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Intelligent Lung Cancer Detection: A Genetic Algorithm Machine Learning Fusion

B. Swarajya Lakshmi

Assistant Professor, Computer Science and Engineering, G. Pullaiah College of Engineering and Technology, Kurnool, Andhra Pradesh, India.

Email ID: *lakshmi.jun@gmail.com*

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Abstract

Early detection of lung cancer is crucial for improving patient outcomes. While Deep Learning (DL) models have shown high accuracy in lung cancer diagnosis, they often require substantial computational resources. This study proposes a novel approach that leverages Genetic Algorithm (GA) to optimize feature selection and dimensionality reduction from lung cancer images. By integrating GA with conventional Machine Learning (ML) models, we demonstrate improved classification accuracy while minimizing computational requirements. Our experimental results show that combining GA with a feed-forward neural network classifier yields exceptional performance, achieving a classification accuracy of 99.70%. This approach offers a promising alternative to DL models for lung cancer detection, particularly in resource-constrained settings.

1. Introduction

Lung cancer is considered one of the deadliest cancer types worldwide [1, 2]. The USA is expected to experience 2,001,140 new cases of cancer and 611,720 deaths related to cancer in 2024 [1]. Lung cancer accounts for approximately 20% of all cancer deaths [1]. The primary causes of lung nodules, which are areas of higher density in the lung, are smoking and chronic contact with airborne pollutants [3]. Early detection of lung cancer is crucial for effective treatment [4, 5]. Immunotherapy has shown promising results for people with lung cancer [6]. However, the objective response varies significantly from patient to patient [7]. Thus, accurately detecting patients with lung cancer who are sensitive to immunotherapy is essential [8]. Computed Tomography (CT) scans are commonly used to detect lung cancer [9]. However, analyzing these images can be time-consuming and prone to human error [10]. Computer-Aided Detection (CAD) techniques could help physicians provide diagnoses with greater accuracy [11]. Several CAD frameworks operate in two phases: reducing false positives and extracting candidate frames [12]. This approach sends unclear nodules detected within the initial coarse imaging scan to the next stage for analysis [13]. Other techniques include intensity threshold and shape curvature [14]. Conventional methods have been used to reduce false alarms in Computer-Aided Detection (CAD) techniques, including gradient, location, density, shape, size, texture, and human data [15]. However, traditional CAD techniques have two major issues: general inefficiency and variability in detection outcomes [16-18]. The advancement of big data and statistical techniques has made Artificial Intelligence (AI) crucial in every aspect of life [19]. AI focuses on developing intelligent models that can think,

reason, and automate tasks [20]. Machine Learning (ML), a subfield of AI, examines large datasets to process and classify information [21]. AI enables machines to make independent decisions [22]. Deep Learning (DL) methods, based on AI and ML, can significantly impact precision medicine, personalized medicine, and biomedical research [23]. Researchers use DL models like Convolutional Neural Networks (CNNs) to classify medical images [24]. Figure 1 illustrates the general architecture for classifying medical images using a DL model. The process involves collecting images through medical scanning technologies, preprocessing images using feature extraction and augmentation, and feeding the images into a DL module for classification [25]. The integration of AI and medicine is an increasingly important research topic [26]. Detecting lung cancer at an early stage is crucial for effective treatment and reducing mortality rates [27]. However, medical images contain numerous features, making classification challenging for traditional ML methods [28]. Therefore, an efficient feature selection technique is necessary to reduce the dimensionality of feature space [29]. This study proposes a novel model integrating a Genetic Algorithm (GA) approach with an ML model to detect lung cancer [30]. The GA selects the most relevant features from lung cancer images, reducing the feature space size. Using conventional ML models instead of CNNs addresses limited computational capabilities in clinics and achieves high classification performance on lung cancer images [31].

