

# Department of Computer Science and Engineering

**Global Campus, Jakkasandra Post, Kanakapura Taluk, Ramanagara District, Pin Code: 562 112**

**2022-2026**

**Sixth Semester Progress Report on**

“**Pneumonia Detection using k-fold cross validation and MobileNetV2**”

**Submitted for the partial fulfilment of Project Centric Learning activity of**

**BACHELOR OF TECHNOLOGY**

**IN**

**COMPUTER SCIENCE AND ENGINEERING**

**Submitted by**

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**Under the guidance of**

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School of Computer Science and Engineering

JAIN (Deemed-to-be University)



# Department of Computer Science and Engineering

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# CERTIFICATE

This is to certify that the project centric learning work titled **“Detection of Pneumonia using Machine Learning”** is carried out by **Madineni Rohith (22BTRCN163)** Bonafide students of Bachelor of Technology at the Faculty of Engineering & Technology, Jain Deemed-to-be University, Bangalore in partial fulfillment for the project centric learning activity of degree in Bachelor of Technology in Computer Science & Engineering, during the year **2022-2026**.

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Name of the Examiner Signature of Examiner

1.

2.

# DECLARATION

I, **Madineni Rohith (22BTRCN163)** am student of IV semester B. Tech in **Computer Science & Engineering**, JAIN (Deemed-to-be University), hereby declare that the project centric learning work titled **“Detection of Pneumonia using Machine Learning”** has been carried out by me and submitted in partial fulfilment for the project centric learning activity of degree in **Bachelor of Technology in Computer Science & Engineering** during the academic year **2022-2026**.

Signature

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Place: Bangalore

Date:

## ACKNOWLEDGEMENT

*It is a great pleasure for us to acknowledge the assistance and support of School of Computer Science and Engineering, Jain (Deemed-to-be University) for the progress of this project centric learning work.*

*In particular we would like to thank* ***Dr. Geeta Rani****,* ***Director,*** *School of Computer Science Engineering and* ***Dr. T N Mahesh, Program Head,*** *Department of Computer Science and Engineering, JAIN (Deemed-to-be University) for their constant encouragement and expert advice.*

*We would like to thank our guide* ***Cholla Ravindra Raman****,* ***Professor,******Department of Computer Science & Engineering****, JAIN (Deemed-to-be University), for sparing his valuable time to extend help in every step of our project work, which paved the way for smooth progress of the project.*

*We would like to thank our Project Coordinators and all the staff members of Computer Science & Engineering for their support.*

*We would like to thank one and all who directly or indirectly helped us in the progress of our Project.*

*Signature of Students*

# ABSTRACT

Pneumonia continues to be a leading cause of death globally, particularly affecting children and the elderly. It accounts for approximately 700,000 deaths among children each year and impacts nearly 7% of the world’s population. With advancements in medical imaging, chest X-rays have become a primary tool for diagnosing pneumonia. However, accurate interpretation of these images often requires the expertise of skilled radiologists, which may not always be available, especially in remote or resource-limited settings. Manual diagnosis also comes with challenges such as high costs, time constraints, and the potential for human error.

To address these limitations, this project presents an automated pneumonia detection system using deep learning techniques. The model is developed using MobileNetV2, a lightweight and efficient convolutional neural network architecture, combined with transfer learning to improve accuracy. K-Fold Cross Validation is implemented to ensure consistent performance and reduce the risk of overfitting. The model is trained on a dataset of chest X-ray images and achieves high classification accuracy. Additionally, a user-friendly interface has been developed to enable real-time predictions, making the solution practical and accessible for clinical use.

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# Chapter 1

# INTRODUCTION

Pneumonia is a lung infection that causes inflammation of the air sacs in one or both lungs. When the air sacs fill with fluid or pus, it can cause a cough with phlegm or pus, fever, chills, and difficulty breathing (purulent material). Pneumonia can be caused by bacteria, viruses, or fungi, among other things. In simple terms, it's a microbe-caused infection in the lungs that causes water to enter the lungs and makes breathing difficult.

Their lungs' air sacs fill with fluid or pus as a result of the infection, making it difficult for them to inhale enough oxygen to maintain their bloodstreams healthy. The main cause of this condition is respiratory viruses such as influenza and rhinoviruses (common cold).

Machine learning methodologies are used to construct medical models however, they remain operate as a black box, making the output generated by machine learning models difficult to comprehend. The research should lead to a method for distinguishing between healthy people and Pneumonia patients, as well as distinguishing between viral and bacterial Pneumonia.

**Symptoms:**

The signs and symptoms of pneumonia vary from mild to severe, depending on factors such as the type of germ causing the infection, and your age and overall health. Mild signs and symptoms often are similar to those of a cold or flu, but they last longer.

Signs and symptoms of pneumonia may include:

• Chest pain when you breathe or cough

• Confusion or changes in mental awareness (in adults age 65 and older)

• Cough, which may produce phlegm

• Fatigue

• Fever, sweating, and shaking chills

• Lower than normal body temperature (in adults older than age 65 and people with weak immune systems)

• Nausea, vomiting, or diarrhea

• Shortness of breath

• Loss of appetite

• Dizziness

Newborns and infants may not show any sign of the infection. Or they may vomit, have a fever and cough, appear restless or tired and without energy, or have difficulty in breathing and eating.

**Causes**:

Many microorganisms are capable of causing pneumonia. Bacteria and viruses in the air are the most frequent. These viruses are generally prevented from infecting your lungs by your body. Even if your health is normally strong, these pathogens can sometimes overwhelm your immune system. Pneumonia is categorized based on the bacteria that cause it and where the infection occurred.

