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Improving lung cancer detection with enhanced convolutional sequential networks

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Lung cancer is the most common cause of cancer-related deaths worldwide, and early detection is extremely important for improving survival. According to the National Institute of Health Sciences, lung cancer has the highest rate of cancer mortality, according to the National Institute of Health Sciences. Medical professionals are usually based on clinical imaging methods such as MRI, X-ray, biopsy, ultrasound, and CT scans. However, these imaging techniques often face challenges including false positives, false negatives, and sensitivity. Deep learning approaches, particularly folding networks (CNNS), have arisen as they tackle these issues. However, traditional CNN models often suffer from high computing complexity, slow inference times and over adaptation in real-world clinical data. To overcome these limitations, we propose an optimized sequential folding network (SCNN) that maintains a high level of classification accuracy, simultaneously reducing processing time and computing load. The SCNN model consists of three folding layers, three maximum pooling layers, flat layers and dense layers, allowing for efficient and accurate classification. In the histological imaging dataset, three categories of lung cancer models are adenocarcinoma, benign and squamous cell carcinoma. Our SCNN achieves an average accuracy of 95.34%, an accuracy of 95.66%, a recall of 95.33%, and an F1 score of over 60 epochs within 1000 seconds. These results go beyond traditional CNN, R-CNN, and custom inception classifiers, indicating superior speed and robustness in histological image classification. Therefore, SCNN offers a practical and scalable solution to improve lung cancer awareness in clinical practice.

Keywords Deep learning, Convolutional neural network, Convolutional sequential network, Lungs cancer, Histological dataset

Lung cancer is one of the deadliest cancers globally, with early detection playing a vital role in improving patient survival[1]. Traditional diagnostic methods such as X-rays, CT scans, and MRIs, though widely adopted, often struggle to detect small or early-stage nodules, especially when affected by noise or overlapping anatomical structures[2]. These approaches are also prone to subjective interpretation, leading to high false-positive and false-negative rates. Overdiagnosis and unnecessary biopsies further complicate the clinical workflow and may negatively affect patient outcomes[3].

Clinical techniques are used for tests that provide images of lung cancer inside human lungs. Clinical techniques like MRI, X-rays, biopsy, ultrasound, and CT scans are used to detect the spread of lung cancer. Ultrasound waves provide pictures of cancer tissues; MRI generates fine-grained pictures of the bodies by vector fields other than the X-ray; and biopsy involves taking a little sample of tissue to examine under a microscope. These are the MRI, X-rays, biopsy, ultrasound, and CT scan methods for detecting lung nodules due to their high resolution[4]. Following are the main issues in the lung clinically[5]:

- When test results suggest a condition occurs false positive, even if it is not present .
- When a test fails to detect cancer even it is present occurs false negative.
- Over diagnosis of certain cancers may not necessarily result in death or decreased quality of life.
- Screening test can potentially result in more harmful tests and procedures.

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- Limited effective screening methods.

Medical imaging techniques like MRI, CT scan, X-ray, and biopsy provide significant representations of tissue and organs. However, they might fail to collect all necessary information. The scientists have used radiomics, a breakthrough in cancer diagnostics that analyzes many body parts using massive amounts of digital data to simplify feature extraction[6].

To overcome these issues, we introduce a Sequential Convolutional Neural Network (SCNN) with a lightweight architecture that minimizes complexity without sacrificing performance. By using fewer layers, efficient preprocessing, and robust feature extraction, SCNN achieves fast, accurate classification and demonstrates resilience under real-world constraints—making it suitable for integration into clinical diagnostic workflows.

While traditional clinical methods methods are widely used, they are often sensitive to noise, leading to imaging mistakes like false positives and false negatives, which can delay accurate diagnosis and treatment. Additionally, these techniques may struggle to detect early-stage lung cancer, where small abnormalities may be difficult to identify, further complicating the early detection process.

We also acknowledge the limitations of existing deep learning models, including traditional Convolutional Neural Networks (CNNs), Region-Based Convolutional Neural Networks (R-CNNs), and Custom Inception Classifiers. While these models have demonstrated some success in medical imaging, they often face challenges in handling noisy datasets, complex histology images, and real-time processing requirements. Many of these models tend to have high false-positive rates due to their sensitivity to image variations and noise, which reduces their diagnostic reliability. Furthermore, their computational complexity and slower processing times make them less suitable for real-time applications, which are crucial in clinical settings for quick and accurate diagnoses.

Recent advances in deep learning, particularly through CNNs and R-CNNs, have introduced automation and improved accuracy in image classification. However, these models frequently exhibit inefficiencies in terms of processing time, computational overhead, and vulnerability to noise and artifacts present in histopathological images. Their deep architectures often result in high inference latency and large memory footprints, which hinder real-time applicability in clinical settings.

Our SCNN model addresses these issues by offering several key innovations. First, it significantly reduces computational complexity with a more streamlined architecture, resulting in faster processing times, making it suitable for real-time or near-real-time applications. Second, the model is designed to be less sensitive to noise and false positives, enabling it to deliver more reliable and accurate classifications. This is particularly important in distinguishing between different types of lung cancer—adenocarcinoma, benign, and squamous carcinoma—where subtle differences in histology images may lead to misclassifications in other models. Lastly, the SCNN model demonstrates enhanced accuracy, precision, and recall compared to traditional deep learning models, thereby offering a more effective solution for early lung cancer detection.

By addressing the limitations of both traditional clinical methods and existing deep learning models, our SCNN model presents a robust and efficient approach to improve the accuracy, speed, and reliability of lung cancer diagnosis. These improvements are critical for early detection, which is key to improving survival rates.

Deep learning is a sub-field of machine learning focused on neural networks with a number of layers, enabling the modeling of intricate patterns and solving complex tasks. Neural networks, composed of interconnected nodes organized into layers, use activation functions for introducing non-linearity. The back propagation algorithm trains these networks by minimizing the error between predicted and actual outputs and adjusting weights accordingly. Therefore, convolutional neural networks (CNNs) specialize in image-related tasks, whereas recurrent neural networks handle sequential datasets by adding memory cells, i.e., long short-term memory and gated recurrent units. The autoencoders learn efficient representations of data, and at the same time, generative adversarial networks (GANs) generate new instances by adversarial training. Transfer learning leverages pre-trained models for improved performance on new tasks. The deep reinforcement learning exemplified by Deep Q Networks (DQN). It combines deep learning with reinforcement learning for decision-making in dynamic environments. This dynamic field continually evolves, pushing the boundaries of artificial intelligence applications[7].

CV enables machine learning[8] and deep learning[9] approaches to efficiently implement a diverse range of practical applications. In the medicinal field, where things are often complicated and interact with each other in many ways. ML methods can be made even better by adding imaging data that are taken from the patient's medical background. The model was created to add new training data and improve the time efficiency to get better performance. One of the goals is to extract all the qualitative and quantitative information in the image and develop it for the detection of the disease. The deep learning is connected with radiology to fulfill the goal. It makes significant enhancements in speed recognition and image recognition, and it is applicable in medical image processing. CV improves to detect stages in various image problems by using mathematical function and transformation. Medical imaging processing algorithms are able to detect and identify the abnormality at the early stage by using the model of convolutional neural networks (CNN) in scientific diagnostic assistance systems.

CNN is the popular tool in natural language processing in image recognition due to its performance in identification of high dimensional input data. It can enhance its optimization parameters and capacity to organize intricate data patterns, thus improving the performance of disease detection, i.e., improving diagnostic accuracy and treatment[10].

CNNs are a type of neural network that has specific layers of architecture. There are four types of CNN layers: Relu layers, pooling layers, and fully connected layers. An image is classified by an image classifier by going through these layers.

In the convolutional neural network model, use Keras as a library in the model because Keras is often used with TensorFlow due to its high-level abstraction, simplicity, and strong community support. The sequential

model is a simple and easy-to-use way to define a deep learning model that consists of a linear stack of layers. The layers are added to the model in sequential order, and the output of a single layer is sent as input for the next layer. Single layers are used to detect the cancer, but the accuracy, precision, recall, and f1-score are improved by increasing of layers. Convolutional neural network model used to compare the key performance measures accuracy, precision, f1-score, and recall with the recent ML/DL model implementation with my own datasets collected from the healthcare department. The proposed sequential model has multiple layers for improved evaluation rather than the previous sequential model.

The primary goal is to build a model that is capable of detecting abnormalities in lung cancer of different stages. This model predicts timely, effective treatments. The analysis of pictures shows a timeline in order to make a new frame and predict abnormality development. The aim is to develop a CNN model to classify cancer detection in the histology image frame. Future developments need evaluation of the effectiveness of model training and the database compatibility of experimental design. As such, frame prediction models are used to find abnormalities in a given data set by using frame reconstruction methods within DL structures. Moreover, novel findings and abnormalities in histology-type pictures are found by using categorization models.

The detection of anomalies is a persistent research challenge in the field of medical diagnostics. The occurrence of a tumor or nodule during cancer preventive therapy. If a nodule fails to exhibit the anticipated outcomes after therapy, it may provide a more grave concern for the patient's well-being compared to the tumor itself. To achieve control over this, there is a need to construct a model that can predict future occurrences. The first focus will be on predicting short-term outcomes, with the ultimate goal of using this approach to anticipate future therapies for patients.

- **Development of SCNN Model:** The proposed sequential convolutional neural network (SCNN) model is designed to reduce processing time and improve performance for lung cancer detection using histology images.
- **Layer Architecture:** The SCNN model employs three convolutional layers, three max-pooling layers, flattening layers, and dense layers, contributing to its efficient and accurate performance.
- **Lung Cancer Classification:** The model is specifically trained to classify lung cancer into three categories: adenocarcinoma, benign, and squamous carcinoma.
- **Improved Performance Metrics:** The SCNN model significantly outperforms existing models like CNN, R-CNN, and Custom Inception Classified in terms of average accuracy (95.34%), precision (95.66%), recall (95.33%), and F1-score.
- **Faster Processing Time:** The SCNN model reduces processing time, achieving a faster classification process within 1000 seconds over 60 epochs.
- **Comparative Superiority:** The SCNN model demonstrates superior performance over CNN, R-CNN, and Custom Inception Classified, making it a more effective and precise model for lung cancer detection.

Related work

Lungs cancer diease

Lung cancer ranks as the leading cause of global mortality, accounting for five million deaths each year. This study aims to identify malignant lung nodules using Computed Tomography scans and categorize them based on severity using advanced Deep learning techniques. The study uses various feature extraction methods, including Fuzzy Particle Swarm Optimization (FPSO), find optimal feature. The innovative FPSOCNN reduces computational complexity, and real-time data from Scan Hospital is used for further evaluation[11].

