AN INTELLIGENT DEEP LEARNING FRAMEWORK FOR LUNG CANCER PREDICTION

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Abstract

Cancer is a multidimensional, multilocational disease, which presents severe health, social and economic impacts globally. Recent identification is paramount and this paper takes advantage of DL, specifically CNNs to forecast and classify lung cancer using medical images, clinical data, and genetic data. The given CNN model demonstrated the 91% accuracy, which is higher compared to other DL and traditional machine learning approaches, whereas precision, recall, and F1-score metrics can definitely indicate its usefulness. The study develops the areas of DL use in cancer risk forecasting, and the errors can be reduced with the addition of physiological parameters and IoM technologies in the future works.

INTRODUCTION

Lung cancer is still one of the primary causes of cancer-related deaths all over the world, and it causes both morbidity and mortality despite development in early cancer diagnosis and subsequent therapies [1]. Historical methods of diagnosis, including histopathological studies and radiographic films, are also costly and time-consuming, as they usually need to be interpreted by an expert, slowing down the response treatment [2]. It is thus desirable to develop automated, precise and efficient methods of lung cancer prediction and classification.

In the modern times, machine learning (ML) and deep learning (DL) have become a potent tool in the medical image analysis and disease prediction. Of particular success is deep learning in the demonstration of complex patterns on high-dimensional data and the precision classification of lung nodules, tumors, and histological subtypes [3]. ML models based on deep learning (DL) principles (FRAMES based on convolutional neural networks, capsule networks, and ensemble learning) have proven to be highly effective in the early diagnosis, progression, and predicting the prognosis of lung cancer [4].

Lung cancer screening is made through the use of CT scans, and chest radiographs. Segmentation and feature extraction method-based deep learning models have enhanced the sensitivity and accuracy in locating nodules and their classification [5]. In addition, whole-slide imaging and large-scale DL models enable automated histopathological analysis [6], which in combination with immunotherapy, enables prognostic analysis of patients.

Recent research paper have also considered the possibility of hybrid solutions that combine use of blockchain with deep learning, cloud processing, and ensemble methods, to provide more reliable, secure, and larger scaling related to lung cancer prediction systems [7]. Furthermore, feature selection and correlation-based procedures have been employed to maximize the model performance, decrease the complexity and increase the interpretability [8]. Such as the scale of required annotated data, working with imbalanced data, and raising analytic complexity to the interpretable level of clinical decisions [9]. Still, combining deep learning with conventional diagnostic routines can prove an incredible potential in the context of lung cancer diagnostics as early diagnosis can be achieved, and the survival rates of more individuals might be enhanced as a result.

1.1 Problem Statement

Cancer diagnosis is not a simple process because most patients are identified at an advanced stage where treatment is not fruitful. Existing diagnostic methods are perhaps precise, but they still require time-intensive human analysis of the medical data. Interpretation of the clinical data and medical images is also subject to inter-observer variability. The possible solution is using deep learning techniques. With the advantage that deep learning models have in being able to identify complex patterns across different information, one can come up with a more efficient and reliable tool in predicting cancer.

1.2 Research Objectives

To Develop an Effective Deep Learning Model:

RO.1: To develop and apply a deep learning-based model namely, a Convolutional Neural Network (CNN) to make predictions on lung cancer diagnosis given the dataset provided.

RO.2: To assess the measurement performance of the proposed CNN model in objectively detecting lung cancer disease using the accuracy, precision, recall, and F1-scores.

RO.3: To benchmark the proposed CNN model with other machine learning and deep learning models developed in previous studies to underline its efficiency and challenges, which could be further improved.

1.3 Research Questions

In order to address the pressing need for improved cancer prediction, this research is guided by the following research questions:

RQ.1: What is the way to implement deep learning in predicting lung cancer diagnosis based on a given dataset?

RQ.2: How does the proposed model perform in detecting lung cancer compared to other studies?

1.4 Significance of the Research

This research can be valuable in the transformation of cancer prediction, as it is possible to enlist the benefits of deep learning algorithms in association with a wide and extensive array of data sources. Traditional techniques of diagnostics usually rely on one kind of data only which can limit the precision of both the timing and the scope of prediction. In contrast to the respective methods, deep learning approaches do not only allow encapsulating complexities across multiple modalities, but also enables a more holistic understanding of the disease and, as a result, increases predictive accuracy. Designing and validating these models can help develop more predictive and accurate cancer systems that cortex could eventually achieve earlier detection, better patient outcomes, and reduce the burden to the society.