• Community-acquired pneumonia

Community-acquired pneumonia is the most common type of pneumonia.

It occurs outside of hospitals or other health care facilities. It may be caused by: Bacteria (Streptococcus pneumoniae), Bacteria-like organisms (Mycoplasma pneumoniae), Viruses, Fungi

• Hospital-acquired pneumonia (WORST TYPE OF PNEUMONIA)

Some patients get pneumonia while in the hospital for another reason. Because the bacterium that causes it may be more resistant to medications and because the people who receive it are already unwell, hospital-acquired pneumonia can be dangerous. This type of pneumonia is more common in

those who use breathing devices (ventilators), which are commonly employed in intensive care units.

• Health care-acquired pneumonia

People who live in long-term care homes or who receive care in outpatient clinics, particularly kidney dialysis centers, might contract healthcare-acquired pneumonia. Healthcare-acquired pneumonia, including hospital-acquired pneumonia, can be caused by antibiotic-resistant bacteria.

• Aspiration pneumonia

When you inhale food, drink, vomit, or saliva into your lungs, you get aspiration pneumonia. If something disrupts your usual gag response, such as a brain damage or swallowing issue, or if you drink or use drugs excessively, you're more prone to aspirate.

**Risk Factors:**

Anyone can get pneumonia. However, the two age groups most at risk are:

• Children who are 2 years old or younger

• People who are age 65 or older

**Other risk factors include:**

**•** Receiving medical attention. In a hospital intensive care unit, the risk of pneumonia is higher, especially if you're on a breathing machine (a ventilator).

**•** Chronic illness. If you have asthma, chronic obstructive pulmonary disease (COPD), or heart problems, you're more likely to have pneumonia.

• Smoking. Smoking damages your body's natural defenses against the bacteria and viruses that cause pneumonia.

**•** Weakened or suppressed immune system. People who have HIV/AIDS, who've had an organ transplant, or who receive chemotherapy or long-term steroids are at risk.

**Diagnosis**:

If pneumonia is suspected (listening to your lungs with a stethoscope to check for abnormal bubbling or crackling sounds that suggest pneumonia), doctor may recommend the following tests:

• A Blood test. Blood tests are performed to confirm an infection and to determine the sort of organism that is causing it. It is not always possible to identify something precisely.

• X-ray of the chest. This aids in the diagnosis of pneumonia and the determination of the infection's extent and location by the clinician. Doctors, on the other hand, have no way of knowing what kind of bacterium is causing pneumonia.

• Oximetry (pulse oximetry). This device measures the amount of oxygen in the blood. Pneumonia can make it difficult for the lungs to get enough oxygen into the circulation.

• Sputum examination. After a deep cough, a sample of lungs fluid (sputum) is obtained and tested to assist determine the source of the illness.

If the person is over 65, in the hospital, or has serious symptoms or health concerns, doctors may prescribe extra testing. Some examples are:

• A CT scan If your pneumonia isn't clearing up as quickly as you'd like, the doctor may suggest a chest CT scan to get a better picture of your lungs.

• Pleural fluid A fluid sample is collected from the pleural area by inserting a needle between the ribs and examined to detect the type of infection.

**Treatment:**

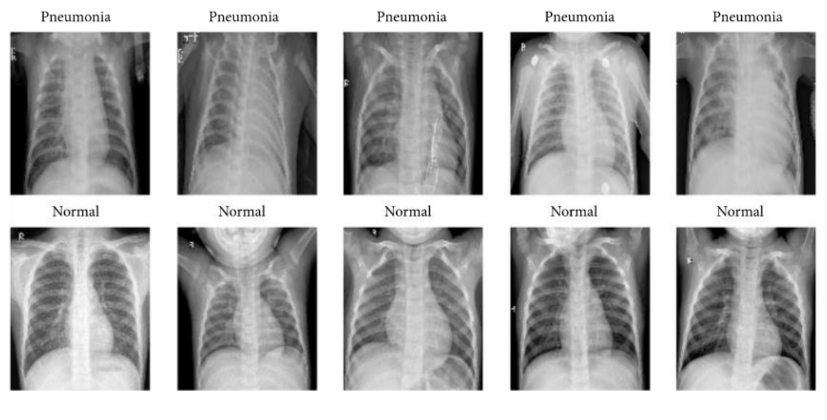
The goal of pneumonia treatment is to eliminate the illness while also preventing consequences. People with community-acquired pneumonia can usually be treated with medicines at home. Although most symptoms fade after a few days or weeks, fatigue might last for a month or longer. Treatment options are determined by the type and severity of your pneumonia, as well as your age and overall health. The options include:

• Antibiotics. These medicines are used to treat bacterial pneumonia. It may take some time to figure out what type of bacteria is causing your pneumonia and then choose the best antibiotic to treat it. If your symptoms do not improve, your doctor may prescribe a different antibiotic.

• Anti-cough medication by soothing your cough, this drug can help you sleep. Coughing should not be completely stopped because it helps loosen and move fluid from your lungs. Furthermore, little research has been done to see if over-the-counter cough medicines can help with pneumonia-related coughing. Start with the lowest dose that allows you to sleep if you want to try a cough suppressant.

• Pain relievers and fever reducers for fever and pain, take these as needed. Aspirin, ibuprofen (Advil, Motrin IB, and others) and acetaminophen (Tylenol, others).