Identifying patients with small cell lung cancer (NSCL) who could benefit from targeted treatments involves looking for biomarkers such as EGFR and PD L1 obtained through tissue biopsies. An alternative method is biopsy involving plasma based DNA which is less invasive, than traditional biopsies and reduces patient risks and discomfort. However liquid biopsy may yield amounts of DNA thus requiring highly precise and specialized technologies to prevent diagnostic errors. This review examines the approaches used to analyze DNA in NSCL patients[12].

The liquid biopsy has transformed the way cancer patients are cared for by identifying cancer markers that can be acted upon and predicting how they will respond to treatment.It also offers information on tumor genotyping determines drug responses and monitors resistance mechanisms.These advancements in technology help, in offering precise. Tailored care to each patient by utilizing next generation sequencing for predictive molecular pathology[13].

Liquid biopsy has greatly enhanced the treatment of cancer by detecting cancer markers and aiding in treatment choices and in depth genetic examinations as well as identifying mechanisms of resistance and monitoring disease progression after treatment to facilitate early detection efforts.The integration of sequencing technology in biopsies improves our comprehension of genetic changes, within tumors[14].

The current working in CAD systems of lung cancer detection, focusing on pre-processing, lung segmentation, and nodule candidate classification. It compares existing approaches and provides a comprehensive overview of the literature[15].

AI is being increasingly utilized in medical imaging, particularly for lungs cell and lung cancer screening. CNN has demonstrated exceptional performance in detecting lung cells and distinguishing between malignant and benign types.Artificial Intelligence tools could help non-invasively characterize tumors and predict patient prognosis. However, clinical implementation is limited due to lack of generalizability and data[16].

Computer-assisted detection methods for lung cancer, focusing on machine learning and image processing methods. A new model is proposed, outperforming existing techniques in terms of accuracy. The model uses Google Colaboratory and uses a marker-controlled watershed algorithm for partition. The computed tomography scan image is converted in grayscale images, noise of the image is remove using Gaussian and Median filters, and

features like area, center, and radius are evaluated. The technique outperforms existing techniques in detecting lung cancer[17].

Lung cancer has become a widespread health issue across the world with regard to its morbidity and mortality. Existing approaches to early detection, treatment and prognosis monitoring suffer from bottlenecks. The use of liquid biopsies (LB), which allow for the detection of tumor-related markers in body fluids, may help alleviate these bottlenecks. This review focuses on membrane-based LB biomarkers and the advancements of sequencing technologies and presents technical updates prospects in clinical use and existing limitations future perspective on existing limitations[18].

Lung cancer, a common variant, is a deadly disease due to pollution, harmful gases, and smoking. Early detection of pulmonary lung nodules is crucial for better diagnosis. Computer-aided systems can assist in image processing, including pre-processing and segmentation. Develop an efficient automatic detection system using soft computing for decision-making[19].

The method of biopsy has been in use for the past two decades as a non intrusive way to identify cancer related biomarkers like circulating tumor DNA. It plays a role in determining the prognosis and monitoring the treatment of individuals with non small cell lung cancer. Identifying mutations in DNA like EGFR, KRAS, ALK or ROS1 is crucial for therapy. Techniques such as qPCR and next generation sequencing are successful, in analyzing DNA.process. This review discusses the use of DNA as a biomarker in patients, with small cell lung cancer[20].

Liquid biopsies provide a method for diagnosing and treating cancer by examining the molecular markers of tumors. Detecting circulating tumoral DNA and cf-RNA can identify targeted treatments for NSCLC patients. Technology developments have improved the effectiveness of liquid biopsy testing; expense and technological limitations are the disadvantages. This technology can revolutionize cancer diagnosis and treatment, enabling real-time patient monitoring, informed treatment options, and improved patient outcomes[21].

Lung cancer is still the deadliest form of cancer worldwide, most patients being diagnosed when the illness is already in its advanced stages. Non-small cell lung cancer (NSCLC) in its early stage has a better prognosis. March 2008 However, sitting firmly in this stage is significantly worse, dropping from 60% at stage II A to 36% at stage III A. Reduction in this burden requires concerted efforts aimed at primary prevention and optimal perioperative systemic therapy. Regarding the pretherapeutic possibilities, the progress in molecular diagnostics and increasing range of targeted therapies indicate further focus on efficient biomarker detection is required. Already used in the management of advanced Spinal NC, liquid biopsies are expected to improve the care of patients with early disease in the future. They are more rapid, easier, and more efficient than conventional tissue biopsies if they are to be used in combinations of screening, diagnosis, and prognosis processes. In addition, they help in therapeutic measures by being able to bypass tumor heterogeneity, assess tumor burden and amount of minimal residual disease (MRD) with circulating tumor DNA after surgery. As studied lung cancer, orel answers some questions about liquid biopsy and goes further into the diagnosis, imaging and prognostic aspects looking on the predictive side of the MRD in this particular context. This review covers the possible role of liquid biopsies in early stage lung cancer[22].

Lung cancer remains the deadliest form of cancer worldwide. While tissue biopsy is the standard method for diagnosing and molecularly stratifying lung cancer, liquid biopsy has emerged as a minimally invasive alternative for detecting biomarkers in body fluids such as blood, urine, sputum, and saliva. Tumor cells release various components—such as cell-free DNA, circulating tumor DNA, exosomes, microRNAs, circular RNAs, circulating tumor cells, and methylated DNA fragments—which can serve as biomarkers for diagnosis, prognosis, and predicting treatment responses. Predictive biomarkers have become a cornerstone in lung cancer management, and liquid biopsy options have gained prominence in recent years. One notable example is the detection of the EGFR p. mutation in plasma, which helps predict treatment responses and monitor lung cancer patients undergoing tyrosine kinase inhibitor therapy. Ongoing efforts are focused on developing more sensitive technologies to enhance the detection of clinically relevant biomarkers. Additionally, liquid biopsy significantly reduces the turnaround time for lab results, expediting the start of treatment and ultimately improving survival rates for lung cancer patients. In this review, we summarize the available and emerging liquid biopsy approaches—covering techniques, biomolecules, and sample types—relevant to lung cancer[23].

This method liquid biopsy does not require invasive procedures and aims at discovering Particles obtaining in body fluids originating from tumors. It achieves this by identifying particular changes in the genome and transcriptome of cells, thus revealing more tumor heterogeneity. Liquid biopsies can also be helpful in the diagnosis of cancer and prediction and alteration of treatment. They provide information throughout the course of disease and make it possible to change the treatment during the course. However, although this appears promising, there are some drawbacks that need to be rectified before the prevalent use of this technology in the clinical setting[24].

Deep learning model

A novel genotype-guided radiomics method that offers high prediction accuracy in small cell of lung non-cancer. Using public datasets, the method uses a hybrid feature fusion, improving prediction accuracy from 78.61 to 83 percent[25].

A deep learning method has been developed to detect lung cancer types from CT images of patients at Shandong Provincial Hospital. The model employs image rotation, translation, transformation, densely connected convolutional networks (DenseNet), and adaptive boosting (adaboost) algorithm. The experimental results demonstrate an identifying accuracy of 89.85 percent, surpassing models like DenseNet, ResNet, VGG16, and AlexNet, indicating an efficient, non-invasive detection tool[26].

3D visualization method using Mask Region-Convolutional Neural Network (Mask R-CNN) and ray-casting for detecting and segmenting pulmonary nodules. The method, consisting of three modules, uses LUNA-16 and Ali TianChi challenge datasets and can detect lung cancer with 88.7 percent sensitivities[27].

A deep neural network model for identifying benign-malignant lung nodules in early lung cancer diagnosis. The model uses a multi-view, knowledge-based collaborative approach, breaking 3D lung nodes into nine fixed views and creating knowledge-based collaborative sub-models for each view. The model can detect lung cancer with 91.60 percent accuracy[28].

Deep learning method for thoracic MR images to detect lung nodules. The Faster R-CNN, consisting of two modules, generates proposed regions for each image and classifies them. The method uses the First Affiliated Hospital of Guangzhou Medical University datasets and can detect 85.2 percent sensitivities of lung cancer[29].

The deep convolutional neural network is being used to automatic classify lung cancer. The DCNN, using 76 cancer cell cases and three convolutional, two fully connected layers, and three pooling layers, successfully classified 71 percent of images without errors[30].

Deep learning-based computer diagnosis system for ultimate lung cancer diagnosis, detecting and characterizing pulmonary nodules with 86.2 percent sensitivity, using LIDC-IDRI and NLST datasets, and predicting malignancy for each detected node[31].

Lung cancer disease are a major cause of cancer deaths worldwide, with 1.76 million deaths in 2018. Computer-aided diagnosis systems have been developed to increase survival rates. The use of VGG16, VGG19, ResNet34, and ResNet50 convolutional neural network architectures for cancer image classification. The ResNet50 architecture showed the best results, with 90.83 precision, 88.89 percent accuracy, and 88.46 percent f1-score[32].

Lung cancer is a major cause of cancer deaths worldwide, with 1.76 million deaths in 2018. Computer-aided diagnosis systems have been developed to increase survival rates. The use of ResNet34, ResNet50, VGG16, and VGG19 convolutional neural network architectures for cancer image classification. ResNet50 architecture achieved the best results with 87.04percent accuracy and 85.71 percent f1 score[33].

Lung cancer are major causes of death globally. Early detection can improve survival rates. A deep neural network was developed to detect lung cancer from omputed tomography images, using a closely connected convolution neural network and adaptive boosting algorithm. The method achieved an accuracy of 90.85 percent on 201 lung images[34].

The early identification of disease reduces the death rates associated with lung cancer. A deep learning-based computer-aided diagnosis (DL-CAD) system was introduced, capable of identifying and categorizing lung nodules with a diameter less than 3 mm. Additionally, it can estimate the probability of these nodules growing into malignant forms. The system's sensitivity was evaluated by testing it with the LIDC-IDRI and NLST datasets, resulting in an accuracy of 86.2 percent[35].

A Deep Convolutional Neural Network (DCNN) is used for the automated classification of lung cancer. The network consists of convolutional, fully connected, and pooling layers. The DCNN was trained using a short dataset consisting of 76 cancer cases, resulting in a classification accuracy of just 71 percent[36].

A reinforcement learning model based on deep learning methods was developed to identify early-stage lung cancer. One significant benefit of this model is that the system is always in a state of learning owing to the reinforcement learning technique. It consistently enhances its learning by incorporating fresh information from each new patient. the LUNA dataset for their tests and achieved a sensitivity of 58.9 percent, specificity of 55.3 percent, and accuracy of 64.4 percent[37].