2. LITERATURE REVIEW

Deep learning analysis was used by [1] to determine lung cancer subtyping based on CT scans. This study revealed that AI models had the potential to differentiate the adenocarcinoma and squamous cell carcinoma without error. This is a clinically-relevant distinction in the course of choosing targeted therapies. A statistically proved eminent value of diagnostic help in complex situations was found to be provided by the model to the radiologists. The authors also stressed the place of AI in precision oncology. Weaknesses were that they rely on annotated data and they are not externally validated.

A correlation-based feature selection approach to lung cancer classification was developed by [2]. Their model helped in minimizing noises in predictive accuracy and enhancing input features as they focused on training rather than using input features that might degrade the model. The method was able to discriminate between malignant and benign cases on the basis of structured clinical data. An advantage was its efficiency in using high dimensional data which is normally not efficiently handled in medical datasets. The study however had limitations on cross- dataset generalization and this necessitated the need to develop larger validation studies.

Proposed the concept of a deep saliency capsule network along with the pretrained models to predict lung cancer. Their architecture was based on taking advantage of the strengths of capsule networks, which is that they can capture spatial hierarchies in images. The algorithm enhanced the accuracy of classification and interpretability compared to traditional CNNs [4].

[5], presented a model of deep feature extraction and ensemble learning classifier to identify lung and colon cancer. They used an ensemble-based hybrid architecture that integrates the Deep CNN features and ensemble methods including random forests and gradient boosting. This combination enhanced more diagnostic accuracy than that of the single-model technique. The study presents a high level of precision in multi cancer detection thus this could be applied in a larger clinical practice. They also highlighted the possibility of such models in reducing the misdiagnosis. However, its applicability was limited by the use of relatively small datasets which rendered its usefulness in various clinical scenarios to be limited.

In case study, [6] dealt with the deep learning of lung nodules based on CT data. They have used the CNNs approach in their framework to discriminate between benign and malignant nodules with a high sensitivity. Outcomes indicated good results in minimizing the false positives that are of great significance in diagnostic imaging. The research tested its model against published online data, doubling up on reproducibility. It also emphasized on the use of automated CAD (Computer-Aided Diagnosis) systems in radiology. It however urged that recognition had to be done through additional validation in multi-center clinical trials.

[7], recently developed a framework that combines the blockchain technology and extended CNN models in detecting lung cancer. Their solution did not only secure and assure privacy to data but also make it more credible in clinical environments. CNN architecture had high accuracy in detection of malignant nodules in imaging datasets. In addition, blockchain integration offered immutability and transparency of medical data. This two-fold innovation is a progressive solution to the AI-Cybersecurity collaboration in the medical roads.

Created a framework of deep learning to screen lung cancer using chest radiographs that is driven by segmentation. Their approach consisted of segmentation of areas of interest and classification tasks where previously end-to-end models were not as accurate. This plan minimized misclassification as a result of irrelevant background features [8]. The study was especially effective in the screening of large population where radiographs are quite common. The authors said it could have an opportunity in low-resource health care systems. However, some difficulties lay in applying the method to a variety of imaging settings.

[9], provided a comprehensive tutorial of different DL applications, architectures, frameworks, and implementation issues in medical research. This paper has discussed CNNs, recurrent neural networks (RNNs), and hybrid methods of predicting the disease. It highlighted the role of workflow optimization and scalability of an AI model in healthcare diagnostics. Noteworthy, the work noted that there is a lack of clarity in data access and AI outcome interpretation. This general review will serve as a guide to other researchers who want to use deep learning in detecting cancer.

Pretrained models increased robustness, which is why the framework can be used to detect the early stage of cancer. The paper stated that pooling operations in CNNs could be overcome using capsule networks. Nevertheless, high computing demands were a problem [10].

[12], demonstrated how a large selection of deep learning algorithms performed in detecting lung disease, including lung cancer. They applied CNNs, deep belief networks and transfer learning models to medical imaging datasets. Their findings indicated that CNN-based networks were the most robust and accurate in all of the techniques. The comparative framework provided the insights into the adaptability of algorithms to the respiratory diseases. The important conclusion was that model generalizability was directly affected by the quality of data. The study, nevertheless, reported the weakness of the diversity in data sets.