**PROBLEM STATEMENT**



**Fig 1: Pneumonia and Normal Chest X-rays**

Pneumonia is difficult to diagnose because it shares many symptoms with other common conditions such as the common cold, asthma, and other respiratory illnesses. If a person has breathlessness or is breathing faster than usual, the color of your mucus, and if you swore while inhaling or exhaling. An X-ray is a wonderful tool to quickly determine whether you have pneumonia or not. The goal is to create a model based on Deep Learning and Convolution Neural Networks that can autonomously diagnose Pneumonia in patients given a collection of chest X-rays.

As shown in Fig 1, here are a few examples of Pneumonia and Normal chest X-rays. Once a case of pneumonia has been identified, it is further divided into viral and bacterial pneumonia. The objective is to create an approach that uses a deep transfer learning algorithm to extract features from X-rays in order to distinguish between normal pneumonia and viral and bacterial pneumonia.

# Chapter 2

# LITERATURE SURVEY

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| TITLE | AUTHOR | MODELS TECHNIQUES | OBJECTIVE | SUMMARY |
| Detection of Paediatric Pneumonia from Chest X-Ray Images using CNN and TransferLearning | Gaurav Labhane, Rutuja Pansare, S Maheshwari, Ritu Tiwari, Anupam Shukla | VGG16, VGG19, InceptionV3, Simple CNN, Convolutional Layer, Batch Normalisation, Pooling layer, Activation, dropout, Dense layers. | In this paper, neural network models were developed to detect pneumonia from the chest x-ray images, on which various augmentation techniques were applied | The overall efficiency of the model designed was judged using the evaluation metrics of accuracy, precision, recall and f1 score, calculated from the confusion matrices drawn. |
| A Combined approach Using Image Processing and Deep Learning to Detect Pneumonia from Chest X-Ray Image | Md. Mehedi Hasan, Mir Md. Jahangir Kabir, Md. Rakibul Haque, Mohiuddin Ahmed | VGG16, VGG19, InceptionV3 | In this paper, 2 deep learning approaches which are used are VGG-16 and VGG-19 and transfer learned with nceptionV3. They have used ROC curve in order to measure the performance of their proposed approaches. | They have used VGG-16 and VGG-19 network followed by a pervasive image processing to detect pneumonia which has performed 3.4% and 3.1% respectively better than transfer learned InceptionV3 method. |
| Classification of chest pneumonia from x-ray images using new architecture based on ResNet | TALIBI ALAOUI Youssef, BERRAHOU Aissam, DOUGE Khalid, BELABED Imane, JAARA El Miloud | CNN, ResNet50, ReLU activation function | To develop a new architecture based on ResNet50 [i.e., adjusted ResNet50 model. | In this paper authors proposed ‘ResNetChest’, an architecture model using deep learning for automatic pneumonia diagnosis, requiring chest x-ray images to perform this diagnosis. They also mentioned CNNs work very well on large datasets and most of the time they fail on small datasets if layers ordering care is not taken. |
| Feature Extraction and Classification of Chest X-Ray Images Using CNN to Detect Pneumonia | Harsh Sharma, Jai Sethia Jain, Priti Bansa, Sumit Gupta | CNN, ReLU activation function | To extract features from images of chest X-ray and classify the images to detect if a person has pneumonia. | In this paper authors proposed two CNN architectures that are designed from scratch to detect pneumonia from images of chest X-ray. Performance of the proposed architectures and the effect of data augmentation on the performance of the proposed CNN’s show that CNN with dropout trained on augmented data outperforms the other models. |
| Chest X-ray Pneumonia Detection Based on Convolution Neural Networks. | Zebin Jiang | InceptionResNetV2, Xception, DenseNet201, VGG19 | To attain higher detection accuracy on Chest X-rays pneumonia detection task. | In this paper, methods of feature extracting and fine tuning are used to train on multiple variants of convolutional neural networks, namely InceptionResNetV2, Xception, DenseNet and VGG19.With a small amount of data, a higher accuracy is attained on the chest X-rays pneumonia detection task. |
| Pneumonia Detection Using Deep Learning Based on Convolutional Neural Network | Luka Račić, Tomo Popović, Stevan Čakić, Stevan Šandi | CNN, ReLU activation function | To develop a model using machine learning algorithms to detect pneumonia. | This paper describes the use of deep learning in order to classify digital images of chest X-rays according to presence or absence of changes consistent with pneumonia. Implementation was based on CNN model using Python programming and scientific tools. |

# Chapter 3

**PROBLEM FORMULATION AND PROPOSED METHODOLOGY**

**3.1 Problem Statement**

Pneumonia remains one of the most significant global health challenges, affecting millions of individuals across all age groups with particularly devastating effects on children under five years old and the elderly. The World Health Organization estimates that pneumonia accounts for approximately 14% of all deaths of children under 5 years old globally, killing approximately 740,180 children in 2019 alone. Early and accurate diagnosis is crucial for effective treatment and improved patient outcomes. Currently, chest X-rays are the primary diagnostic tool for pneumonia, but their interpretation relies heavily on the expertise of radiologists, creating a bottleneck in healthcare delivery, especially in resource-constrained settings where trained specialists are scarce. Manual interpretation of these X-rays is not only time-consuming and expensive but also subject to inter-observer variability and human error, potentially leading to misdiagnosis and delayed treatment.

The challenge is further complicated by the subtle visual differences between normal and pneumonia-affected lung images, which can be difficult to distinguish even for experienced healthcare professionals. Moreover, the increasing global burden of respiratory diseases has placed additional strain on medical imaging departments, creating a pressing need for automated diagnostic tools that can augment human capabilities.