1.1. The contributions of this research include

- Implementing GA to select the optimal subset of features from lung cancer images, reducing redundant features and improving classification accuracy with ML models [32].
- Studying the classification performance of common ML models to evaluate the effectiveness of using GA with ML models [33].
- Comparing the classification performance of the proposed model (GA-FFNN) with state-of-the-art classifiers on the same dataset [34]. Figure 1 shows General pipeline for classifying medical images.

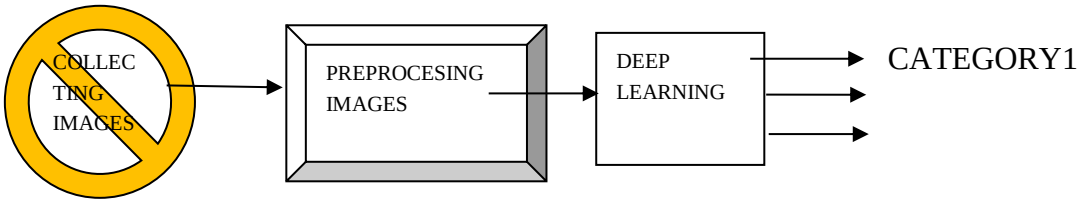

Figure 1 General pipeline for classifying medical images.

2. Related Works

Various researchers have proposed different methods for detecting lung cancer. For instance, a method called Sybil was presented in [35], which utilized Low-Dose Computed Tomography (LDCT) images. Sybil requires LDCT images without the need for radiologist annotations and can run in real-time. Another approach, proposed in [36], is the LungNet-SVM algorithm, an enhanced version of the AlexNet architecture. This algorithm uses a combination of convolutional and fully connected layers to extract features from CT images and classify them as benign or malignant.A hybrid approach, proposed in [37], combines a Convolutional Neural Network (CNN) with a Recurrent Neural Network (RNN) to detect lung cancer from CT images. This approach uses the CNN to extract features from the images and the RNN to analyze the temporal relationships between the features.Other approaches, such as the ones proposed in [38] and [39], use a combination of machine learning algorithms and feature selection techniques to detect lung cancer from CT images. These approaches use techniques such as Support Vector Machines (SVMs), Random Forests, and Gradient Boosting to classify the images as benign or malignant. A deep learning approach, proposed in [40], uses a combination of two pre-trained CNN models, SqueezeNet and ResNet101, to extract features from CT images and classify them as benign or malignant. Another approach, proposed in

[41], uses a combination of machine learning algorithms and feature selection techniques to detect lung cancer from CT images. This approach uses techniques such as SVMs, Random Forests, and Gradient Boosting to classify the images as benign or malignant. A hybrid approach, proposed in [42], combines a CNN with an XGBoost algorithm to detect lung cancer from CT images. This approach uses the CNN to extract features from the images and the XGBoost algorithm to classify the features as benign or malignant.Finally, an ensemble approach, proposed in [43], combines the predictions of multiple machine learning models to detect lung cancer from CT images. This approach uses techniques such as bagging and boosting to combine the predictions of the individual models and improve the overall accuracy of the system.

3. Methodology

3.1. Proposed Model Overview

This study presents a novel detection model for lung cancer, which classifies Computed Tomography (CT) images into three distinct categories: normal, malignant, and benign. The proposed model leverages a Genetic Algorithm (GA) to select the most optimal features, thereby minimizing redundancy and eliminating irrelevant features. This feature selection process enhances the classification performance of Machine Learning (ML) models when performing classification tasks. Therefore, the proposed model integrates GA with an ML model to achieve improved accuracy in lung cancer detection. Figure 2 illustrates the flow diagram of the proposed model, outlining the steps involved in its implementation. The process commences with loading the lung cancer dataset, comprising images corresponding to three distinct classes: normal, malignant, and benign. To address the issue of class imbalance, which can lead to overfitting, an oversampling technique is employed. Following dataset balancing, each image is passed through the AlexNet pre-trained neural network to extract features. Subsequently, the Genetic Algorithm (GA) parameters are defined to configure the algorithm and optimize feature selection. Adjusting GA variables, such as population size, mutation rate, crossover probability, and the number of generations, enables GA to identify the most relevant features in the images. This process reduces the dimensionality of the data by selecting only valuable features, thereby achieving high classification accuracy. The GA is utilized to select the most relevant features and reduce feature space, enhancing the performance of Machine Learning (ML) in detecting lung cancer. Once optimal features are selected, an ML classifier is employed to classify patient diagnoses into three categories. In summary, this method integrates image oversampling, AlexNet, GA, and ML to detect lung cancer. Figure 2 shows Flow diagram of the proposed approach.