A study was conducted by [13] to analyze how environmental degradation affects the health of humankind with special reference to cancers. They presented the case that pollutants, toxins, and climatic-induced shifts negatively affect the immune system and expose people to carcinogenic substances indirectly causing the prevalence of cancer. Their examination expressed the fact that industrialization, urbanization, and environmentally harmful activities are silent accelerators of the disease. The paper proposes that ecological sustainability should be part of the preventive medicine strategies in their policy enforced by the respective governments. The work is especially pertinent to the cancer epidemiology as it sees the correlation between environmental hazards and oncological effects.

[14] investigated the capability of whole-slide imaging (WSI) and deep learning to be utilized in forecasting cancerous outcomes. E-reading slide images and implementing AI models on top of images, the research provided evidence of a higher precision and efficiency than manual histologic study. These modalities allowed high throughput evaluation, eliminating human error and inter-observer variability. Also, Lee emphasized the principles of WSI as a way of pretentious treatment planning. The study makes digital pathology a foundation stone in implementing AI in cancerous diagnoses.

[15] implemented the use of machine learning connected with image processing to classify lung cancer. Their experimentation involved steps in processing the images to improve the quality of images followed by classification algorithms. The results showed that there was better accuracy than the conventional diagnostic models. The authors emphasized the role of cross-breed workflows incorporating the enhancement of images and AI learning. This technique has the potentiality to be applied as a cost-effective screening technique in a low-resource setting [16, 17]. Nonetheless,

the paper recommended improvement of algorithms to deal with noisy data in the real world.

Designed a hybrid deep learning model with the ability to diagnose lung as well as colon diseases. They incorporated transfer learning as a part of ensemble. The model proved much adaptable in multi-cancer environments in that the model showed promise of universal diagnostic tools. Notably, it minimized training costs in terms of computation and did not sacrifice accuracy. The authors pointed out its use in the use of an integrated cancer screening system. However, due to the limitations of the dataset [17], it could not be tested with rare-cancer types.

[18], developed a DL-based system to detect and stage lung tumors that runs in a cloud environment. These were architected to enable real-time image processing and capability to scale to large-scale hospital capacities. Since it was a cloud-based framework, telemedicine applications were made feasible as it can be accessed remotely. The paper showed good results in terms of tumor staging, which could be used in preparing therapies. Using cloud infrastructure, the method also decreased the load on local machines. The authors, however, mentioned some issues in privacy of data and network dependence.

In a study by [19], presenting a systematic review of research on identification of microsatellite instability (MSI) in colorectal cancer histology using deep learning, it was shown that a deep-learning-based system could be used to identify the microsatellite instability. This review showed that the AI models had a high likelihood of detecting MSI status, which is vital in therapy and prognosis. The results indicated the effectiveness of DL to complement the conventional histopathological assessment. The authors also identified problems connected to interpretation of black-box AI models. Still, their contribution preconditioned the rise of precision oncology on the basis of computational pathology.

Table 1: Comparative Literature Review

Study	Methods	Dataset	Results	Limitations
Ali et al. (2023)	Deep learning (CNN)	ELISA & PCR test results.	High accuracy in HBV classification.	Limited dataset size, generalizability concerns.
Zhang et al. (2023)	ML (Logistic Regression, Random Forest)	1,000+ patient records	Random Forest had highest sensitivity & specificity	Missing data & imbalanced samples
Khan et al. (2024)	Hybrid CNN–LSTM	Hospital records & PCR over 5 years	Strong prediction of HBV progression	Lack of interpretability for clinicians
Patel et al. (2024)	Ensemble learning (XGBoost, Gradient Boosting)	800 patient diagnostic records (ICT, ELISA, PCR)	Superior classification accuracy	High computational cost, low-resource adoption issues
Rahman et al. (2025)	Explainable AI (SHAP-based interpretation)	1,200 patient records	Improved transparency & biomarker identification	Trade-off between performance & interpretability

3. MATERIALS AND METHOD

This section suggestions an explanation of the data employed by us and an in-depth discussion of the process undertaken to predict the risk of lung cancer. The methodology aims at addressing the issue of early cancer diagnosis with deep learning models. The method is systematic, and comprises of data acquisition and partitioning, pre-processing, feature extraction, and application of the deep learning models.