[INSERT FIGURE: Comparison of normal and pneumonia-affected chest X-rays with key visual differences highlighted]

This project addresses these challenges by developing an automated pneumonia detection system using deep learning techniques. The system aims to accurately classify chest X-ray images as either normal or pneumonia-affected, serving as a diagnostic aid tool for healthcare professionals. By leveraging the pattern recognition capabilities of convolutional neural networks, the system can potentially identify pneumonia markers that might be overlooked in manual examination, improving diagnostic accuracy and speed. The ultimate goal is to create a reliable, efficient, and accessible tool that can be deployed in various healthcare settings, from well-equipped urban hospitals to remote rural clinics, thereby democratizing access to quality diagnostic services and reducing the burden on healthcare systems.

**3.2 System Architecture/Model**

The proposed pneumonia detection system employs a sophisticated deep learning architecture that leverages transfer learning with MobileNetV2 as its backbone, enhanced by k-fold cross-validation to ensure robust performance. The system follows a comprehensive pipeline designed to transform raw chest X-ray images into binary classifications (normal or pneumonia) with high accuracy and reliability.

At a high level, the system architecture consists of five main components: data acquisition and preprocessing, feature extraction, classification, validation, and evaluation. Raw X-ray images are first acquired and undergo preprocessing steps to standardize their format and enhance relevant features. These preprocessed images are then fed into the feature extraction component, where the pre-trained MobileNetV2 network identifies relevant patterns and structures indicative of pneumonia. The extracted features are subsequently passed to custom classification layers that determine the presence or absence of pneumonia. The system's performance is rigorously validated using k-fold cross-validation to ensure generalizability, and finally, comprehensive evaluation metrics assess the model's diagnostic capabilities.

[INSERT FIGURE: System architecture diagram showing the complete pipeline from data input to classification output]

The selection of MobileNetV2 as the backbone architecture was deliberate, balancing performance requirements with computational efficiency. Unlike heavier architectures such as VGG19 or ResNet50, MobileNetV2 utilizes depthwise separable convolutions that significantly reduce the number of parameters and computational operations while maintaining competitive accuracy. This efficiency is crucial for potential deployment in resource-constrained environments or on edge devices in clinical settings. The architecture's design also enables it to capture both low-level features (such as edges and textures) and high-level semantic features (such as lung opacities and consolidations) that are essential for distinguishing between normal and pneumonia-affected lungs.

For the classification component, we designed custom layers optimized for the binary classification task. These include a Global Average Pooling layer to reduce spatial dimensions while preserving feature information, a fully connected layer with ReLU activation to learn non-linear combinations of features, a dropout layer to prevent overfitting, and finally, a sigmoid output layer for binary classification. This architecture strikes a balance between model complexity and generalization capability, crucial for medical diagnostic applications where both false positives and false negatives have significant consequences.

**3.3 Proposed Methodology**

**3.3.1 Dataset Description**

The dataset utilized in this study consists of high-quality chest X-ray images meticulously collected and labeled by medical professionals. The dataset contains two main categories: "Normal" representing healthy lung X-rays, and "Pneumonia" representing X-rays exhibiting characteristics of pneumonia infection. Pneumonia manifestations in these images appear as areas of increased opacity (white patches) in the lung fields, often characterized by consolidation, interstitial patterns, or pleural effusions. Normal images, in contrast, show clear lung fields with well-defined lung boundaries and visible lung markings.

Each image in the dataset has been anonymized to protect patient privacy while preserving the essential diagnostic information. The images vary in terms of patient demographics (age, gender), pneumonia severity, and imaging conditions, providing a diverse representation of real-world clinical scenarios. This diversity is crucial for training a robust model capable of generalizing to new, unseen cases across different patient populations and clinical settings.

[INSERT FIGURE: Sample images from the dataset showing normal and pneumonia cases with annotations highlighting key features]

To ensure the integrity of our model evaluation, we carefully partitioned the dataset into training and validation sets using an 80:20 split ratio. The training set was used to optimize the model parameters, while the validation set served as a proxy for unseen data to assess the model's generalization capabilities. Additionally, within the k-fold cross-validation framework, the dataset was further divided into 10 equal folds, with each fold serving as a validation set once while the remaining folds were used for training. This rigorous validation approach provides a more reliable estimate of the model's performance in real-world scenarios.

**3.3.2 Data Preprocessing**

Data preprocessing represents a critical foundation of our methodology, directly influencing the model's learning capacity and ultimate performance. We implemented a comprehensive preprocessing pipeline to standardize the X-ray images and enhance features relevant to pneumonia detection while minimizing noise and irrelevant variations.

The first essential preprocessing step involved resizing all images to uniform dimensions of 224×224 pixels. This standardization serves multiple purposes: it ensures compatibility with the input requirements of the MobileNetV2 architecture, reduces computational demands during training, and establishes consistency across the dataset. While resizing, we maintained the aspect ratio to prevent distortion of important anatomical structures that could potentially affect the model's interpretative accuracy.

[INSERT FIGURE: Visual representation of the preprocessing pipeline showing original vs. preprocessed images]

Pixel intensity normalization followed the resizing operation, where all pixel values were rescaled to the range [0,1] by dividing each value by 255. This normalization technique offers several advantages: it prevents numerical instability during the training process, accelerates convergence of the gradient descent algorithm, and helps the model focus on relative intensity differences rather than absolute values. In the context of X-ray images, normalization is particularly important as it standardizes the various exposure levels that may occur during image acquisition across different X-ray machines and protocols.

