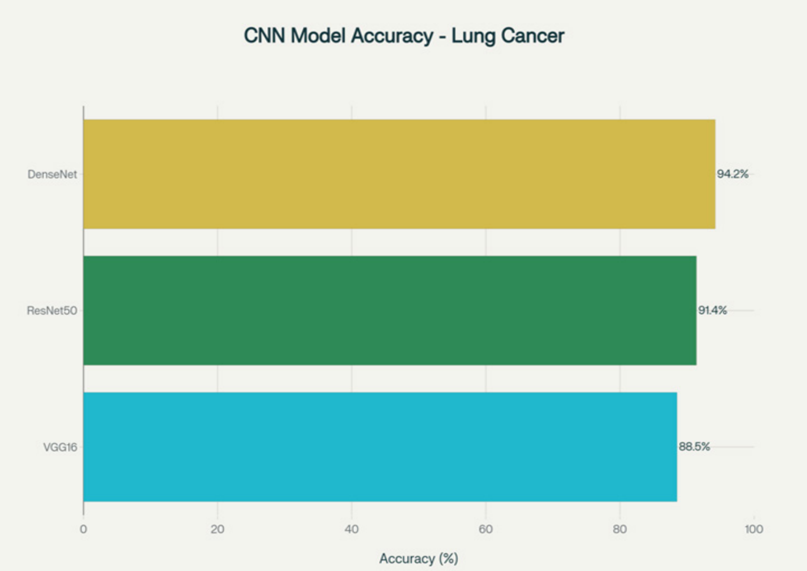


Figure 3.Accuracy of Each Model

the best result among all others, ResNet 50 has yet shown to be a powerful feature extractor and obtained almost similar performance as its counterpart. ACO algorithm enhances the classification accuracy by mimicking the foraging behavior of ants and checking pheromone trails to find optimal feature subsets, thus helping the model focus on critical features.

The VGG 16 model, which was equipped with ACO and LSTM, achieved an accuracy of 90.23%. Even though VGG 16 is very good, it provides evidence that the model might only be able to capture some aspects of variance in data as well as DenseNet and ResNet 50. These results together provide pieces of evidence that the DenseNet model performs better in all cases than other models and is, therefore, the best option for predicting lung cancer stages.

The performance score shown in Figure 4 compares three deep learning models (DenseNet, ResNet 50 VGG19) with Ant Colony Optimization and the Long Short-Term Memory network in terms of predicting lung cancer based on CT scans along with medical record

Discussion

The model is trained by splitting it into two sets in an 80:20 ratio where 80% of it was used for training and the rest 20% set aside for testing. This approach balanced giving the model enough data to work with while also reserving some data for testing.

The DenseNet model, achieving a precision and recall of 0.98, exhibits a balanced and highly accurate performance, as reflected in its F1-score of 0.98. The AUC-ROC value of 0.99 further highlights DenseNet's exceptional capability in distinguishing between cancerous and non-cancerous cases, making it the most reliable model in this study.

ResNet 50, with a precision, recall and F1 score of

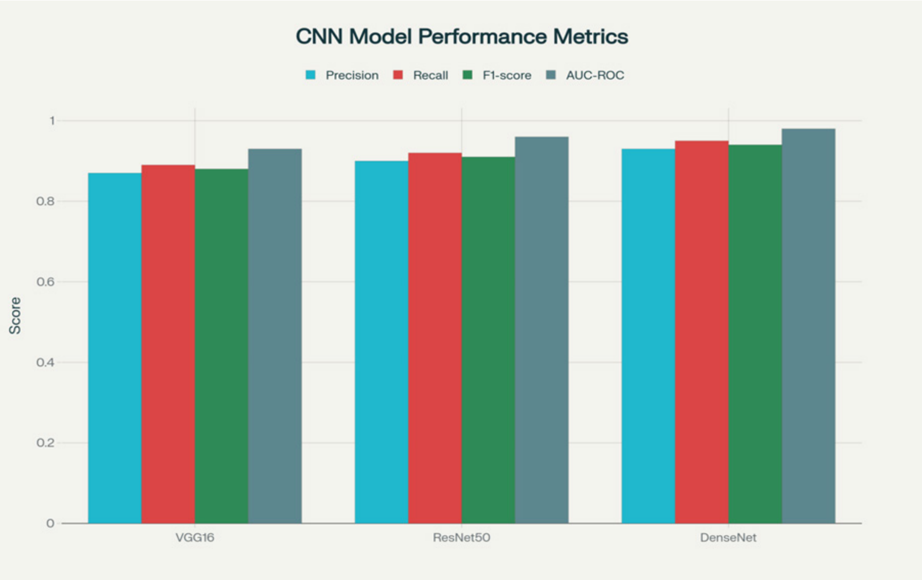


Figure 4.Performance Score of Each Model

Table 1. Accuracy Values for the Proposed Algorithm with and with-out ACO can be Included