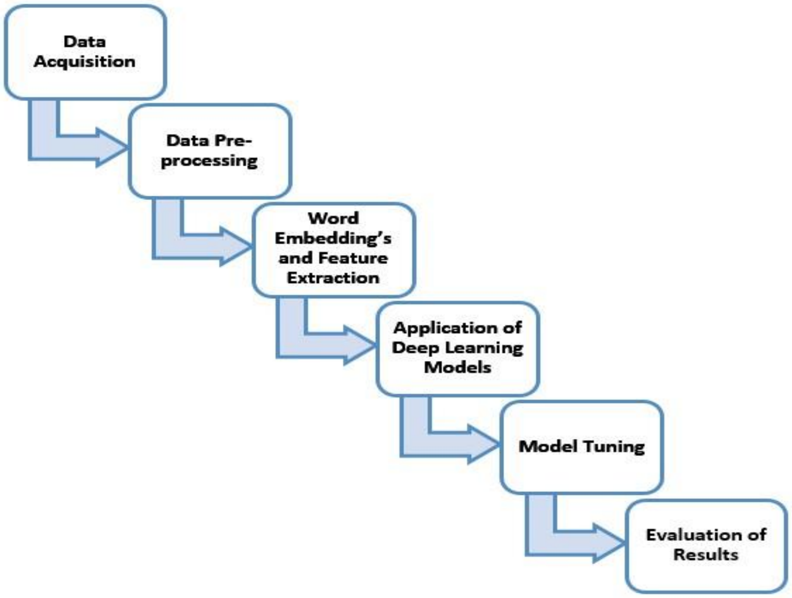

Fig.1: Overview of the Suggested Procedure.

3.1 Data Collection and Data Splitting

Data Acquisition

The data used in this study was obtained on Kaggle and comprises of 750 images into which three experts have classified as having three different lung conditions:

i Normal Class: Histologic features of healthy lung.

ii Lung Adenocarcinomas: 1. Anchors and eyes: Can be identified by this pattern, which is based on the anchors and eyes. 2. Bronchial adenocarcinoma: Can be classified as such based on the color of anchors and eyes which forms bronchial adenocarcinoma.

Lung Squamous Cell Carcinomas: Appearances of this type of cancer which starts in the squamous cells on the lung.

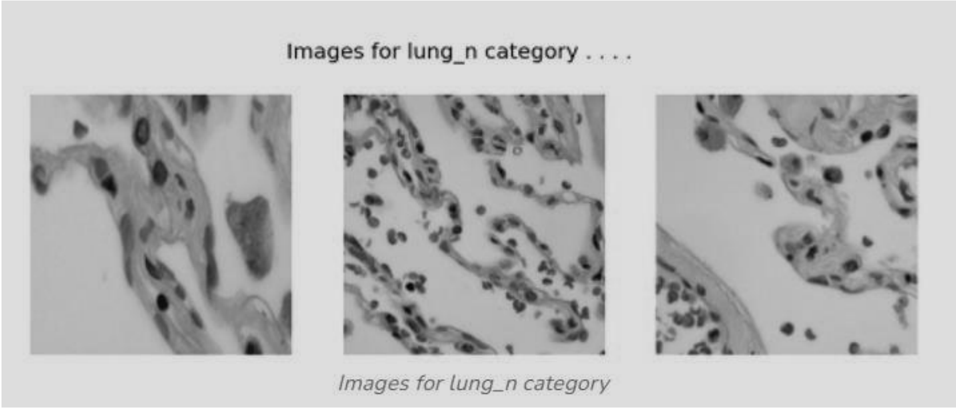

Fig.2: Lung_n Images Category

Fig.3: Lung_aca Images Category

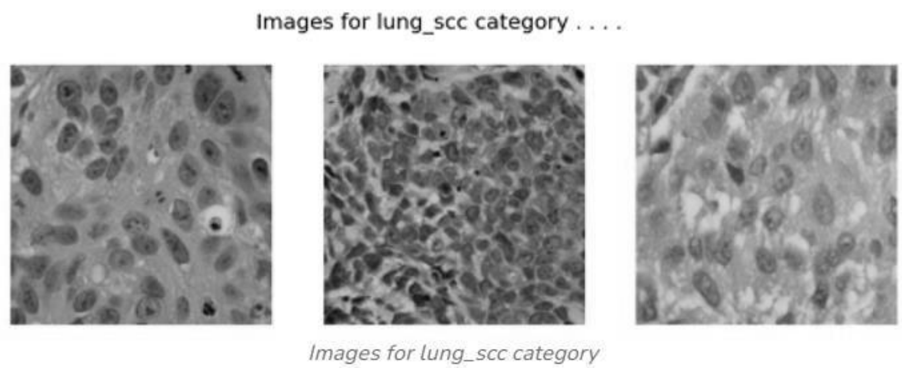

Fig.4: Lung_scc Images Category

Table 4.1: Detail of Lungs Cancer Prediction Data Set

Category	**Disease**	**Image Count**
Normal_Class	Lung's cancer	250
Lung_Adenocarcinomas	Lung's cancer	250
Lung_Squamous_Cell Carcinomas	Lung's cancer	250
Total		**750**

To produce these images in each class, 250 original images were augmented.