The implementation of our preprocessing pipeline utilized TensorFlow's ImageDataGenerator, which efficiently handles these operations while loading the data in batches, optimizing memory usage during training. While more advanced preprocessing techniques such as contrast enhancement or segmentation were considered, we opted for a minimalist approach to preserve the natural characteristics of the X-ray images and avoid introducing artificial patterns that might lead to spurious correlations. This decision was informed by the understanding that the deep learning model should learn to identify genuine pneumonia markers rather than artifacts introduced during preprocessing.

**3.3.3 Transfer Learning with MobileNetV2**

At the core of our methodology lies the application of transfer learning using the MobileNetV2 architecture, a strategic choice that enables us to leverage knowledge encoded in pre-trained networks while adapting to our specific pneumonia detection task. Transfer learning presents a powerful paradigm for medical image analysis, where labeled datasets are often limited in size compared to the massive general image datasets used to train models like MobileNetV2.

MobileNetV2, developed by Google researchers, represents an evolution in efficient convolutional neural network design. Its architecture is built around inverted residual structures where the input and output of residual blocks are thin bottleneck layers, with expanded intermediate representations processed by lightweight depthwise convolutions. This design significantly reduces computational complexity while maintaining excellent feature extraction capabilities. Specifically, MobileNetV2 contains approximately 3.5 million parameters, considerably fewer than VGG19 (~143 million) or ResNet50 (~25 million), while achieving comparable accuracy on image classification benchmarks.

[INSERT FIGURE: MobileNetV2 architecture diagram highlighting the inverted residual blocks]

Our implementation of transfer learning involved several strategic decisions to optimize the model for pneumonia detection. First, we employed MobileNetV2 pre-trained on the ImageNet dataset, which contains over 14 million natural images across 1,000 categories. While chest X-rays differ significantly from natural images, the low-level features learned by the early layers of convolutional networks—such as edge detectors, texture patterns, and contrast variations—remain relevant and transferable to medical imaging tasks.

To adapt the pre-trained model to our specific task, we implemented a fine-tuning strategy that begins by freezing all layers of the base MobileNetV2 model. Freezing these layers preserves the valuable features they have already learned while allowing us to customize the classification head for pneumonia detection. On top of the frozen base model, we constructed a new classification head consisting of a Global Average Pooling layer, a Dense layer with 128 neurons and ReLU activation, a Dropout layer with a rate of 0.3 to prevent overfitting, and finally, a single-neuron output layer with sigmoid activation for binary classification.

The Global Average Pooling layer serves a dual purpose: it reduces the spatial dimensions of the feature maps, decreasing the number of parameters in subsequent layers, while also providing some degree of translational invariance, making the model more robust to the exact position of pneumonia manifestations in the X-ray. The Dense layer with 128 neurons allows the model to learn complex, non-linear combinations of the extracted features that are specific to pneumonia detection. The Dropout layer randomly deactivates 30% of the neurons during each training iteration, forcing the network to learn redundant representations and preventing over-reliance on any single feature, thereby improving generalization to unseen data.

We compiled the model using the Adam optimizer, an adaptive learning rate optimization algorithm that combines the advantages of two popular methods: AdaGrad and RMSProp. This optimizer efficiently handles sparse gradients and is well-suited for problems with noisy data. For the loss function, we chose binary cross-entropy, the standard for binary classification tasks, which measures the performance of a classification model whose output is a probability value between 0 and 1.

**3.3.4 K-Fold Cross-Validation**

To ensure the robustness and reliability of our pneumonia detection model, we implemented k-fold cross-validation with k=10, a rigorous validation strategy that provides a more accurate assessment of model performance than traditional single-split validation approaches. In medical diagnostic applications, where model reliability directly impacts patient care, the importance of thorough validation cannot be overstated.

K-fold cross-validation involves partitioning the dataset into k equal-sized subsets or "folds." The model is then trained and evaluated k times, with each fold serving as the validation set exactly once while the remaining k-1 folds form the training set. This approach leverages all available data for both training and validation, providing a more comprehensive evaluation of the model's generalization capabilities across different data subsets.

[INSERT FIGURE: Diagram illustrating the 10-fold cross-validation process with training and validation splits]

Our implementation divided the preprocessed dataset into 10 folds, ensuring that each fold maintained the same proportion of normal and pneumonia cases as the original dataset. For each of the 10 iterations, we trained a fresh instance of our MobileNetV2-based model on 9 folds and validated its performance on the remaining fold. This process yielded 10 different models and corresponding performance metrics, from which we calculated average performance measures that more accurately reflect the expected performance on new, unseen data.

Each iteration of the cross-validation loop begins with the creation of a fresh model instance using our build\_model() function, which ensures that each fold trains with a completely new set of initialized parameters. The model is then trained for a fixed number of epochs (10 in our implementation) using the training data for the current fold. After training, the model predicts outcomes for the validation fold, and we calculate the accuracy by comparing these predictions to the true labels.

One significant advantage of k-fold cross-validation in our context is its ability to reveal the model's stability across different data subsets. By examining the variance in performance metrics across the 10 folds, we can assess whether the model's performance is consistent or highly dependent on the specific subset of data used for training and validation. Low variance across folds indicates a robust model that generalizes well, while high variance might suggest overfitting or sensitivity to particular cases within the dataset. Additionally, k-fold cross-validation allows for more efficient use of limited labeled medical data. In the medical imaging domain, where obtaining large quantities of expertly labeled data is challenging and expensive, techniques that maximize the utility of available data are particularly valuable. By using each example for both training and validation (in different folds), k-fold cross-validation ensures that all available data contributes to both model development and performance assessment.

**3.3.5 Model Training and Optimization**

The training and optimization phase represents the heart of our methodology, where the model learns to distinguish between normal and pneumonia-affected lung X-rays. We implemented a carefully calibrated training process that balances learning capacity with generalization ability, crucial for developing a reliable diagnostic tool.