"Automatic Lung Cancer Prediction from Chest X-ray Images Using Deep Learning Approach" used a technique that included using a convolutional neural network called DensNet-121, which consists of 121 layers. They combined this network with transfer learning to categorize chest images. The model is trained on two datasets, namely Chest X-ray 14 and JSRT, to accurately detect and identify nodules. The model achieved an accuracy of around 74.43±6.01 percent, with a sensitivity of about 74.68 ± 15.33 percent and a specificity of around 74.96 ± 9.85 percent. This indicates models potential usefulness in assisting lung cancer prediction from chest xray providing early diagnosis and detection[38].

CNN predictor is designed to identify early-stage adenocarcinoma (ADC) and squamous cell carcinoma (SCC) in individuals with lung cancer. CNN has been verified using real-time patient data from Massachusetts General Hospital, specifically from individuals with early-stage non-small cell lung cancer (NSCLC). The database contains a total of 311 recorded data phases. The CNN model, based on the VGG network, achieved a prediction rate of 71 percent AUC[39].

The CNN models includes VGG model, InceptionV3 model, RestNet model, DenseNet121 model and a custom CNN model to improve cancer detection of histology image using tranfer learning and advanced data techniques. Utlize a cancer detection from kaggle dataset these model of histopathology characteristics by applying transfer learning from general image dataset i-e medical imaging datasets. CNN architecture is analyzed for a unique combination to extract feature with advance data augmentation strategy. Previous approaches to counter the challenge of insufficient annotated data have not been successful in detecting histopathologic cancer but these methods improve our models detection performance. Detailed evaluation of performance metrics show the proficiency of each model in revealing subtle histological patterns is displayed. The results call for careful choice of CNN architectures in respective tasks, while also propelling the field of automated histopathologic analysis towards widerapplicability which can have potential impact on early cancer diagnosis and treatment planning[40].

Histopathological images have proven to be highly useful for examining biological structures and disease diagnosis including cancer. Digital pathology makes it possible to get accurate diagnostic results with higher quality images, in more detail and with various viewing and group annotations where the pathologists work and contribute to the evaluations. These improvements facilitate prompt initiation of therapies and enhance the

chances of success of the therapies and the wellbeing and survival rate of the patients. But, reviewing these images remains a monotonous and labor-intensive task for the pathologists. Therefore, need for fast and dependable automated methods for differentiating between normal and cancerous images is on the rise. The focus of this paper is a deep learning based image classification approach making use EfficientNet and its variants B0 to B7 at image resolutions that vary from 224 x 224 to 600 x 600. To avoid overfitting the model, some methods of parameter tuning and transfer learning were applied. The dataset which was utilized in this research was the Lung colon cancer histopathology image LC25000 dataset which has 25000 histopathological images split into five classes of lung adenocarcinoma, lung squamous cell carcinoma, benign lung tissues, colon adenocarcinoma and benign colon tissue. First the dataset was prepared to remove images containing unnecessary noise and other forms of image contamination as well as recognition confusion[41].

Lung cancer is the most common cause of cancer death. This is why early lung cancer diagnosis is essential. Such systems can increase the level of lung cancer diagnosis as well as relieve the burden of the workload on pathologists. The CancerDetecNN learning algorithm was designed to determine whether lung whole-slide images contain tumor tissue with relatively low computational efforts. The CancerDetecNN algorithm in five different versions, supplemented by three deep learning models in existence, was implemented to train and test the datasets of the primary tumor plus no tumor tiles obtained from lung WSIs. CancerDetecNN Version 5 was the fifth version developed which at this stage trumped all the other provided architecture, CNN model, predicting all on the dataset given below of a precision of 0.972, AUC of 0.923, F1 score of 0.897 within which cnn model was resnet50. It also used on average less training time by 1 hr and 51 minutes compared to that of the best CNN model ResNet-50. There is a caveat regarding size and diversity of the used dataset relative to the sample analyzed within the work[42].

Ovine pulmonary adenocarcinoma (OPA) is a contagious lung tumor caused by the Jaagsiekte Sheep Retrovirus (JSRV). Integrative virology induces lung cancer in JSRV infected sheep. Though the laboratory pathologist provides histopathological diagnosis as the ultimate means of detecting OPA, craniofacial anatomy assistant interpreting traditional pathology images is quite complicated and highly operator dependent. Recently, the most competent image analysis of pathological specimens was performed with the mask R-CNN. In this work, 54 typical OPA-wsi were used to collect 7167 representative images about OPA's outward appearance from OPA FIGURE OUT STRUCTURAL MORPHOLOGY. Owing to the large number of images, a pi dataset was created that was targeted to the pathology of OPA. This dataset was then split 80% for the training and 20% for the testing of the model based on the number of images used. The model evaluation was carried out using mean average specificity (mASp) and average sensitivity (ASe). Out of the six WSI level pathological images, three were OPA and three were non-OPA, and these were not included in the dataset for anti-peeking validation. For this purpose, additionally, 500 randomly selected images without the underlying conditions were collected for comparative study of the model and pathologists. The key points that were evaluated are accuracy, sensitivity, specificity, and the concordance rate of the methods. The model obtained mASp and ASe values of 0.573 and 0.745, respectively, which suggests that it was able to detect the lesions effectively and also match the annotations provided by the experts. In validation, the model was still able to achieve accurate result when task with detecting OPA and also telling the difference between OPA and OPA-free images. When diagnosing a random sample of 500 images, the model scored an accuracy of 92.8% with no errors of omission and sensitivity of 88%. The concordance in the scores of junior and senior pathology experts was 100% and 96.5%, respectively. Finally, the diagnostic model for OPA based on Mask R-CNN provides effective and timely diagnosis with potential use in everyday practices[55].

Rapid tumor cell proliferation in lung tissues is risk prone and requires appropriate therapeutic intervention such as early detection. In this study, we present DenseNet for detecting lung cancer whereby the approach utilizes continuous feature propagation which blurs the model parameters and enhances the learning of local features within the lung cancer detection system. This assists in achieving structural complexity and unevenness of the CT and histopathological images. In this enhancement, the attention mechanism is integrated into the model bringing ATT-DenseNet; this ensures critical parts are given attention thus increasing the chances of making correct diagnoses. With up to 20% accuracy improvement on average and additional 19.66% and 24.33% increases in precision and recall respectively ATT-DenseNet achieves greater and brighter expectations in lung carcinoma detection modalities than existing methods. DenseNet's ability to analyze complex medical images promises better outcomes[43].

Breast cancer is one of the most common types of cancer in women and significantly improves treatment outcomes. Machine learning (ML) and deep learning (DL), particularly folding networks (CNNS), methods, have demonstrated promising BC diagnosis, even in areas without medical professionals. Due to limited medical imaging data, the new approach used the EfficientNet-B5 with the ensemble-PRE training model, the DenseNet-121, and the Support Vector Machine (SVM) classification, and used a metaheuristic optimizer for hyperparameter tuning. This model was tested on Abriest Data Record and achieved high performance with 99.9% accuracy, sensitivity and AUC. This has proven effective in BC classification[44].

Instance segmentation is a complex computer vision task in which individual objects are identified by one image, generating accurate segmentation masks for everyone who combines both semantic segmentation and object recognition elements. One of the broader models for this task is Mask R-CNN. This extends faster R-CNN by including additional branches that predict the object mask in addition to detection of bounding boxes. This study presents a comparative analysis of 15 different versions of the mask R-CNN framework highlighting differences and improvements in these common variants. Most versions were evaluated using CoCo data records specifically designed for instance segmentation tasks[45].

Acute lymphoblastic leukemia (ALL) is a severe blood and myeloid carcinoma, characterized by the rapid growth of immature lymphoblasts. The use of artificial intelligence (AI) in medical diagnosis brings promising advances in early and accurate recognition for all by improving diagnostic accuracy and minimizing human

error. This study introduces two new AI-based architectures for all awareness. The initial knowledge of Nevestro Classification (KNC) uses two optimized teacher models trained with Adam and Nadam optimizers. The second approach, Nevestro Densenet (50) (Dan), is a custom variant of Densenet, improved with the attention mechanism and fine-tuned with the Nadam Optimizer. Experimental results show the high effects of these models, accuracy, sensitivity, specificity, accuracy, and F1 score values of 0.991, 0.9945, 0.9924, 0.9945 or 0.9945[46].

Early identification and timely management of brain small vascular disease (CSVD) can effectively slow progression to more severe stadiums such as Class II and III. This study used the possibilities of artificial intelligence (AI) and developed an automated computer-aided diagnostic system for accurate detection of CSVD grade 1 using non-dominant brain MRI scans. Patients with Fazekas Grad 1 CSVD over 40 years were confined, and MRI data were processed into 3D formats of axis disk normalization, resizing and dimensioning (120, 128, 128, 128, 1). The 3D Folding Network (CNN) is built from scratch and consists of four foldable layers and three fully connected layers. This model achieved an accuracy of 93.12% when using 3D stack images. These results highlight the effectiveness of the 3D-CNN model in detection of CSVD in the early stages, providing a promising tool for supporting clinical diagnosis and potentially the risk of vascular dementia[47].

Covid-19 is making rapid research efforts to explain the global pandemic and develop effective devices for early detection and accurate diagnosis. This study examines the application of artificial intelligence technologies (AI), including machine learning (ML) and deep learning (DL), to identify Covid-19 using clinical laboratory results. Six models have been evaluated: K-Nearest Neighbor (KNN), Decision Tree (DT), and Naive Bayes (NB) with ML approaches and deep neural networks (DNN), folding networks (CNN), and long-term short-term memory (LSTM) as DL methods. Using 5,644 records from the Israeli Albert Einstein Hospital in Brazil, models were assessed using accuracy, accuracy, recall and F1 scores using 10% Covid 19 positive cases and 18 related attributes. The ML model showed moderate performance (NB: 76%, KNN: 84.56%, German: 85%), while the DL model significantly exceeded them. Under these, the LSTM model achieved a maximum accuracy of 96.78% and an F1 score of 96.58%, highlighting the effectiveness of the diagnosis of Covid 19[48].

This Table 1 compares different deep learning techniques for the diagnosis of lung disorders, enlighten their images dataset sizes, performance parameters weaknesses and strengths. ResNet50,DenseNet and VGG16 technique demonstrate higher accuracy specificity and sensitivity but their computational complexity and interpret-ability and suitability for real time application may vary.Methods like R-CNN and MV-KBC transcend in extraction of features and combining multiple prospective but encounter problems with large dataset and practical implementation. Techniques like LUNA and DL-CAD pivot around continuous learning and early detection emphasizing scalability and its application in real-time, however they are limited by quality of dataset and interpretibilitation. Grossly the Table 1 accentuate the trades-offs between performance computational requirments and practical deployment in clinical settings.

Proposed convolutional sequential networks

The data-set used for training, validation and testing the classification system, the preprocessing step taken for the input data, the classifiers that were design, the metrics used to evaluate their performance and applying DL techniques to extract addition information fron the classifier. The final stage of the project involved analyzing the results and make recommendation for the future improvement. Figure 1 shows the flow chart of proposed sequential model proposed in this work.