Data Splitting

The whole dataset is structured into the analytic, training and evaluation of data. Explicitly, the data has been divided to 80 percent as the training set, 20 percent as validation set, and 20 percent reserved as a testing set. The data is also grouped into three subsets of data further distinguished:

Training Set: This was utilized to train the machine learning models. It is crucial in computing model parameters like the weight and bias [4]. In this paper, 80 percent of the data set is allocated to training, both target and predictor variables.

Validation Set: Helps to address concerns of overfitting and improper underfitting by offering independent data to test the model throughout the training. In this case 10 percent of the data is used to validate. Depending on the framework used, such as Keras, model parameters are customizable manually or automatically; to be more objective in this study, automatic validation is used [8].

Testing set: Test set used to compare the performance of the final model on unseen data. In the given research, ten percent of the data will be held out as the test set to provide an impartial estimation of the generalizability of the model. The accuracy of the model is tested by matching predictions to their actual results. The data is divided with 90/10 percent, both to train and validate the data, and the parameters are optimized with the aid of the validation set [17].

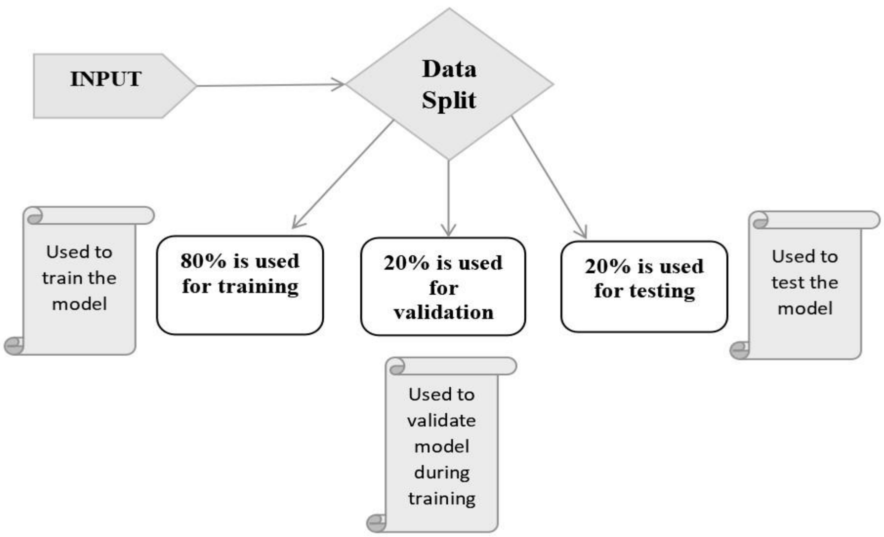

Fig.5: Splitting Data Process

3.2 Preprocessing for Lung Cancer Prediction Using CNN

Preprocessing is also an essential procedure in training a CNN model and achieving higher accuracies in its prediction. Proper preprocessing will provide high quality data that is consistent and will make models perform well. The critical steps entail the following:

i **De-missing Missing Values:**

The problem of missing values needs to be tackled well because it may skew a model or make its predictive ability lower. Standard imputations or methods are mean, mode, and median. When missingness is not random, more sophisticated techniques of predictive imputation may be used.

ii **Outlier Detection and Treatment:**

The existence of outliers in numeric attributes has a negative impact on the accuracy of the model. Outliers are usually estimated by using statistical methods like the z-score or the interquartile range (IQR). As soon as outliers are identified, they may be omitted in case they were introduced by data entry errors or corrected with the help of such methods as standardization.

Standardization and normalization:

To guarantee that all the numeric features make the same contribution to the model and to increase the rate of convergence during training, scaling of features is done to a standard range.