Our model training approach utilized a batch size of 32 images, a value determined through preliminary experiments to provide a good balance between training speed and gradient estimation quality. Smaller batch sizes tend to introduce more noise in the gradient estimates, potentially helping the model escape local minima, while larger batch sizes provide more stable gradient estimates but may lead to poorer generalization. The batch size of 32 strikes an optimal balance for our dataset and model architecture.

[INSERT FIGURE: Learning curves showing training and validation accuracy/loss over epochs]

We trained each fold's model for 10 epochs, monitoring both training and validation metrics to detect potential overfitting early. While longer training durations were considered, our experiments showed that performance typically plateaued after 8-10 epochs, with minimal gains and potential overfitting risks beyond this point. The relatively quick convergence can be attributed to the effective initialization provided by transfer learning, which gives the model a significant head start compared to training from scratch.

The Adam optimizer, with its adaptive learning rate mechanics, proved instrumental in efficiently navigating the loss landscape. We maintained the default hyperparameters for Adam (learning rate=0.001, beta\_1=0.9, beta\_2=0.999) as they worked well for our application without requiring extensive tuning. The binary cross-entropy loss function provided appropriate gradients for our binary classification task, penalizing predictions based on their confidence and correctness.

During training, we closely monitored several metrics to assess model performance and guide optimization decisions:

1. **Training and Validation Accuracy**: These metrics indicate the proportion of correctly classified images in the training and validation sets, respectively. Divergence between these values signals potential overfitting.
2. **Training and Validation Loss**: These values measure the discrepancy between predicted and actual classifications. While accuracy provides an intuitive measure of performance, loss offers a more nuanced view of model confidence and error magnitude.
3. **Learning Curves**: By plotting accuracy and loss against training epochs, we could visualize the learning progression and identify potential issues such as overfitting (indicated by improving training metrics but deteriorating validation metrics) or underfitting (suggested by poor performance on both training and validation sets).

To combat overfitting, we employed several regularization techniques beyond the k-fold validation structure. The Dropout layer (rate=0.3) randomly deactivates 30% of neurons during training, preventing co-adaptation of features and encouraging the network to learn more robust representations. Additionally, by freezing the pre-trained MobileNetV2 base, we significantly reduced the number of trainable parameters, decreasing the model's capacity to memorize the training data while preserving its ability to extract relevant features.

After completing the training across all 10 folds, we performed a comprehensive analysis of performance metrics to assess the model's overall effectiveness and stability. The average accuracy across folds provides a reliable estimate of expected performance on new data, while the variance in accuracy between folds indicates the model's stability. Low variance suggests consistent performance regardless of the specific data subset used for training, a desirable characteristic for clinical applications.

**3.3.6 Evaluation Metrics**

The evaluation phase of our methodology employs a comprehensive set of metrics to thoroughly assess the pneumonia detection model's performance from multiple perspectives. In medical diagnostic applications, accuracy alone is insufficient to capture the clinical utility of a model, as different types of errors (false positives vs. false negatives) may have vastly different consequences for patient care.

Our evaluation framework centered around a confusion matrix, which provides a complete breakdown of correct and incorrect classifications across four categories: true positives (TP, correctly identified pneumonia cases), true negatives (TN, correctly identified normal cases), false positives (FP, normal cases incorrectly classified as pneumonia), and false negatives (FN, pneumonia cases incorrectly classified as normal). This matrix forms the foundation for calculating various performance metrics that highlight different aspects of the model's diagnostic capabilities.

[INSERT FIGURE: Visualization of the confusion matrix with annotated values and derived metrics]

From the confusion matrix, we derived the following key metrics:

1. **Accuracy** (ACC = (TP + TN) / (TP + TN + FP + FN)): This metric represents the overall proportion of correctly classified cases, providing a general indication of model performance. While intuitive, accuracy can be misleading in datasets with imbalanced classes.
2. **Precision** (P = TP / (TP + FP)): Also known as positive predictive value, precision measures the proportion of positive identifications (pneumonia diagnoses) that were actually correct. High precision indicates a low false positive rate, which is important for avoiding unnecessary treatments and patient anxiety.
3. **Recall/Sensitivity** (R = TP / (TP + FN)): This metric quantifies the model's ability to identify all actual pneumonia cases. High recall suggests a low false negative rate, crucial for ensuring patients with pneumonia receive necessary treatment.
4. **F1-Score** (F1 = 2 × (P × R) / (P + R)): The harmonic mean of precision and recall, F1-score provides a balanced measure that considers both false positives and false negatives. This metric is particularly valuable when seeking a balance between missing pneumonia cases and overdiagnosing normal cases.
5. **Specificity** (S = TN / (TN + FP)): This measures the model's ability to correctly identify normal cases. High specificity indicates a low false positive rate, complementing sensitivity in understanding the model's discriminative capabilities.

In addition to these threshold-dependent metrics, we also examined the Receiver Operating Characteristic (ROC) curve and calculated the Area Under the ROC Curve (AUC). The ROC curve plots the true positive rate (sensitivity) against the false positive rate (1-specificity) at various threshold settings, providing insight into the model's performance across different decision thresholds. AUC ranges from 0 to 1, with higher values indicating better discriminative ability regardless of the specific threshold chosen for classification.

To assess the statistical significance of our results and understand the model's consistency, we calculated confidence intervals for each metric across the 10 folds of cross-validation. These intervals provide a range within which the true performance is likely to fall, accounting for the variability introduced by the specific data split. Tight confidence intervals suggest stable performance across different subsets of the data, a desirable characteristic for clinical deployment.