The algorithm processes each output feature map I in a convolutional layer by iterating over every position (m, n) within the output feature map's dimensions, where m ranges from 0 to $M-1$ and n ranges from 0 to $N-1$. For each position, it initializes a variable $\texttt{sum}$ with the bias value for the current output feature map, $\text{bias}[I]$. It then performs the convolution operation by iterating through each input feature map k and each position $(s1, s2)$ in the convolution kernel. The weight used in the convolution is $\text{weight}[k][I][s1][s2]$, and the corresponding input data value is $\text{input}[k][m+s1][n+s2]$. The algorithm updates the $\texttt{sum}$ by adding the product of the weight and input data for each kernel element. Once the sum is computed for each position, an activation function is applied to transform the result into the final output value, which is stored in $\text{output}[I][m][n]$. This process is repeated for every position in each output feature map, ensuring that the convolution and activation are performed across the entire feature map set. Illustrated in Algorithm 1.

```
for I = 0 to L do
    for m = 0 to M do
        for n = 0 to N do
            sum ← bias[I];
            for k = 0 to K do
                for s1 = 0 to S1 do
                    for s2 = 0 to S2 do
                        sum ← sum + weight[k][I][s1][s2] × input[k][m+s1][n+s2];
            output[I][m][n] ← activation_func(sum);
```

Algorithm 1. Sequential Based Convolutional Layer

Technique	Images	Disease	Parameter Name	Strength	Weakness
ResNet50[25]	20,000	Lungs	Accuracy, Sensitivity, Specificity	Deep Architecture with Skip Connections, effective deep neural network training, Improves image recognition task performance.	High computational intensity, Overfitting potential, Large memory footprint, Limited interpretability, High training requirements, Real-time application challenges.
DenseNet[26]	4000	Lungs	Accuracy	Facilitates feature reuse, Mitigates vanishing gradient problems, Enables efficient parameter usage, Improves training efficiency and performance.	High memory consumption, High computational intensity, Parallelization challenges, Interpretability issues, Sensitivity to hyperparameters, Limited applicability to specific tasks.
DL-CAD[27]	1500	Lungs	Sensitivity, Specificity, Accuracy	Boosts creativity, Optimizes, Personalizes, Predicts maintenance.	Reliance on large labeled datasets, Potential interpretability limitations, Can hinder practical applications.
ResNet50[28]	2763	Lungs	Accuracy, Recall, Precision, F1-score	Enables effective deep neural network training, Improves image recognition task performance.	High computational intensity, Overfitting potential, Large memory footprint, Limited interpretability, High training requirements, Real-time application challenges.
R-CNN[29]	7000	Lungs	Sensitivity, Accuracy	Employs region-based strategies, Effectively localizes and classifies objects.	Slow inference speed during object detection, Requires multiple region proposals and individual forward passes, Not suitable for real-time applications.
VGG16[30]	6000	Lungs	Precision, Accuracy, F1-score	Its simplicity and uniform architecture, making it easy to understand and implement.	Large number of parameters increases computational requirements, Predisposition to overfitting, especially with smaller datasets.
MV-KBC[31]	8000	Lungs	Accuracy	Combines multiple perspectives, Utilizes limited data.	Relies on fixed views, May not capture comprehensive nodule characteristics.
ResNet50[32]	5015	Lung	Precision, Accuracy	Balances model complexity, computational efficiency, Suitable for various tasks, effective network training.	Limited ability to capture complex hierarchical features, Potential challenges with vanishing gradient, parameter efficiency.
ResNet50[33]	10015	Lungs	Accuracy	Learn hierarchical features and spatial hierarchies, Capture intricate patterns with translational variance.	Expensive for training and inference, Less suitable for realtime, resource-constrained applications.
DenseNet[34]	201	Lungs	Accuracy	Improved feature reuse through dense connectivity, Enhanced gradient flow.	High memory usage and computational cost, Sensitivity to parameters, Potential difficulty in transfer learning.
DL-CAD[35]	346	Lungs	Accuracy	Early detection capability, Potential to reduce mortality rates, Probability estimation for malignancy.	False positives/Negatives, Limited to small nodules, Dependence on dataset quality.
D-CNN[36]	76	Lungs	Accuracy	Automated classification, feature learning, potential for Scalability.	Limited dataset size, Generalizability, potential biases, interpretability.
LUNA[37]	888	Lungs	Accuracy, Senstivity, Specificity	Continuous learning, Adaptive to dynamic environments, Potential for personalized medicine,Utilization of deep learning methods.	Moderate sensitivity, specificity, and accuracy, Interpretability, Dependency on quality of data, Computational complexity.
Dense-Net121[38]	247	Lungs	Accuracy, Senstivity, Specificity	Utilization of deep learning, Transfer learning, Multi-Dataset Training.	Limited performance metrics, Evaluation on limited datasets, Complexity, Interpretability.
VGG[39]	311	Lungs	Accuracy	Specialized classification, High prediction rate, utilization of VGG network.	Limited prepreocessing, room for improvement in accuracy, Dependency on single dataset.
CNN[40]	277485	Lungs	Accuracy	Excellent for pattern analysis, Efficient for image differentiation and object detection	complex model visual information processing, High computational costs, Difficult to capture long-range dependencies, Reliance on large datasets.
Efficient-NetB2[41]	25000	Lungs	Accuracy	Strong in efficiency and accuracy, high-performance tasks on both high-end and resource-constrained platforms.	Limited computational resources, small datasets, or real-time requirements, alternative architectures might be more suitable.
Cancer-DetecNN[42]	2042	Lungs	Precision, F1-score	Combine precision and efficiency, outperform traditional CNN models.	Relies on small, limited dataset, may affect generalize to diverse and large dataset.
R-CNN[55]	500	Lungs	Accuracy, Sensitivity, Specificity	R-CNN accuracy region-based object detection, transfer learning based significant influence model detection techniques.	The main weakness are slow performance, model complexicity, heavy trainable model.
DenseNet[43]	750	Lungs	Accuracy, Recall, F1-score, Precision	Efficient parameter use, improve gradient flow and enhance feature reuse.	High memory and computational cost due to dense connection, which can make it challenging to scale to very deep networks or large datasets.

Table 1. Summary table of related work on deep learning

Dataset description

To create a strong, dependable and reliable system, dataset including a substantial number of histological images are required. The dataset used in this model are taken from three different places are lungs cancer Inmol, lungs cancer NIH[52] and lungs cancer kaggle dataset[53]. It contain lungs data of three types that is benign, adenocarcinoma and squamous carcinoma. The number of images in each class is illustrated in Table 2. The defected image portion biopsy tissue examin using a microscope. All effected tumour tissue cases in the database are non-small lungs cancer. It is crucial that the samples collected from the dataset have undergone immunochemistry procedures to amplify the characteristics that differentiate cancer cells from healthy cells. The most prevalent form of non-small cell lung cancer are squamous cell carcinoma and adenocarcinoma. Non-small cell lung cancer often exhibits lower sensitivity to chemotherapy and radiation in comparison to small cell lung cancer. The dataset contain three types of cells are benign, adenocarcinoma and squamous cell carcinoma to train and test my model.

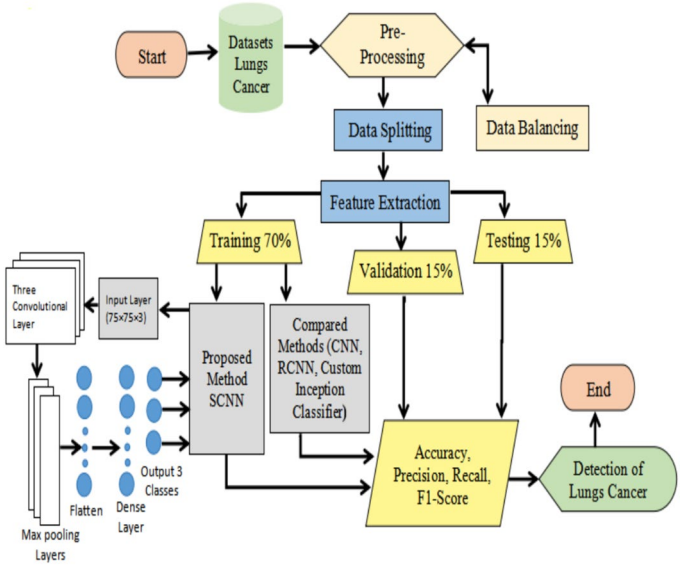

Fig. 1. Proposed methodology flow chart.

Data Set	Lung adenocarcinoma	Lung squamous cell carcinoma	Benign lung tissue	Total
Inmol Hospital	170	170	170	510
NIH	1000	1000	1000	3000
Kaggle	4900	1050	1050	7000
Total	6070	2220	2220	10510

Table 2. Data set classes.

Institute	Training	Validation	Testing	Total
Inmol Hospital	357	77	76	510
National Intitute of Health	2100	450	450	3000
Kaggle	4900	1050	1050	7000
Total	7357	1577	1576	10510

Table 3. Number of images in class.

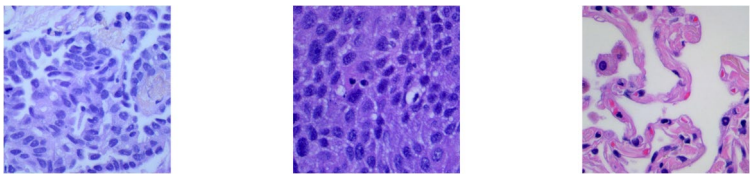

Fig. 2. Images from dataset: (left) Adenocarcinoma tissue, (middle) Squamous Carcinoma, (right) Benign cell.

The dataset contain 510 images from Inmol hospital, 3000 images contain National institute of health science and 7000 images contain from internet source kaggle. All images have the resolution of 768 X 768 pixels in jpeg format. The distribution of images for institute and each class are describe in the given Table 3.

Adenocarcinoma is the common type of non-small cell in the lungs called cancer generating from glandular cells. The symptoms of cancer are cough, shortness of brath and chest pain and often shows up on imaging investigations as peripheral nodules or masses. The treatment of this cancer involves surgery, chemotherapy, radiation based on stage of the cancer and molecular characteristics of the cancer. This type of cancer structure is as seen in the below Figure 2.

The benign tissues indicate non-malignant abnormalities in the lungs. These cells do not grow or extend to other body parts. Medical expert must diagnose these tissues for proper treatment. The images are distinguished in the below Figure Figure 2.

Squamous cell carcinoma of the lungs is a kind of non-small cell lung cancer that arises from the squamous cells. It presents as a centrally located tumor or hollow space in the lung, along with symptoms. The standard treatment for this cancer is surgary and radiation therapy depend on the stages. The image are distinguished in the Figure 2.