Normalization scales a feature xxx to a range [0, 1]:

$$x_{\text{norm}} = \frac{x - x_{min}}{x_{max} - x_{min}} \text{.....................(1)}$$

Standardization transforms a feature x to have zero mean and unit variance:

$$x_{\text{std}} = \frac{x - \mu}{\sigma} \text{....................(2)}$$

where σ is the mean and σ is the standard deviation of the feature.

Through these preprocessing procedures, the quality and homogeneity of the dataset is improved, which allows the CNN model to learn more efficiently and provides accurate lung cancer classification results based on medical images.

3.3 Word Embeddings and Feature Extraction

i. Word Embeddings

Word embeddings represent words as a high dimensional dense vector in which semantically related words are clustered near one another. The embeddings represent the contextual and meaning connections of the words and are usually trained on large textual corpora via neural net methods (Word2Vec, GloVe, or FastText).

$w_i \in R^d$.....................(3)

Where:

- w_i represents the vector embedding of the i word.
- d is the dimensionality of the embedding space.

ii. Feature Extraction

Feature extraction is a process of converting raw data into a series of informative and representative features that would be inputted into the machine learning models. This is the primary step in a natural language processing (NLP) process that often involves the conversion of text-based data into a numeric representation that can be efficiently acted upon [10], allowing effective learning and prediction.

$$S = [w_1, w_2, \ldots, w_n] \ldots\ldots\ldots\ldots\ldots\ldots\ldots (4)$$

Where S is the feature matrix for a sentence of n words.

Application of Deep Learning Models

The essentials of our methodology are the use of DL models to forecast lung cancer in its initial stage, and these include CNN mainly. These techniques are fed with pre-processed image data and will automatically learn and detect useful patterns representative of cancer.

i. Convolution Layer

Snaps on convolutional layers filters (K) over small parts of the input image (X) to recognize features like (edges or textures). The convolution operation is defined to be

$$S_{i,j} = (X * K)_{i,j} = \sum_{m=0}^{M-1} \sum_{n=0}^{N-1} K_{m,n} \cdot X_{i+m,j+n} \ldots\ldots\ldots\ldots\ldots\ldots\ldots (5)$$

This learning constructs a hierarchical model of features by attaching a spatial relationship and successively deriving higher-level structure.

ii. Max Pooling

Pooling transforms the spatial dimensions of feature maps by replacing each feature-map location with the maximum value of one of a set of non-overlapping windows [17], allowing salient information to be retained at a lower computational cost and facilitating translation invariance.

iii. Full Connected Layer

The fully connected (dense) layer reduces valid feature map produced by the convolutional and pooling layers into a vector v to do the classification:

$$v = [f_1, f_2, \ldots, f_n] \ldots\ldots\ldots\ldots\ldots\ldots\ldots (6)$$

Each element f_i represents a learned feature from the input image.

iv. Dropout Layer

Dropout randomly removes a proportion p of neurons during training in order to avoid overfitting:

$$v' = v \odot r, \quad r_i \sim \text{Bernoulli}(1 - p) \ldots\ldots\ldots\ldots\ldots\ldots\ldots (7)$$

Here r is a binary mask and $\odot$ is point-wise multiplication.

v. Dense Layer

The dense layer executes a fully-connected procedure and combines all the features of inputs to learn complex relations.

vi. Output Layer

In binary classification the output layer activates the sigmoid and produces a probability between 0 and 1:

$$\hat{y} = \sigma(z) = \frac{1}{1 + e^{-z}} \ldots\ldots\ldots\ldots\ldots\ldots\ldots (8)$$

That is z input to the output neuron and $\hat{y}$ the estimated probability of class 1.

Training utilizes backpropagation and gradient descent and performance is measured using accuracy, precision, recall and f1-score.

4. RESULT AND DISCUSSIONS

In this study, presents an observational data collected as a result of many research studies held to solve the problem.

4.1 Answer to the Research Questions

Research Question 1: What is the way to implement deep learning in predicting lung cancer diagnosis based on a given dataset?

In answering this question, we developed a CNN that diagnoses lung cancer. A number of different deep learning models were compared, and the CNN parameters were determined by iterative experiment in the best possible way and to optimize performance of the multiple layers. There are various parameter configurations which were analyzed to determine an effective configuration. The most important aspects of the development of the proposed CNN model and the related settings are summarized in Table 2.