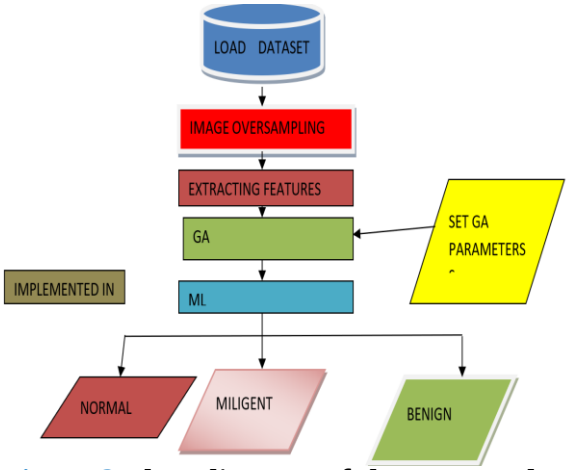

Figure 2 Flow diagram of the proposed approach.

3.2. Dataset

This study utilized the IQ-OTH/NCCD dataset, comprising a collection of Computed Tomography (CT) scan slices. The dataset was collected from Iraqi hospitals over a three-month period in 2019. Each CT scan slice represents an image of the human chest, captured using a Siemens SOMATOM CT scanner with a protocol of 120 kV, 1 mm slice thickness, and varying window widths and centers for reading, ranging from 350 to 1200 Hounsfield Units. The dataset consists of 1,097 images, divided into three classes: Benign, Malignant, and Normal, as outlined in Table I. However, the dataset suffers from class imbalance, particularly in the Benign class, which can lead to overfitting in classification tasks. To address this issue, the proposed model employs oversampling techniques to increase the number of images in the underrepresented classes. This involves identifying the class with the highest number of images (Malignant class with 561 images) and then increasing the other classes to match the class with the highest number of images. Table 1 shows Classes of the IQ-OTH/NCCD Dataset.

Table 1 Classes of the IQ-OTH/NCCD Dataset

Category	Number of original images	Number of images after oversampling
Benign	120	561
Malignant	561	561
Normal	416	561
Total	1,097	1,683

3.3. Theory of Genetic Algorithm (GA)

Genetic Algorithm (GA) is a optimization technique inspired by the natural selection process [38]. GA starts with a sample of individuals in a population and generates a new one using genetic operators to find the best individual fit [39].GA employs the concepts of population, chromosome, gene, fitness function, selection, crossover, mutation, and termination to solve complex problems. A population represents a group of solutions to the problem, as shown in Equation (1):

$$P(n) = \{S1, S2, ..., Si\} \quad (1)$$

where P refers to the population, n is the generation number, S is the individual solution or chromosome, and i is the index of the solution.A chromosome represents an individual solution to the problem, typically encoded as a binary string, as shown in Equation (2):

$$Si = \{G1, G2, ..., Gm\} \quad (2)$$

where G refers to a gene and m is the length of the chromosome. Each gene can take a binary value (0 or 1).A fitness function is used to evaluate the individual solution (chromosome), as shown in Equation (3):

$$F(Si) \rightarrow R \quad (3)$$

where F is a fitness function that can be formulated depending on the problem and R is a real number. Selection is used to select the best individuals, which is also known as survival. Crossover is a method used to combine parts from two parents to produce offspring. Mutation is used to alter some parts of the offspring. To understand the operation of GA, assume that we want to find the minimum solution of the following function:

$$f(x) = (x - 2) \quad (4)$$

Assume also that the value of x is an integer between 0 and The aim is to find a value between 0 and 15 that gives the smallest solution of $f(x)$. At the beginning, a random population is generated, and each population is represented as a 4-bit binary string. Therefore, the first population could be:

- Value of $x = 4$ (binary: 0100)
- Value of $x = 15$ (binary: 1111)
- Value of $x = 2$ (binary: 0010)

As the objective is to find the minimum solution for $f(x)$ in (4), the smallest value is the best solution.