Pre-processing

The proposed SCNN model uses the Tensorflow, Keras, and NumPy libraries. Keras and TensorFlow libraries are used for the management and storage of image files as datasets to process the model. Tensorflow is a dependable and efficient library for importing and preprocessing image data. functions Keras is a neural network library at a higher level, and it works well with the TensorFlow library. It offers a favorable setting for building complex neural network models. Keras uses the 'image.dataset.directory' function from the 'tensorflow.keras.preprocessing' module to create a dataset from the photos saved on the disk. The proposed SCNN train model is used to predict the label in the test dataset. First, normalize the image by dividing the image pixel by 255.0, resize the image to the desired shape, and display the normalized image The numpy array is used to standardize the image division, resulting in an evaluation within the range of 0 to 1 in the deep learning model. Next, make a prediction for the label of the image and compare it with the actual label of the image to evaluate the performance of the model. The normalization as show in Figure 3.

Firstly, the image was compressed from the image size of 768 x 768 pixels to lower pixels of 75 x 75. The dataset contains images that are organized into batches size of 32, with each image having 3 channels representing the RGB color to manage the model complexity. Normalization ensures that the pixel values of the input are limited to a certain range; scaling ensures consistency in the size of the image; and turning the image into a NumPy array and reshaping it prepares it for input into the model.

The Gaussian Noise layer introduces random noise, drawn from a Gaussian distribution with a standard deviation of 0.1, into the input data. This noise disrupts the input characteristics, causing them to be less predictable and more robust. By training the autoencoder to recreate the original input without any noise from the perturbed input, the model acquires the ability to comprehend the fundamental structure of the data while eliminating the interference caused by the noise. The Gaussian noise layer functions regularize the approach, reduce overfitting by introducing dissimilarities to the training data and promoting the acquisition of more universally applicable representations by the model. In general, this allows the autoencoder to acquire decoding skills, improving its capacity to handle and reconstruct clear pictures from inputs that include noise.

The Gaussian noise layer is used during training to enhance the model's resilience by introducing random Gaussian noise to the input data. The denoising is shown in Figure 4.

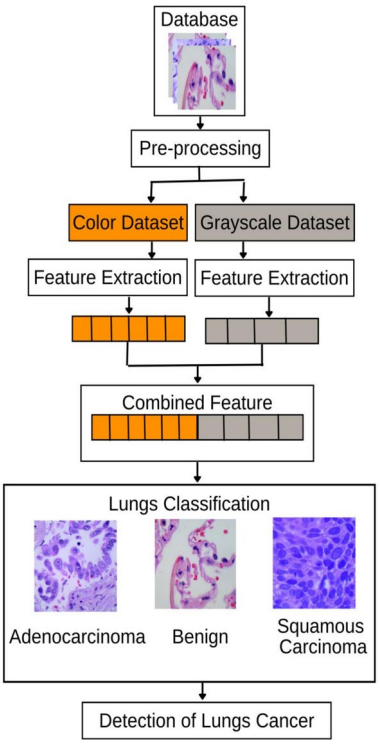

Fig. 3. Image Normalization.

Fig. 4. Noise in pathology image.

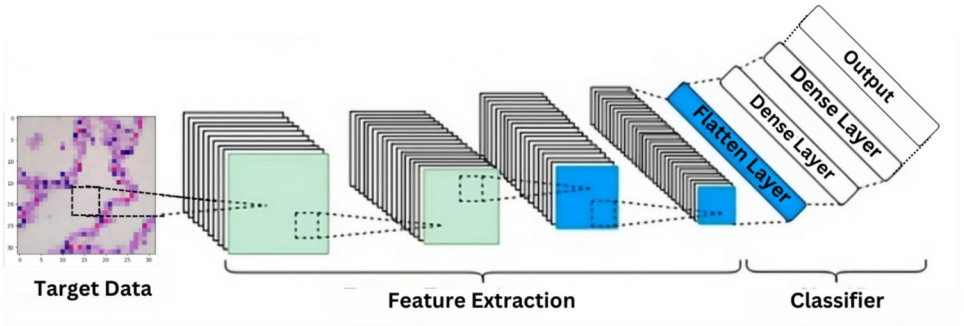

Fig. 5. Transfer learning-based feature extraction.

Data splitting

Lungs cancer histopathology images are used and divided into three subsets: training, holdout validation, and testing, described in Table 3. Specifically, 70 percent of the dataset is allocated for training purposes, while 15 percent is set for holdout validation, and another 15 percent is left for testing. Holdout validation split the data into training and validation set with fixed ratio in my case (70 percent training 15 percent validation and remaining for testing). The training set is used to train the model and performance is evaluated by holdout validation Prediction of the cancer is one of the main concerns in the performance evaluation of CNN model.

Transfer learning-based feature extraction

The dataset of lungs cancer is used to train the model of proposed SCNN so it is called as source code. It consist of images with three classes. Here, feature extraction can be done as part of transfer learning. The transfer learning approach used to adjust the weight of the whole network at small learning rate to prevent the loss factor of the original weights. The fully connected layer are ignored and new layer can be consider as target layer. As illustrated in Figure 5.

The following parameters are use in transfer learning to identify the classification of the image, T: target, m: target dataset size, S:Source, n: Source dataset size, $\phi(.) : objective function$, $\mathcal{F}$:feature space, P(x): marginal probability distribution and learning samples: X=$\{x_1, x_2, \ldots, x_n\} \in \mathcal{F}$, Υ= label space: K=$\{\Upsilon, \varphi(.)\}$, $n \gg m$.

An image domain, D, is define as having two components: a feature space,*F*, and a probability distribution, P(X):

$$\mathcal{D} = \{\mathcal{F}, P(X)\} \tag{1}$$

For a source domain, S, the dataset is $X_S = \{x_{S1}, x_{S2}, \ldots, x_{Sn}\} \in \mathcal{F}_S$. The source domain data can be denoted by:

$$\mathcal{D}_S = \{(x_{S1}, y_{S1}), (x_{S2}, y_{S2}), \ldots, (x_{Sn}, y_{Sn})\} \tag{2}$$

Where $x_{Si} \in \mathcal{F}_S$ is a data, and $y_{Si} \in \Upsilon_S$ is the corresponding class label.

For the target domain,T, the target domain can be denoted by:

$$\mathcal{D}_T = \{(x_{Tm}, y_{Tm}), (x_{Tm}, y_{Tm}), \ldots, (x_{Tm}, y_{Tm})\} \tag{3}$$

where $x_{Ti} \in \mathcal{F}_T$ is the data instance, and $y_{Ti} \in \Upsilon_T$ is the corresponding class label.

A task,K, consists of two components: a label space,Υ, and an objective function, $\phi(\cdot)$:

$$\mathcal{K} = \{\Upsilon, \phi(\cdot)\} \tag{4}$$

Assuming a specific domain, $\mathcal{D}_S$, learning activity, $\mathcal{K}_S$, an objective domain, $\mathcal{D}_T$, its learning activity, $\mathcal{K}_T$, Transfer learning is a technique that is enhance the learning rate of desired predictive function $\phi_T(\cdot)$ in $\mathcal{K}_T$ information is used in $\mathcal{D}_S$ and $\mathcal{K}_S$, where $\mathcal{D}_S \neq \mathcal{D}_T$ or $\mathcal{K}_S \neq \mathcal{K}_T$. $\mathcal{D}_S$ representation of the image dataset in our research, its learning activity, $\mathcal{K}_S$, where $\mathcal{K}_S = \{\Upsilon_S, \phi_S(\cdot)\}$, Υ_S is a source of label space, $\phi_S(\cdot)$ is

the source of predictive function. It is used to create a visual representation of a fresh image x_i to the label y_i. $\mathcal{D}_T$ representation of histopathology dataset in our research work and its learning activity, $\mathcal{K}_T$, where $\mathcal{K}_T = \{\Upsilon_T, \phi_T(\cdot)\}$.Enhance the $\phi_T(\cdot)$ of the histopathology image dataset, $\mathcal{D}_T$, using the image dataset, $\mathcal{D}_S$, and the objective function, $\phi_S(\cdot)$ of $\mathcal{K}_S$.

Inception V3

The Inception V3 transfer learning system employs proposed Sequential Convolutional Neural Networks for the purpose of image classification. The Inception V3 is an improved iteration of the original Inception V1 model[49]. Overfitting occurs when a model included many layers of convolutions. inception v3 works on over fitting and stops overfitting. The V1 model uses the concept of several filters of different diameters on the same level. Consequently, our inception models no longer consist of complex layers but rather parallel layers, resulting in a bigger system than a simple one. Consequently, our inception model uses a parallel proposed SCNN model to reduce the expensive computational cost. One of the great benefits of the Inception model is considerable dimension reduction.

The Inception v3 model employs the libraries of TensorFlow and Keras API modules to train and operate simultaneously with a Sequential convolutional neural network (SCNN) model using a dataset of histology images. The model is initialized with training weights from the Image dataset, which allows it to capture learning features during training on a large-scale picture classification task. The input dataset are dimensions of 75x75 and consists of RGB channels. The input shape of (75, 75, 3) is distinct. Transfer learning applies the feature extraction skills of the InceptionV3 model, modifying the top layers to reach a specific target domain. By applying the InceptionV3 model to make proposed SCNN architecture more efficient, it becomes feasible to refine and train the model using a particular dataset. This approach results in enhanced speed and precision in the categorization of images. InceptionV3 accelerates the model development process of proposed SCNN model, which is particularly advantageous in situations where there is a lack of labeled data or limited computer resources. Applying and modifying models may enable researchers and practitioners to achieve state-of-the-art performance in many computer vision applications.

Proposed sequential based convolutional neural network model

In Proposed SCNN model, training dataset $\Phi = \{(\mathrm{x}_i, \mathrm{y}_i)\}_{i=1}^{N}$, N is the size training dataset and $(\mathrm{x}_i, \mathrm{y}_i)$ is a single training example, $\mathrm{x}_i \in \Phi$ is the training images, $\mathrm{y}_i \in \Phi$ is the respective label of each image x_i, θ is the model parameters, and $\hat{y}_i$ is the predicted label using the function $f(\mathrm{x}_i; \theta)$. The purpose of training a machine learning classifier can be described as minimizing the loss equation (5):

$$L = \frac{1}{N} \sum_{i=1}^{N} L_i(f(\mathrm{x}_i; \theta), y_i) \tag{5}$$

The loss function is the cross-entropy loss function,which is define as in equation (6):

$$L(\hat{y}_i, y_i) = -\sum_{i=1}^{N} y_i \log \hat{y}_i \tag{6}$$

given that $\hat{y}_i = f(x_i; \theta)$

the cross-entropy loss function is define as in equation(7):

$$L_{BCE}(\hat{y}_i, y_i) = -\frac{1}{N} \sum_{i=1}^{N} [y_i \log \hat{y}_i + (1 - y_i) \log(1 - \hat{y}_i)] \tag{7}$$

The proposed SCNN operation composes the convolution layer is a mathematical operation combines two signals, which can define in equation (8):

$$o[u, v] = f[m, n] \cdot g[u, v] = \sum_{m} \sum_{n} f[m, n] \cdot g[u + m, v + n] \tag{8}$$

where f[m, n] is the convolution filter, g[u, v] is the input image, o[u, v] is the result feature. The working of SCNN model as shown in Figure 6.