Table 2: Model Characterization of the CNN model

Parameters	Values	Parameters	Values
model	sequential	Dense	32
image_size	256	Dropout	0.2
Input vector_size	10	Filter_size	32
Test_size	0.2	Pool_size	2
Max Pooling	(2,2)	Activation function	softmax
verbose	1	Epochs	10
Kernel_size	(5,5)	Batch_size	64

By conducting tests on CNN models having the parameter settings provided in Table 2, their performance was evaluated based on test accuracy, test loss and training time. It was found that CNN with 32 filters performed on the test data with 91.0% accuracy.

Table 3: CNN Performance Assessment

Performance Evaluations	Values
Accuracy	91%
Precision	100%
Recall	92%
F-1 score	96%

i. Accuracy

Accuracy is used to measure the correctness of the test relative to the total number of predictions of the model. It is computed as

$$\text{Accuracy} = \frac{\text{Number of correctly predicted records}}{\text{Total number of records}} \ldots\ldots\ldots\ldots$$

An accurate one works best where there is a balanced distribution of classes in the data set It can be misleading in the cases of class imbalances in the data representation of the model performance.

ii. Precision

Precision tests how accurate the positive predictions of the model were. It is ascribed as

$$\text{Precision} = \frac{\text{True Positives (TP)}}{\text{True Positives (TP)} + \text{False Positives (FP)}} \ldots\ldots\ldots\ldots\ldots\ldots (10)$$

Acute accuracy is important in cases where false-positives have serious ramifications, as with medical diagnosis.

iii. Recall (Sensitivity)

Recall is the ability of the model to correctly predict all actual positives including those it would have otherwise missed:

$$\text{Recall} = \frac{\text{True Positives (TP)}}{\text{True Positives (TP)} + \text{False Negatives (FN)}} \ldots\ldots$$

Recall is crucial in processes where collecting all positive cases is crucial, i.e. disease detection.

iv. F1-score

F1-score is a single measure balancing precision and recall a weighted average compiled of precision and recall:

$$\text{F1-score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \ldots\ldots\ldots\ldots\ldots\ldots (12)$$

A high F1-score would be used to indicate good performance in both precision and recall and thus a F1-score would prove useful when evaluating models with imbalanced outcomes.

Research Question 2: How does the proposed model perform in detecting lung cancer compared to other studies?

To answer this question, the proposed CNN model performance was contrasted with a few conventional machine learning (ML) and deep learning (DL) methods.

Comparison to Machine Learning Models

To compare the performance of the proposed CNN to the traditional ML models based on the patient data, the assessment was performed using accuracy, precision, recall, and F1-score metrics. Logistic Regression (LR) model had the highest accuracy of about 70 percent. A more comprehensive assessment of the results obtained in the proposed CNN model and the traditional ML classifiers is described in Table 4.

Table 4: Comparisons between the machine learning models and the proposed CNN model.

ML Model	Accuracy (%)	Precision (%)	Recall (%)	F-1 score (%)
SVM	67	68	96	79
DT	65	74	71	73
LR	70	71	95	81
RF	69	71	90	79
KNN	69	71	93	81
Proposed CNN	**91**	**100**	**92**	**96**

Comparison of Proposed CNN Model with the Other Deep Learning Models

To determine the effectiveness of the suggested CNN based model in classifying liver diseases using the data provided on the patient, comparisons were made with other approaches to deep learning such as BiLSTM, RNN, ANN and LSTM. Evaluation metrics were accuracy, precision, recall and F1-score. The results of these models as well as those of the proposed CNN model are given in Table 5.

Table 5: Comparison Between Deep Learning Models and proposed CNN model.

DL Model	Accuracy (%)	Precision (%)	Recall (%)	F-1 score (%)
BILSTM	75	76	94	84
RNN	83	77	89	82
ANN	80	76	93	84
LSTM	74	81	86	83
Proposed CNN	**91**	**100**	**92**	**96**

The review shows that the presented CNN DL model is (compared to other DL solutions) more effective to measure accuracy, F1-score, recall, and precision. This excellent output is achieved by use of comparative experiments that make use of a mixture of two different machine learning models and feature selection models that lead to favored classification.

To determine its efficacy the suggested CNN model was compared with the other studies in the areas of lung cancer diagnosis. The comparison emphasizes the model achieved a higher performance compared with the prevailing approaches (see Table 6). Nevertheless, the comparisons to published works are also difficult because of differences in datasets and methodologies applied, which could also distort generalizability of performance measurements.