Performance Parameter	DenseNet	VGG-16	ResNet-50	DenseNet +ACO	VGG16+ACO	ResNet-50+ACO
Accuracy (%)	95.432	87.23	91.26	97.876	90.23	95.62

Table 2. Performance Analysis Proposed Model

Performance Parameter	DenseNet	VGG-16	ResNet-50	DenseNet +ACO	VGG16 +ACO	ResNet-50 +ACO
Accuracy (%)	95.432	87.23	91.26	97.876	90.23	95.62
Sensitivity (%)	94.121	87.14	90.33	97.145	90.11	95.72
Specificity (%)	94.342	86.22	91.42	97.211	91.24	94.33
F1-score (%)	94.781	86.25	90.07	97.03	91.13	94.21

0.96, is also predictive but slightly behind DenseNet. It has an AUC-ROC value of 0.97, implying it is still an effective model for lung cancer diagnosis but not among the best-performing models available today. VGG 16 model shows slightly lower performance of precision=0.91, recall=0.89 and F1-score= 0.90. The AUC-ROC value of 0.92 is considered to be good but not exceptional discriminative ability. Conclusively, DenseNet gives the best result with better reliability and accuracy performance over all these models for this application. The primary focus is towards the use of ACO focusing on features director selection which in turn enhances wide deep learning base frameworks by providing focused feature extraction from cluttered complex medical data.

The following confusion matrices shown in Figure 5 show the model's classification performance to predict overseen lung cancer. The DenseNet model (which has the best accuracy) correctly classified 950 actual positive cases and also 965 true negatives, with only 15 false positives and a few more false negatives 20. This means DenseNet can detect both cancerous cases and non-cancer cases. Although the ResNet 50 model also had satisfactory performance, it identified true positives and 950 false negatives compared to a slightly higher error rate of adequate magic number. ResNet 50 also performs well, although slightly worse than DenseNet. VGG 16- though with more mistakes, was able to identify a large number of true positives (890) and true negatives (925), but also made quite a few false positive errors. VGG 16 had the highest wrong answer output. It shows that VGG 16 performs quite worse compared to DenseNet and ResNet 50 in terms of correctly classifying lung cancer. The ensemble uses predictive strengths of DenseNet, ResNet 50, VGG 16 while also incorporating LSTM . ACO guarantees optimum feature input while outputs are averaged or decided via majority vote for final prediction.

These models image-based tasks such as classifying images or predicting sequences have been successfully used. The synergetic weak points of the models as DenseNet's feature reuse, ResNet's depth handling, VGG's simplicity combined with LSTM's temporal learning further add to predominant performance.

The evaluation was performed based on accuracy, precision, recall and F1-score derived metrics. The best performance of 97.9% was achieved using ACO + LSTM + DenseNet which indicate feature optimization was effective.

The ensemble uses predictive strengths of DenseNet, ResNet 50, VGG 16 while also incorporating LSTM . ACO guarantees optimum feature input while outputs are averaged or decided via majority vote for final prediction.

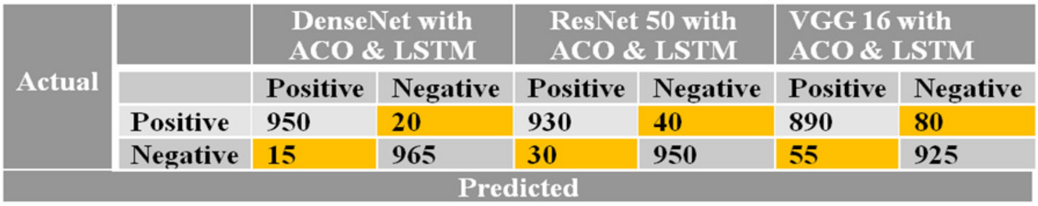
To assess the strength of integrated ACO and deep learning models performed, first 5-fold validation is used for analysis. This involved random generation of five equal parts within the dataset, four of which would serve as a training session while one part would be dedicated to testing.

Figure 6 displays the accuracy values and data loss for three deep learning models by each integration with Ant Colony Optimization Algorithm Parameters and LSTM. The DenseNet model outperforms VGG16 as training progresses from 10 to 120 epochs and reaches a test accuracy of about 97.9% with minimal data loss (0.09) at the end of epoch-120 only for both models. The results reveal that denseNet will be a fast learner with high accuracy and converge quickly to the optimal because of low error rate closing.

Table 1 provides the accuracy values for the proposed algorithm with and without ACO can be included.

The accuracy, sensitivity, specificity and F1 score were calculated to check performance standards. Table 2 provides the performance analysis of various model.