The layers of Sequential based CNN involve the input image with a small grid shape, which is called the kernel, convolution filter starts from the top left corner of the image. The convolutional filter is used to extract features from the input layer of images that will help in classifying the image. The weight of the convolutional filter is the most important in Sequential based CNN, which is learned from the iterative nature of the back propagation algorithm. Many filters are used to extract as many features from the image as shown in the possible to attract the correct classification of the image.

The proposed SCNN employs a strictly sequential architecture implemented in Keras' sequential API, with levels placed on a linear stack from input to output. In contrast to more complex architectures that use skip connections or multiple branches (such as reset or initiation), SCNN maintains simple flows that improve interpretability and reduce computing efforts. This simplicity makes it suitable for clinical applications that

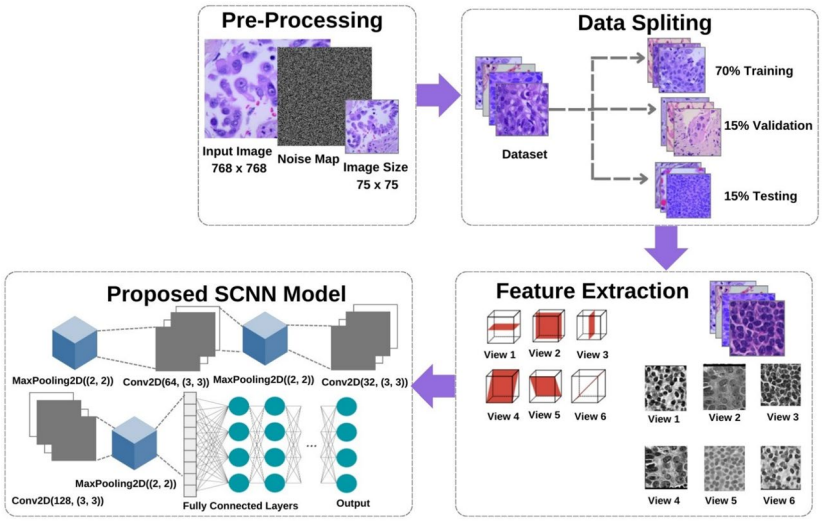

Fig. 6. Framework of our Proposed SCNN Algorithm.

require efficient and reliable processing. To illustrate this design, a detailed block diagram of the SCNN architecture is shown in Figure 6.

Training procedure

The relu activation function uses to decide a neuron fire or not. Relu activation are applied with hidden layer. In sequential model defines two dense layers having 256 and 3 nodes. first dense layer use relu function and softmax function uses for activation because this is multi-class classification. Then created model is compiled using compile() method. The categorical cross entropy method used to calculate the metrices accuracy.

The adaptive moment estimation is uses to train the model due to learning rate method, combining momentum and RMSprop algorithm for efficient descent optimization.

Evaluation metrics

Calculate the performance of our proposed SCNN technique to diagnose lungs cancer using histological image dataset. Performance is calculated as accuracy (ACC), Recall, precision (PRE) and F1-score[50].

Validation strategy

Holdout validation is the widely used method in the proposed SCNN model of machine learning, which is used to assess a proposed model's performance. The working of validation in given datasets contains a data point that categorizes into different classes and groups, which are randomly shuffled from the original sequence. After shuffling the dataset of images, The dataset is split into three different categories: training sets, validation sets (which is called holdouts), and test datasets. The large portion of the training dataset is used to train the proposed model with the help of identifying patterns and relations within the dataset. The holdout validation dataset is employed during the training to train the proposed model parameters and prevent the model from becoming overly specialized to the training dataset and maintain its ability to generalize. The test dataset is kept separate from the training and validation processes, which are used to evaluate the proposed model's final performance on an unseen dataset, performance during the testing phase, adjustment of the model, and training process can be made, and the validation procedure is repeated as needed. Holdout validation is an effective and efficient technique to ensure a proposed model is robust, reliable, and capable of performing well in real-world applications. The importance of structured evaluation in machine learning pipelines to develop the proposed SCNN model, which can handle unseen datasets confidently, is shown in Figure 7

Holdout validation approach used for validation in proposed SCNN model.The available dataset is partition in to training, validation and testing data. The proportion of dataset used for each set depends on the number of available images in the data. The data variability and the characteristics of model being used. The proportion of the validation set are assigns to the training data needs to large when working with a small datasets. 70 percent dataset are used for training, 15 percent dataset are used for validation and remaining 15 percent dataset for testing the model. Although the percent matters. The ratio between the validation and testing set smaller because validation sets intrinsically large and better reflects the data. Training data and validation dataset are used for CNN model training. The training dataset are uses to learn the model parameters. The validation dataset are used to to determine the model hyper-parameter during the process called as hyper tuning. Distinguishing between the model parameter and hyper-parameter is essential. Model parameters refer to the variables that represent the attributes of a model. These variables are learnt during the training of an algorithm using the training set.

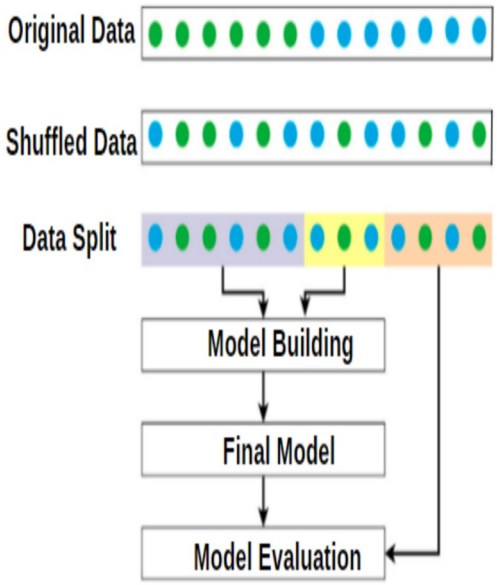

Fig. 7. Holdout validation.

Experiment	Accuracy	Observation
Full Model	97%	Baseline Acuuracy with all components
Without Image Pre-processing	85%	Accuracy drops indicates preprocessing significant improves image quality.
Without Feature Extraction	75%	Performance drops drastically showing features are critical for classification.
Inception V3	92%	Accuracy drops indicates Inception V3 significant improves processing time.
Without Proposed Sequential Convolutional Neural Network	82%	Indicates the current classifier is better optimized for the task.

Table 4. Ablation Study of Proposed SCNN Model.

Clinical relevance and practical implementation

The clinical relevance of the proposed SCNN model lies in its potential to serve as a diagnostic support tool for pathologists and radiologists, enhancing the early detection and classification of lung cancer from histopathological images. Its high accuracy and sensitivity suggest it could assist in reducing diagnostic errors and accelerating the analysis process, especially in high-throughput clinical environments. To evaluate real-world applicability, we conducted tests simulating noisy and incomplete data conditions. The model maintained robust performance under moderate levels of Gaussian noise and partial occlusion, demonstrating its resilience. Similarly, further validation is performed with diverse real-world datasets from multiple institutions like Inmol, NIH and Kaggle for confirming the generalizability. For clinical integration, the SCNN model can be deployed as part of a computer aided diagnosis system integrated into existing digital pathology platforms. This would enable real-time inference, flagging suspicious regions for further examination by clinicians. Future work will focus on developing a user-friendly interface and conducting prospective trials in collaboration with healthcare institutions to assess clinical utility and workflow compatibility.

Ablation study

The analysis of several experiments determine the contribution of various components as show in Table 4. The full model achieves the highest accuracy of 97%, serving as the baseline with all components enabled. When image pre-processing is removed, accuracy drops to 85%, indicating that pre-processing significantly enhances the image quality. Simultaneously, the removal of feature extraction, the result of accuracy dropping to 75%, demonstrates its critical role in classification performance. Without using Inception V3 achieves an accuracy of 92%, which shows a reduction compared to the full model but highlights improved processing time. Finally, with the removal of the proposed sequential convolutional neural network, reduce the accuracy to 82%, indicating that the current classifier is better optimized for the task. These findings emphasize the importance of each component to achieve the highest performance and efficiency.

Ethical statement

All methods in this study were carried out in accordance with relevant guidelines and regulations. The research protocols involving the use of lung cancer data from INMOL Cancer Hospital Lahore, the National Institute of Health Islamabad, and publicly available datasets from Kaggle were reviewed and approved by the Institutional Review Board (IRB) of Riphah School of Computing & Innovation, Riphah International University, Lahore.

Where applicable, necessary permissions were obtained from the respective institutions for the use of anonymized and secondary data, ensuring compliance with data protection and ethical standards under letter number 059271 dated 22-04-24.

Results and discussion

The main goal is to enhance the classification of accuracy of the purposed model SCNN. The specific paramenter use to assess the experimental assessment of the proposed SCNN architecture.

Computational complexity analysis

Time Complexity: The time complexity of CNN based model is generally scale withe the numbers of layer and the size of convolutional filters. Our SCNN model, through careful architecture design, reduce unnecessary convolutional operation, which result in a computational load compare to deeper or more complex model like ResNet or DenseNet. The time complxity of our proposed SCNN is approximate $O(n^2 * k^2 * d)$, where n is input size, k is the filter size, k is filter size, and d is depth. This compares with deeper models that may exhibit higher complexity $O(n^3 * d^2)$ due to additional layers or complex connection.

Space Complexity: Our proposed SCNN model also optimzes memory usage by reducing the numbers of parameter through the use of efficient convolutional filters and reduce the depth of certain layers possible. This make the proposed model more scalable and efficient for real-time applications.

Comparison with Other Models:

- When deep learning models ResNet-50 or DenseNet-121, our proposed SCNN model demonstrates reduced computational requirement, making it more suitable for real-time applications where quick response time are critical, in real time lungs cancer detection or medical diagnose.
- The Computational complexity of proposed SCNN model is lower, which contributes to faster training times and inference speeds. This is especially beneficial to scale large datasets, reduce computational burden allow for better scalability without significant compromise on accuracy.

Benefits to Real-Time Applications and Scalability:

- **Reduced Latency:** The lower comptational complexity allows our proposed Scnn model to process inputs more quick, which is a significant advantage in real time application medical imaging and autonomous systems.
- **Scalability:** The reduce computational load also ensures that the model can handle large datasets more efficient without require extensive hardware resources. This makes the SCNN model more adaptable to application where both scalable and efficiency are important.