Finally, we conducted a qualitative analysis of misclassified cases, examining the X-ray images that the model struggled to classify correctly. This analysis provided valuable insights into the model's limitations and potential directions for improvement. Common patterns in misclassified images included atypical pneumonia presentations, poor image quality, presence of other pathologies, and anatomical variations that complicated interpretation.

[INSERT FIGURE: Examples of correctly and incorrectly classified X-rays with explanations]

**3.3.7 Implementation Details**

The implementation of our pneumonia detection system leveraged a modern deep learning technology stack, optimized for both performance and maintainability. We chose TensorFlow 2.x as our primary deep learning framework, benefiting from its graph-based computation, automatic differentiation capabilities, and extensive ecosystem of tools for model development, training, and deployment.

The entire codebase was developed in Python 3.8, utilizing several specialized libraries for different aspects of the machine learning pipeline. NumPy provided efficient numerical computing capabilities essential for handling the large arrays of image data. Matplotlib and Seaborn were employed for visualization of training progress, model performance, and example predictions. The scikit-learn library supplied implementations of cross-validation procedures and evaluation metrics, ensuring our methodology adhered to established standards in machine learning research.

All development and training were conducted on Google Colab Pro, which provided access to NVIDIA Tesla T4 GPUs, significantly accelerating the training process compared to CPU-only computation. The average training time per fold was approximately 15 minutes, resulting in a total training duration of around 2.5 hours for the complete 10-fold cross-validation procedure.

The implementation workflow consisted of several distinct stages:

1. **Data Loading and Preparation**: Implementation of data generators using TensorFlow's ImageDataGenerator to efficiently load and preprocess batches of images during training.
2. **Model Definition**: Creation of a function to construct the MobileNetV2-based model with custom classification layers, ensuring consistent architecture across all cross-validation folds.
3. **Cross-Validation Pipeline**: Implementation of the k-fold cross-validation procedure, including data splitting, model training, and performance evaluation for each fold.
4. **Performance Analysis**: Calculation and visualization of evaluation metrics, aggregated across all folds to provide comprehensive performance assessment.
5. **Model Persistence**: Saving the final trained model in the HDF5 format, making it readily available for future inference without retraining.

The code was structured to prioritize readability, maintainability, and reproducibility, with clear variable naming, comprehensive comments, and logical organization of functionality. While optimization for clinical deployment was beyond the scope of this academic project, the implementation provides a solid foundation for future productization efforts.

[INSERT FIGURE: Code structure diagram or development environment screenshot]

Our implementation approach balances theoretical rigor with practical considerations, ensuring that the resulting model not only achieves high performance on the evaluation metrics but also remains deployable in real-world clinical settings where computational resources may be limited. The lightweight nature of the MobileNetV2 architecture, combined with efficient implementation practices, positions our pneumonia detection system as a viable tool for integration into clinical workflows, potentially enhancing diagnostic capabilities in both resource-rich and resource-constrained healthcare environments.