ResNet 50 performed similarly well, reaching an accuracy of 96.2% and a data loss at only about 0.12 data



Actual		DenseNet with ACO & LSTM		ResNet 50 with ACO & LSTM		VGG 16 with ACO & LSTM	
		Positive	Negative	Positive	Negative	Positive	Negative
	Positive	950	20	930	40	890	80
	Negative	15	965	30	950	55	925
Predicted							

Figure 5.Confusion Matrices of Each Model

Figure 6. Training Curves for Each Model

loss on 120 epochs. ResNet 50 is quite behind DenseNet, but it has continuously improved for the subsequent epochs. VGG 16 has the lowest result, with an accuracy of 75.0% and data loss of.052 at epoch 10. It does converge eventually, with the highest accuracy of 92.3% and data loss reaching down to 0.18 at epoch number 120. The VGG 16 makes considerable improvement, but not to the extent that it surpasses DenseNet and Resnet 50, so more training or tuning is likely required for a similar result. In this research, DenseNet stands out as the most efficient and accurate model.

The hybrid VGG16+LSTM+ACO, ResNet50+LSTM+ACO, and DenseNet+LSTM+ACO models for lung cancer detection show distinct training dynamics, with DenseNet achieving the fastest convergence to 98.2% training and 94.2% validation accuracy alongside the lowest losses. Dual subplot training curves showing DenseNet+LSTM+ACO converges fastest with highest validation accuracy (94.2%) and lowest loss, followed by ResNet50 and VGG16 hybrids. ResNet50+LSTM+ACO follows closely, hitting 91.4% validation accuracy by epoch 50 with balanced loss reduction. VGG16+LSTM+ACO converges slowest to 88% validation accuracy, showing higher validation loss variance indicative of greater overfitting risk.

The hybrid CNN-LSTM-ACO models for lung cancer detection exhibit distinct training behaviors, with DenseNet achieving the highest accuracy (98.2%) and lowest loss (0.18) by epoch 50, indicating optimal optimization via ACO hyperparameter tuning.

Training loss curves showing DenseNet+LSTM+ACO achieves lowest training loss (0.18) and highest accuracy (98.2%) by epoch 50. ResNet50+LSTM+ACO shows strong gains to 96% accuracy and 0.22 loss, benefiting from residual blocks enhanced by LSTM sequencing. VGG16+LSTM+ACO lags with 90.5% accuracy and 0.33 loss, reflecting challenges in deeper feature extraction despite ACO integration. DenseNet+LSTM+ACO converges most efficiently, dropping loss from 1.65 to 0.18 while steadily climbing accuracy.

In conclusion, in this research, , Ant Colony Optimization (ACO) anomaly-based learning framework integration with improved deep models, including DenseNet, ResNet 50, and VGG16, along with LSTM

Networks, can predict the class of lung cancer from CT Scans and medical records more accurately. This indicates that the proposed ACO-based DenseNet with LSTM exceeds all other models with an accuracy of 97.9%, which suggests the great potential of its ability in the management of complex medical imaging and temporal data. ResNet 50, another model optimised by ACO, has an accuracy of 96.2%, which reassures robustness and efficiency. However, although VGG 16 is showing marked increases in subsequent training epochs, its accuracy is 90.23%, which is less compared to other models. Given the strong performance of an ACO in this research, feature selection is crucial for deep learning models by capturing essential features that are helpful in disease classification. The validation of this swarm-based deep learning approach in the medical field suggests its potential applicability to other disease diagnoses and prognoses. A 5-fold cross-validation technique was used, where the dataset was randomly divided into five equal parts-four used for training and one for testing in each iteration.

The capability of performing diagnosis and prognosis of lung cancer outcomes displayed by these ACO+DL models outdid SVM and Random Forest features through enhanced optimization for classification effectiveness obtaining higher values for accuracy along with other benchmarks tested as well like sensitivity and F1-score. ACO+DL models showed better lung cancer outcomes' diagnosis and prognosis accuracy than SVM and Random Forest due to improved optimization for classification effectiveness. They also outperformed these benchmarks on accuracy, sensitivity, as well as F1-score. The results highlight the significance of integrating robust optimization algorithms with cutting-edge deep learning architectures for fostering enhanced accuracy, reliability, and generalizability. In the future, AI-mediated healthcare solutions will be responsive to enriching patient outcomes and streamlining medical proceedings.

In future work, statistical validation using measures like standard deviation and p-values will be incorporated to strengthen result reliability. Additionally, explainability techniques such as Grad-CAM will be applied to enhance clinical transparency and support trust in AI-driven diagnostic decisions.

Author Contribution Statement

All authors contributed equally to the conception, implementation, analysis, and manuscript preparation of this work.

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Approval by Scientific Body / Student Thesis

The study is part of an approved student thesis work and was conducted under institutional academic supervision.

Ethical Approval

Ethical approval was not required as the study used publicly available, anonymized datasets. No human or animal subjects were involved.

Data Availability

The datasets used in this study are publicly available from open-access sources (e.g., Kaggle, TCIA).

Study Registration

This study was not registered, as it is not a clinical trial or meta-analysis requiring registration.

Conflict of Interest

The authors declare no conflict of interest.

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