- $f(4) = (4 - 2) = 2$
- $f(15) = (15 - 2) = 13$
- $f(2) = (2 - 2) = 0$

$x = 2$ is the best solution since it produces the minimum value. Now, the fittest population is chosen to produce the next generation, which can be $x = 4$ (binary 0100) and $x = 2$ (binary 0010), since they generated the smallest fitness values. The crossover method can be applied to the selected individuals, Parent 1: 0100 and Parent 2: 0010. This is done to produce Offspring 1 and Offspring 2. Assume that the first offspring is generated from the first two bits of Parent 1 and the second two bits of Parent 2. Then Offspring 1 is 0110. Offspring 2 is generated from the last two bits of Parent 1 and the first two bits of Parent 2, which gives 0000. Therefore, in the case of Offspring 1, $x = 6$, and for Offspring 2, $x = 0$. The mutation method can be used to ensure diversity in the population. This can be done by flipping the last two bits of Offspring 2, for example. Offspring 2 now becomes 0011 ($x = 3$). Therefore, the new population is $x = 6$ and $x = 3$. The evaluation of the fitness function using the new population gives:

$$f(6) = (6 - 2) = 4$$

$$f(3) = (3 - 2) = 1$$

The smallest value of the fitness function using the new population is $f(3)$. However, it is not smaller than $f(2)$, thus the algorithm is terminated as the optimal solution has already been selected.

3.4. Feature Selection Using GA

Algorithm 1 describes the GA feature selection approach. In the input, the dataset that contains lung cancer images is loaded and each image is read. Then AlexNet is used to extract all features from each image. After that, the following GA parameters are set: population size, max generation, and number of features. The value of each parameter was selected based on experiments. The expected output of the algorithm is the most important features

organized in columns, and each row is labeled with the class to which it belongs (Normal, Malignant, Benign). Oversampling is performed to increase the number of images since the dataset is not balanced. The oversampling technique used is random duplication of images, so the number of images in each class matches the class that has the maximum number of images. Subsequently, AlexNet is used to extract all features from the images, and the results are fed to GA to select the most important features. Finally, the GA output is saved in a CSV file to be used later by the ML model.

Algorithm 1: Feature Selection Using GA Input:

- Load dataset Read images Load AlexNet
- Set GA parameters: Set populationSize Set maxGenerations Set numFeatures
- Output: importantFeatures.csv
- Procedure:
- Perform oversampling
- Extract features using AlexNet Run GA
- Save relevant features to importantFeatures.csv
- End Algorithm.

4. Results and Discussion

This section presents the experimental results of this research. It begins by showing a defined set of parameters used for each classifier. Then, it provides a comparative study of various ML classifiers that integrate the GA approach to evaluate their effectiveness. Finally, this section describes a comparative analysis of the proposed model with recent studies using the IQ-OTH/NCCD dataset. Table 2 provides information about each classifier and the corresponding parameters used to classify lung cancer images. Default values were used with each classifier to achieve fairness. The Random Forest (RF) classifier uses Gini impurity as the splitting criterion, and the splitter is set to the best. The Decision Tree (DT) classifier also uses the Gini criterion and 100 decision trees. The SVM classifier uses a linear kernel, and the regularization is set to 1.0 to avoid overfitting. The K- Nearest Neighbor (KNN) classifier relies on Singular Value Decomposition (SVD). The hidden layer of the Feedforward Neural Network (FFNN) classifier consists of 100 neurons, uses the Rectified Linear Unit (ReLU) as the activation function, and Adam as an optimizer. The Linear Discriminant Analysis (LDA) classifier employs five neighbors. The performance comparison of ML models used along with the GA algorithm is displayed in Table 3.