Table 6: Comparison of the Deep Learning models and proposed CNN model.

Reference	Techniques	Accuracy
(***Chaunzwa***, et al., 2021)	Deep learning classification of lung cancer histology using CT images.	71%
(***Trebeschi***, et al., 2021)	Prognostic value of deep learning-mediated treatment monitoring in lung cancer patients receiving immunotherapy. *Frontiers in oncology.*	75%
Proposed CNN	**Lung Cancer Prediction using Deep Learning (CNN)**	**91%**

Confusion Matrix

Confusion matrix is one of the most important technologies to measure the results of a classification model. It gives a breakdown line by line of the model prediction and actual results, which would enable researchers to know the results of the model where the model is performing well and where it is underperforming.

In terms of disease prediction, i.e. detecting lung cancer, the matrix will involve a comparison between Actual labels (real state of the patient) and

Prediction labels (model output). It is made up of four major parts:

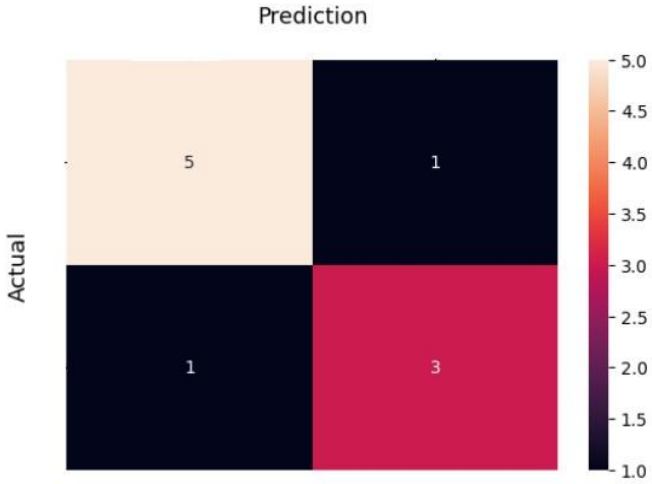

Fig.6: Visualization of confusion matrix

The Analysis of the Proposed Model

The proposed model is based on the Convolutional Neural Network (CNN) to classify the cases of lung cancer diseases. As shown in Table 6, the CNN model achieves a better performance than other available alternatives in the diagnosis of lung cancer. The success of the model can be explained by the fact that the balanced datasets paired up with efficient feature selection techniques and a sturdy CNN architecture have resulted in the successful performance of the model. Moreover, the BiLSTM layer mentioned will allow maintaining information regarding context, which is vital in terms of correct classification. The model is quite effective as reflected on the experimental results with the accuracy of 91%, precision of 100%, recall of 92%, and an F1-score of 96.

5. CONCLUSION

In the present research, a deep learning system with pretrained generic CNNs followed by a softmax layer was implemented to classify lung cancer images. The proposed model was stringently contrasted to the existing state-of-the-art methodologies as have been published in the literature. Experimental data show a high-performance level of the model with 91% accuracy. Also, a Tkinter based user-friendly interface was also provided making the product accessible to general users. This work can show a viable and feasible way to automate the lung cancer classification of images with results that almost correlate with the clinical ones.

In the future other physiological factors important in determining the development of lung cancer in the human body will be identified and used as predictive factors. Blood pressure, oxygen saturation, and body temperature are parameters which will be analyzed in regards to predictive significance. An Internet of Medical Things (IoMT) application will be designed to implement those physiological measurements into the predictive model. Such an end-to-end strategy is likely to enhance the quality, reliability, and clinical utility of the lung cancer prediction models, eventually facilitating better healthcare outcomes.

Future work

Defining Essential Predictive Features: Examine genetic markers, lifestyle, environmental exposures and comorbidities to provide enhanced lung cancer predictive features.

Combination of Physiological Parameters: Add blood pressure, oxygen levels and body temperature to enhance prediction accuracy.

OMT Application Development: Design Internet of Medical Things applications to enable data collection of patient information in real-time and constant monitoring.

iv Advanced Deep Learning Techniques: Learn ensemble learning, transfer learning, and other deep learning techniques to make a model robust across a suite of datasets.

v Clinical Validation: Partner up with healthcare providers in the validation of models and effectiveness of early interventions and detection.

vi User Interface and Ethical Consideration: Optimize the UI to ensure interface is user-friendly, the data is secured, and ethical considerations taken, as well as regulatory compliance.

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