Potential Limitations: While the proposed SCNN model provide significant computational advantages, it is possible that reduce the complexity could lead to slight comromise in performance metrics, particular for extremely complex data representation. However, our experimental result have shows the proposed SCNN achieve comparable accuracy, precision, f1-score and recall. In future work, we plan to explore further optimization to balance complexity with performance for even better results on more challenging dataset.

Experimental detail

The proposed SCNN model use the device Intel Core i5 4300M, which has 8 cores and 8 threads. It has the capability of attaining a maximum speed of 4.9 GHz making it suitable for such a power-hungry function. The system contains an Intel HD Graphics 4600 GPU which is an efficient data processor with 2944 CUDA cores and 4 gigabytes of DDR4 2944 MB memory, allowing for quick training of deep networks. Further DDR4 memory at 3200 MHz with 4 GB capacity is facilitating the use of large data sets at the same time. The Proposed SCNN model uses Python 3.8 on the assumption that most of it libraries are utilized and it is very efficient using Google Colab which is a web based platform offering free access to fast GPU resources.

Our SCNN models experimental setup require preparation of data preprocessing steps and fine tuning of hyperparameters in order to correctly predict lung cancer efficiently. Initially resizing the images to 75 x 75 pixels helped maintain input dimensions before normalizing pixel values, within the range [0 1] ensuring smoother and more reliable training processes. The models architecture was structured with three layers utilizing ReLU activation and gradually increasing the number of filters (32 to 64 to 128) enabling the capture of intricate hierarchical features. After each convolution operation in the model architecture design process included MaxPooling layers to decrease dimensions and computational complexity effectively. The model structure concludes with a Flatten layer that preprocesses the data for integration in a layer with 256 units for feature analysis and another Dense layer with Softmax activation to generate class probabilities. The optimization of hyperparameters involved tuning the learning rate and batch size along with determining the optimal number of training epochs to enhance the models learning capability, from the training dataset while preventing overfitting issues. The design of the structure was thoughtfully selected to strike a balance between the intricacy of the model and its effectiveness, in identifying and categorizing lung cancer from image data.

The impact of each part of the architecture of the proposed SCNN model, the third Conv2D layer which has 128 filters and MaxPooling2D layer were removed and this has made a reduction in its performance compared to the initial SCNN hence underlining their role in aggregating elaborate and high level information. The Flatten layer was considered to be indispensable since its deletion led to a shape mismatch and hindered the shifting from 2D feature maps into 1D dense neuron. The Dense(256) layer was lowering the efficiency of the classifications of extracted features and thus efficiency was reduced as well. Furthermore, the exclusion of

Models	Accuracy	Precision	Recall	F1-score	Time	Epochs
CNN[50,51]	0.82	0.84	0.83	0.82	172	50
R-CNN[54,55]	0.74	0.74	0.74	0.73	3591	60
Custom Inception Classifier[56,57]	0.79	0.84	0.79	0.79	148	50
SCNN	**0.94**	**0.94**	**0.94**	**0.94**	**158**	**60**

Table 5. Lungs cancer detection of Inmol hospital.

Models	Accuracy	Precision	Recall	F1-score	Time	Epochs
CNN[50,51]	0.76	0.77	0.77	0.77	9552	15
R-CNN[54,55]	0.77	0.85	0.73	0.68	16710	60
Custom Inception Classifier[56,57]	0.86	0.86	0.86	0.86	809	60
SCNN	**0.97**	**0.97**	**0.97**	**0.97**	**906**	**60**

Table 6. Lungs cancer detection from National Institute of health.

MaxPooling2D layers improved ability to preserve spatial information but it increased computational cost as well as the chances of overfitting. Every part of the SCNN architecture is important in the improvement of the performance of the model on the image classification and if any of them is eliminated, then the performance of the model will reduce.

Evaluation metrics

The classification of these models is evaluated using a confusion matrix, and the accuracy, precision, recall, and f1-score are evaluated. Where the TP, FP, FN, TN are the output measures as true positive, false positive, false negative and false negative for the training of the models.

Case I: Lungs cancer detection from Inmol hospital

The result of the proposed SCNN model is compared with the results of other previous models in the last three years. The previous known models of lung cancer detection are CNN, R-CNN, and Custom Inception Classifier. The 510 images in the dataset of lung cancer are classified into three classes: adenocarcinoma, benign, and squamous carcinoma. The dataset is used to calculate the accuracy, precision, recall, and f1-measure score; compare these parameters of metrics with the previous models. The SCNN model demonstrate the best performance with 0.94 accuracy, 0.94 precision, 094 recall and 0.94 f1-measure score. Comparison Table 5 shows the detail of accuracy, percision, recall and f1-measure score, time, and epochs achieved by all models. The proposed model by SCNN gives the highest performance values for the parameter compared with the other models.

The results of the proposed SCNN model are compared with those of previous models in the field of lung cancer detection, specifically CNN, R-CNN, and Custom Inception Classifier. The dataset, which consists of 510 images, is classified into three categories: adenocarcinoma, benign, and squamous carcinoma. The key factors involves accuracy, precision, recall and f1 measure score are calculated using the predicted image. These measurements are subsequent compared to results of the previous models and compare the performance.

The proposed SCNN model give an idea of high performance with an accuracy of 0.94, precision of 0.94, recall of 0.94 and f1-measure score of 0.94. These results shows that the proposed SCNN model continuously and correctly classifies images across all categories. Comparison Table 5 shows detailed information on precision, accuracy, recall, F1-measure score as well as time number of epochs achieved by all models.

The proposed SCNN model attain high performance values of all parameters compare with other previous models are CNN, R-CNN and Custom Inception Classifier. This shows the proposed SCNN model is highly effective in lungs cancer detection, offer significantly improvement in accuracy and performance The high precision, recall and f1-measure scores highlights the proposed SCNN model reliability and robustness and diagnose accurate lungs cancer.

The model accurately predicted the label as Adenocarcinoma. The output of proposed SCNN model uses to classifies as an input data point and it performs the prediction that match the actual label. The true label is Adenocarcinoma means that it is cancer the proposed SCNN model predicted the same label as true label. The process of prediction takes 206 milliseconds per step. The speed and accuracy of prediction are essential for patient care ensure the diagnoses makes quickly and correctly.

Case II: Lungs cancer detection from National Institute of health

The result of the proposed SCNN model is compared with the results of other previous models in the last three years. The previous known models of lung cancer detection are CNN, R-CNN, and Custom Inception Classifier. The 3000 images in the dataset of lung cancer are classified into three classes: adenocarcinoma, benign, and squamous carcinoma. The dataset is used to calculate the accuracy, precision, recall, and f1-measure score; compare these parameters of metrics with the previous models. The proposed SCNN model demonstrate the best performance with 0.97 accuracy, 0.97 precision, 0.97 recall and 0.97 f1-measure score. Comparison Table 6

Models	Accuracy	Precision	Recall	F1-score	Time	Epochs
CNN[50,51]	0.84	0.83	0.83	0.83	16294	10
R-CNN[54,55]	0.9	0.89	0.9	0.89	20903	30
Custom Inception Classifier[56,57]	0.88	0.9	0.87	0.87	22641	30
SCNN	**0.95**	**0.96**	**0.95**	**0.95**	**1936**	**60**

Table 7. Lungs cancer detection from kaggle.

Models	Accuracy	Precision	Recall	F1-score	Time	Epochs
CNN	0.8067	0.813	0.81	0.8067	8672.67	25
R-CNN	0.803	0.8267	0.79	0.767	13734.67	50
Custom Inception Classifier	0.843	0.867	0.84	0.84	7866	46.67
SCNN	**0.953**	**0.9567**	**0.953**	**0.953**	**1000**	**60**

Table 8. Average Table.

shows the details of accuracy, precision, recall and f1-measure score, time, and epochs achieved by all models. The proposed model by SCNN gives the highest performance values for the parameter compared with the other models.

The model accurately predicted the label as Squamous_carcinoma. The output of proposed SCNN model uses to classifies as an input data point and it performs the prediction that match the actual label. The process of prediction takes 90 milliseconds per step. The speed and accuracy of prediction are essential for patient care ensure the diagnoses makes quickly and correctly.

Case III: Lungs cancer detection from kaggle

The result of the proposed SCNN model is compared with the results of other previous models in last three years. The previous known models of lung cancer detection are CNN, R-CNN, and Custom Inception Classifier. The 7000 images in the dataset of lung cancer are classified into three classes: adenocarcinoma, benign, and squamous carcinoma. The dataset is used to calculate the accuracy, precision, recall, and f1-measure score; compare these parameters of metrics with the previous models. The proposed SCNN model demonstrate the best performance with 0.95 accuracy, 0.95 precision, 0.95 recall and 0.95 f1-measure score. Comparison Table 7 shows the details of accuracy, precision, recall and f1-measure score, time, and epochs achieved by all models. The proposed model by SCNN gives the highest performance values for the parameter compared with the other models.

The model accurately predicted the label as Benign. The output of proposed SCNN model uses to classifies as an input data point and it performs the prediction that match the actual label. The true label is benign means that it is non-cancer the proposed SCNN model predicted the same label as true label. The process of this prediction takes 131 milliseconds per step. This correctness is accurate and crucial for patient care.

Average performance of models

Calculate the average performance of the models for each of the indicated situations discussed in the previous three sections. Conduct the calculation and compare each of the previous models with the anticipated model. Unlike other models, the suggested model stands out for its superior efficiency, achieved via decreased complexity and time-saving features. Select four models from three situations and compute the mean. The suggested model exhibits the utmost degree of performance. The proposed SCNN model has superior performance, with an average accuracy of 0.953, precision of 0.9567, recall of 0.953, and f1-measure score of 0.953 across 1000 seconds of time and 60 epochs.The average performance of all parameters in four models is shown in the average Table 8.

Improvement of proposed SCNN model

In the improvement section, calculate the improvement of proposed SCNN proposed model. The values of the improvement of parameter of the three models are shown and gives a demonstration of much proposed SCNN is advanced on the other compared models. The parameters are involved for the performance are include accuracy, precision, recall, f1-measure score, time, and epochs. The significance of enhancements achieved from the proposed model SCNN is highlighted in Table Table 9. The comparison highlights the efficiency and robustness of proposed SCNN in the confusion metrics, providing clear proof of its effectiveness. The results indicate the practical implementation of proposed SCNN, particularly in the domain that needs to be very accurate and efficient. The average performance of all the parameters is shown in improvement model Figure 8.