Table 2 Classifier Parameters

Classifier	Parameters
RF	Criterion: Gini, splitter: best
SVM	Kernel: linear, regularization: 1.0
KNN	Solver: SVD
FFNN	Hidden layer sizes: 100, activation: ReLU, solver: Adam
LDA	Number of neighbors: 5
DT	Number of decision trees :100, criterion: Gini

These models were evaluated using metrics including precision, recall, F1- score, and accuracy. The RF classifier achieves an impressive performance whereas the SVM classifier performs a perfect balanced performance. In addition, the SVM classifier exhibits identical accuracy with the RF classifier, which shows its proficiency in the context of lung cancer classification. The KNN classifier shows an accuracy of 97.92%, which is lower than that of RF and SVM. The FFNN classifier outperforms all the ML methods considered in this study, with perfect precision reaching 100%. In addition, the classifier shows reliable and strong performance with recall, F1-score, and accuracy of 99.72%, 99.86%, and 99.70%, respectively. The LAD classifier yields classification performance close to the SVM classifier, and it produces an identical accuracy to RF and SVM. LDA results do not outperform the FFNN, but it shows a solid performance compared to the other ML methods. The DT is asimpler classifier, and according to the results, it is not one of the top performers in context of lung cancer classification. The DT classifier shows the lowest scores across all metrics compared with RF, SVM, KNN, FFNN, and LDA Table 3 shows ML Classification Performance Using GA

Table 3 ML Classification Performance Using GA

Model	Precision	Recall	F1-score	Accuracy
RF	98.88%	99.16%	99.02%	99.11%
SVM	98.77%	98.77%	98.77%	99.11%
KNN	97.88%	97.69%	97.40%	97.92%
FFNN	100%	99.72%	99.86%	99.70%
LDA	98.72%	98.87%	98.77%	99.11%
DT	94.93%	95.12%	94.95%	94.36%

Table 4 presents a comparative analysis of research studies conducted in 2023-24. These studies used different classifiers on the IQ-OTH/NCCD dataset, which is the same dataset used in this study. According to their results, most studies achieved classification accuracy greater than 99.00% except [36, 43] which obtained 98.32% and 98.54%, respectively. In [44], a CNN with BiLSTM achieved 99.20%. In [34], ResNet101 with SqueezeNet reached 99.09%. In [35, 37], comparable results were obtained, with 99.64% and 99.54% accuracy, respectively. This study, using GA with FFNN, outperformed these models by achieving 99.70% accuracy.

Table 4 Comparison of Different Classifiers Evaluated on IQ OTH/NCCD

Study	Model	Accuracy
[34]	ResNet101 + SqueezeNet (Hybrid model)	99.09%
[35]	CNN + SMOTE	99.64%
[36]	LCSCDM	98.54%
[37]	MENet (Xception, InceptionResNetV2, MobileNetV2)	99.54%
[43]	binary count ratio	98.32%
[44]	CNN-Bi LSTM	99.20%
This study	GA-FFNN	99.70%

Conclusion

Medical images are often analyzed using DL models that require a lot of computational resources. This study proposed an approach that leverages the power of GA and ML to detect lung cancer. GA was applied to select the most important features from lung cancer CT images, helping to reduce feature space size and enhance classification performance when using conventional ML models. This approach used GA to select the most relevant features and ML to perform the classification task. A comparative analysis was performed to evaluate the effectiveness of the proposed model with various ML models. The proposed model was compared with state-of-the-art classifiers on the same dataset. The experimental results confirm that the proposed model achieved high classification performance by integrating GA and FFNN. In the future, the proposed model should be tested with more diverse datasets to validate its robustness and generalizability.

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