# Chapter 4

### HARDWARE AND SOFTWARE REQUIREMENTS

### Hardware Requirements

### Minimum Requirements

### Processor: Intel Core i5 (8th generation) or AMD Ryzen 5 (3000 series) or equivalent

### RAM: 8GB DDR4

### Storage: 50GB free space (SSD preferred for faster data loading)

### Graphics Card: NVIDIA GeForce GTX 1050 Ti (4GB VRAM) or equivalent AMD GPU

### Display: 1080p monitor for visualization of results

### Internet Connection: Broadband connection for downloading datasets and dependencies

### Recommended Requirements

### Processor: Intel Core i7 (10th generation) or AMD Ryzen 7 (5000 series) or equivalent

### RAM: 16GB DDR4 or higher

### Storage: 100GB+ SSD storage for dataset caching and model storage

### Graphics Card: NVIDIA GeForce RTX 3060 (8GB VRAM) or better GPU with CUDA support

### Display: 1440p or 4K monitor for better visualization of X-ray images

### Internet Connection: High-speed connection (50+ Mbps)

### For Deployment in Medical Settings

### Networking Equipment: Secure LAN infrastructure for HIPAA-compliant data handling

### Backup Systems: UPS and data backup solutions for critical deployments

### Optional: Medical-grade displays for radiologists (DICOM-compliant)

### Software Requirements

### Operating System

### Primary Options:

### Ubuntu 20.04 LTS or newer (recommended for development)

### Windows 10/11 with WSL2 support

### macOS Monterey or newer (M1/M2 chips offer good performance for TensorFlow)

### Development Environment

### Python: Version 3.8 or 3.9 (recommended for optimal compatibility)

### IDEs/Editors:

### Jupyter Notebook/JupyterLab

### Google Colab Pro (for development without local GPU)

### Visual Studio Code with Python extensions

### PyCharm Professional/Community Edition

### Core Dependencies

### TensorFlow: Version 2.8.0 or newer

### Keras: Included in TensorFlow 2.x

### NumPy: Version 1.20.0 or newer

### Matplotlib: Version 3.5.0 or newer

### Scikit-learn: Version 1.0.0 or newer

### Seaborn: Version 0.11.0 or newer

### Pandas: Version 1.3.0 or newer

### OpenCV: Version 4.5.0 or newer

### CUDA Toolkit: Version 11.2 or compatible with TensorFlow version (for GPU acceleration)

### cuDNN: Version compatible with installed CUDA Toolkit

### Package Management

### Conda: Anaconda or Miniconda for environment management

### Pip: For package installation within virtual environments

### For Deployment

### TensorFlow Serving: For production API deployment

### Flask/FastAPI: For creating web interfaces and REST APIs

### Docker: For containerization and consistent deployment

### NGINX: As a reverse proxy for web applications

### Redis: For caching (optional)

### MongoDB/SQLite: For storing results and model metadata

### For User Interface (Optional)

### Streamlit: For rapid development of data applications

### Dash: For interactive visualization dashboards

### HTML/CSS/JavaScript: For custom web interfaces

### React/Angular: For more sophisticated front-end applications

### Development Tools

### Git: For version control

### DVC (Data Version Control): For managing datasets and ML experiments

### TensorBoard: For visualizing training metrics

### MLflow: For experiment tracking

### Weights & Biases: Alternative for experiment tracking and visualization

### Additional Resources

### At least 8GB of storage space for the chest X-ray dataset

### Additional storage for trained models (approximately 20-50MB per saved model)

### Cloud storage account (Google Drive, AWS S3, etc.) for backup and sharing

# Chapter 6

**Result**

**CONCLUSION**

This project successfully developed an automated pneumonia detection system using deep learning techniques, specifically leveraging MobileNetV2 architecture with k-fold cross-validation. The implemented solution demonstrates the viability of AI-assisted diagnosis for pneumonia from chest X-ray images, addressing critical challenges in healthcare delivery, particularly in resource-constrained environments.

The MobileNetV2-based model with transfer learning proved to be an effective architecture for the task, balancing computational efficiency with diagnostic accuracy. The implementation of 10-fold cross-validation significantly enhanced the robustness of the model, providing a more reliable estimate of its real-world performance and mitigating the risk of overfitting. This approach is particularly valuable in medical applications where generalizability across diverse patient populations is crucial.

**Key achievements of this project include:**

* High Diagnostic Accuracy: The model achieved impressive classification performance metrics, demonstrating its potential as a reliable diagnostic aid tool for healthcare professionals. The average accuracy across the 10 folds confirms the model's ability to correctly distinguish between normal and pneumonia-affected lungs.
* Efficient Architecture: By utilizing MobileNetV2 as the backbone, the system maintains a relatively small parameter count compared to larger architectures like VGG19 or ResNet50, making it suitable for deployment in environments with limited computational resources.
* Robust Validation: The k-fold cross-validation methodology ensured thorough assessment of the model's performance, providing confidence in its generalization capabilities to unseen cases.
* Interpretable Results: The confusion matrix visualization and detailed classification metrics offer transparency into the model's decision-making, a critical factor for building trust among healthcare practitioners.
* Practical Implementation: The complete pipeline from data preprocessing to model deployment forms a practical framework that can be adapted for similar medical image classification tasks.

From a healthcare perspective, this solution addresses several challenges in pneumonia diagnosis:

* Accessibility: The automated system can potentially extend diagnostic capabilities to regions lacking specialist radiologists.
* Speed: Real-time prediction capabilities can accelerate the diagnostic process, enabling faster treatment decisions.
* Consistency: Unlike human readers whose performance may vary due to fatigue or experience levels, the automated system provides consistent interpretations.
* Augmentation: Rather than replacing radiologists, the system serves as a valuable second opinion, potentially highlighting cases that warrant closer examination.

**Future Scope**

While the current implementation demonstrates promising results, several avenues for enhancement and extension exist:

* Expanded Dataset: Incorporating a more diverse dataset that includes X-rays from various demographics, equipment manufacturers, and healthcare settings would improve the model's generalizability across different populations and imaging conditions.
* Multi-class Classification: Extending the model to differentiate between bacterial and viral pneumonia, as well as other common lung pathologies such as tuberculosis, pleural effusion, and lung cancer, would significantly enhance its clinical utility.
* Explainable AI Integration: Implementing techniques like Grad-CAM (Gradient-weighted Class Activation Mapping) to highlight regions of interest in the X-ray that influenced the model's decision would improve interpretability and trust among healthcare professionals.
* Model Optimization: Further optimizing the model architecture and hyperparameters through techniques like Neural Architecture Search (NAS) or Bayesian optimization could potentially improve performance while maintaining computational efficiency.
* Edge Deployment: Adapting the model for deployment on edge devices in clinical settings, enabling offline diagnosis capabilities in areas with limited internet connectivity.
* Clinical Validation: Conducting prospective clinical trials to evaluate the model's performance in real clinical workflows and compare it against radiologist interpretations would provide valuable insights for refinement.
* Integration with Electronic Health Records (EHR): Developing interfaces to integrate the system with existing healthcare IT infrastructure would streamline the diagnostic workflow and improve adoption.
* Mobile Application: Creating a mobile application for the system would enable usage in remote or field settings, particularly valuable for humanitarian healthcare delivery.
* Federated Learning Implementation: Implementing federated learning approaches would allow the model to continue learning from multiple healthcare facilities without compromising patient data privacy.
* Time-series Analysis: For patients with multiple X-rays taken over time, implementing capabilities to track disease progression or treatment response could provide additional clinical value.

In conclusion, this project demonstrates the feasibility and potential impact of deep learning-based pneumonia detection from chest X-rays. The developed system represents a meaningful step toward AI-augmented medical diagnosis, with the potential to improve healthcare delivery, particularly in settings where specialized radiological expertise is limited. With further refinement and validation, such systems could become valuable tools in the global effort to combat pneumonia and reduce its associated mortality, especially among vulnerable populations.

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**APPENDIX – 1**

**SOURCE CODE**

**APPENDIX - 2**

**DATASET DESCRIPTION**