The Figure 8 shows improvement of proposed SCNN model as compared to other three classifier CNN, R-CNN and Custom Inception Classifier across four parameters of metrics accuracy, precision, recall and F1-score. SCNN shows the significant improvement from CNN particularly in ACC(18.18), Precision(18.18), Recall(18.18) and F1-score(18.18). SCNN shows the significant improvement from R-CNN particularly in ACC(18.67), Precision(15.72), Recall(20.67) and F1-score(24.34). SCNN shows the significant improvement from Custom Inception Classifier particularly in ACC(18.67), Precision(10.38), Recall(13.49) and F1-score(13.49). The yellow line represent the overall average of improvement of old models.

Models	Accuracy	Precision	Recall	F1-score	Time	Epochs
CNN	18.18	17.62	17.69	18.18	−88.46	140
R-CNN	18.67	15.72	20.67	24.34	−92.71	20
Custom Inception Classifier	13.043	10.38	13.49	13.49	−87.28	28.57
Average Improvement	**16.63**	**14.57**	**17.28**	**18.67**	**89.49**	**62.85**

Table 9. Improvement Model.

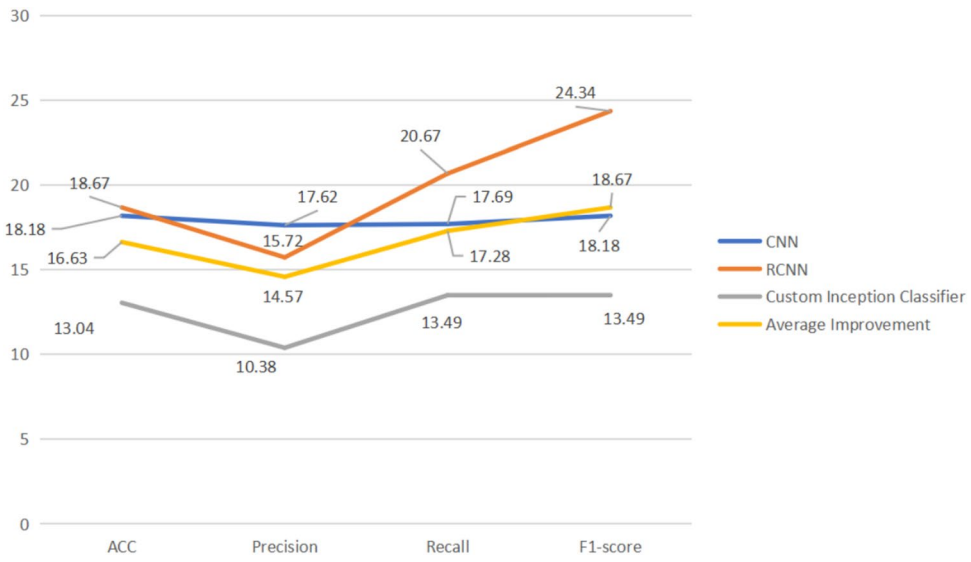

Fig. 8. Improvement Classification of Proposed SCNN Model.

Metric	SCNN	DenseNet[43]	R-CNN[55]	CancerDetecNN[42]	CNN[40]	D-CNN[36]
Image	10510	750	500	2042	277485	76
Accuracy	95.3	94.50	92.8	-	88	71.1
Precision	95.67	94.56	84.7	97.2	-	-
Recall	95.3	94.47	100	92	-	-
F1-score	95.3	94.48	91.7	89	–	-
Time(sec)	1000	10800	-	4140	-	28800
Epochs	60	1000	65	-	25	60000

Table 10. Comparison of proposed sequential based convolutional neural network.

Comparison of proposed sequential based convolutional neural network

The proposed SCNN model demostrate the performance across multiple attributes when compared to the other models such as DenseNet, R-CNN, and CancerDetectNN as shown in Table 10. With an accuracy of 95.3%, it surpass most competitor, while maintain strong 95.3% F1 score, precision 95.67% and recall 95.3% highlight its ability to accurate identify and classify cancer types with minimal false positive and miss cases. That's why shows the balance and robustness of the model across the dataset.The proposed SCNN model requires 1000 seconds for training over 60 epochs, making it much faster then other models like DenseNet in term of efficiency, which takes over 10000 seconds. The proposed SCNN model stands out as a highly accurate, efficient and balance model make it a competitive solution in cancer detection tasks.

Experimental analysis

In this section, we discuss the key improvements introduced by our Sequential Convolutional Neural Network (SCNN) model over traditional methods such as CNN, R-CNN, and the Custom Inception Classifier. Our SCNN model is designed to offer significant advancements in terms of computational efficiency, processing speed, and classification accuracy, specifically for the task of lung cancer detection using histology images. The SCNN model is designed with a streamlined architecture consisting of three convolutional layers, three max-pooling layers, and deserial layers, which significantly minimizes computational overhead. Unlike more intricate architectures like R-CNN and Custom Inception Classifier, which involve additional layers and complex operations, the

SCNN maintains simplicity while achieving comparable or better performance without requiring excessive computational resources. In terms of processing speed, the SCNN model demonstrates a notable reduction in processing time, completing training and classification in 1000 seconds over 60 epochs. This marks a significant improvement over traditional CNNs and models like R-CNN, making the SCNN model highly suitable for real-time or near-real-time applications, such as lung cancer detection in medical imaging, where speed is critical. Accuracy and performance are also key strengths of the SCNN model. It achieves an average accuracy of 95.34%, precision of 95.66%, recall of 95.33%, and a high F1-measure score. These metrics highlight the SCNN's superior ability to classify lung cancer histology images with high precision and minimal errors, surpassing traditional CNNs, R-CNN, and Custom Inception Classifier in medical imaging tasks. Furthermore, the SCNN model is particularly adept at classifying lung cancer histology images into three categories—adenocarcinoma, benign, and squamous carcinoma—with greater accuracy. Traditional CNNs and R-CNN may struggle with similar datasets, especially when dealing with fine details in medical images. The SCNN, however, delivers more precise classification results. Optimized specifically for medical imaging, the SCNN model preserves critical image features while reducing false positives and negatives. This tailored approach enhances its effectiveness in clinical settings, making it a robust and efficient tool for image-based medical diagnostics, particularly in lung cancer detection.

Limitations of the proposed SCNN model and future enhancements

The proposed SCNN model demonstrate strong performance in lungs cancer. It has several limitations needed to address in future. One is the primary limitation is to reliance on large and small dataset to train the model, which may not always available or diverse enough to ensure the model robustness across different populations and types of lungs cancer. When the model is applied to new unseen data or other medical conditions. The model computational efficieny is strength, it may still struggle with real-time application on small devices, limitation its deployment in resources constrained environment. The SCNN model are easier for healthcare professionals to use without needing advanced technical knowledge.

To address these limitations future work will focus on integration of medical parameter such as patient demographics, clinical history, and genetic marker to provide a large diagnostic tool. This integration improves the model accuracy and relevance medicine. The improvement of diversity and quality of the datasets uses to train the model, potentially through data augmentation techniques or collaboration with medical institutions to access more varied and extensive dataset. The proposed SCNN model is user friendly interface developed ensure that it can be easily used by healthcare profession without any extensive technical expertise. The proposed SCNN model is more versatile, scalable and applicable in real world clinics.

Conclusion and future

Lung cancer is a disease causing abnormal cell growth. Lung cancer is the leading cause of cancer related to death. The highest death rate in Pakistan is due to lung cancer, which is one of the deadliest forms of the disease.In early stage, the symptoms of disease are not clear. To detect the cancerous lungs nodules and classify the cancer of lungs. The proposed SCNN model detect cancer at the early stage.A proposed model SCNN technique is used and reduce computational complexity and time. The cancer detect at early stage for the better treatment. Lungs cancer dataset are classified in to three classes adenocarcinoma, benign and squamous carcinoma. The proposed model used best feature extraction of transfer learning rate, Gaussian noise and normalization. The proposed SCNN model consist of CNN model with training procedure of flatten, dense layers and adam optimization. The SCNN model is used to perform on dataset collected from Inmol hospital, National Institute of health science and kaggle dataset. The three previous models CNN, Custom Inception Classifier and R-CNN are used to detect cancer and make comparison with the proposed SCNN model. The experimental results show that proposed SCNN model perform better the then other models.

The proposed model is used to improve accuracy and time efficiency compared to the previous model. The working comparison of four models, including SCNN, is divided into three cases with respect to the dataset. Case I show the comparison with the proposed model shown in the Table 5. The SCNN model demonstrated the best performance with 94 % accuracy, 94 % precision, 94 % recall, and 94 % f1-measure score using the Inmol dataset. Case II shows the comparison with the proposed model shown in the Table 6. The SCNN model demonstrated the best performance with 97 % accuracy, 97 % precision, 97 % recall, and 97 % f1-measure score, using the National Institute of Health Sciences dataset. Case III shows the comparison with the proposed model shown in the Table 7. The SCNN model demonstrated the best performance with 95 % accuracy, 95 % precision, 95 % recall, and 95 % f1-measure score using the Kaggle dataset. Table 8 and Table 9 shows the average and improvement of the proposed SCNN model as compared to the other models.

In future work, enhance cancer detection performance. We will implement an automated report creation feature that includes the measurement of oxygen level, blood pressure, and other relevant parameters associated with cancer prediction. The report generated will include detailed information about the identified cancer. An IOMT application can be developed to extract the generated report. This report will help doctors understand and analyze the disease, save time for both doctors and patients, and treat the cancer disease timely and appropriately. Which will make a model user-friendly. Moreover, these improvements will make the SCNN model more accurate and reliable. The SCNN model will work with various types of cancer datasets. To improve the performance of the cancer evaluation, we needed to include a large dataset to make the model more efficient. The capsule Neural Network will be the advancement of AI, using class equivalence to make a copy of the complexities of human vision. The fundamental significance of this system is its capacity to achieve outstanding precision even when trained on limited datasets, indicating a shift towards more efficient and precise visual recognition systems. The progress of CapsNet is the capacity to alter the boundaries of machine learning.This

might potentially result in the development of innovative applications across several industries, characterized by outstanding efficiency and reliability.

Data availability

The data used in this study consisted of publicly available datasets of the lungs cancer Inmol, Lung cancer NIH and the lungs cancer kaggle dataset, references for these datasets is given in the paper.

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Author contributions

Conceptualization, U.H.; formal analysis, J.U.; funding acquisition, Y.J.; investigation, I.K.; methodology, U.H.; project administration, J.K.; resources, I.K.; software, I.K.; validation, S.R.; visualization, M.Y.; writing—original draft, U.H., J.U., and J.K.; writing—review and editing, U.H., J.K., I.K., and Y.J. All authors have read and agreed to the published version of the manuscript.

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Declarations

Competing Interests

The authors declare that there are no competing interests regarding the publication of this paper.

Informed consent

Informed consent was obtained from all individual participants included in the study.

Additional information

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