**Deep Learning Tuberculosis Prediction from Chest X-Rays**

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**Thesis Report**

**January 2023**

**Dedication:**

**Dedicated To Mother, Father and Brother**

**Acknowledgement:**

I am immensely grateful towards my family and friends who helped me get information on my thesis. My family encouraged me and helped me in this humongous task of writing a thesis when I had no any idea on how to write it. I thank my friends for giving me advice and correcting my mistakes, when I asked doubts, my friends and family correct me and helped in every possible way to complete the thesis.

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# **List of Abbreviations:**

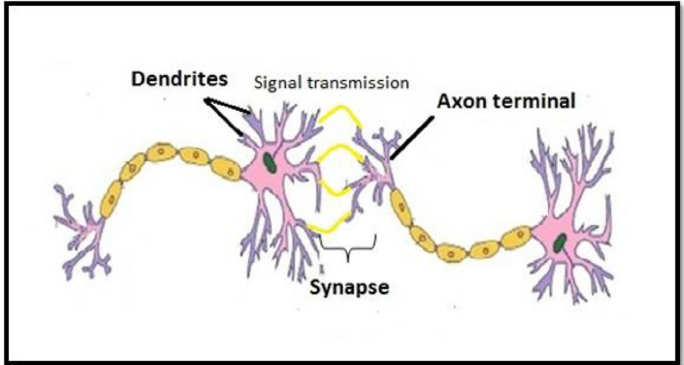
* WHO ………………… World Health Organization
* HIV …………………… Human Immunodeficiency virus
* TB ……………………. Tuberculosis
* SDG …………………. Sustainable Development Goals
* AI ……………………. Artificial Intelligence
* CAD …………………. Computer Aided Detection
* GDG …………………. Generation Data Group
* CNN …………………. Convolutional Neural Network
* SVM …………………. Support Vector Machine
* RGB …………………. Red Green Blue
* GLCM ………………. Gray Level Co-occurrence Matrix
* DWT …………………. Discrete Wavelet Transform
* LBP …………………… Local Binary Pattern
* NLM …………………. National Library of Medicine

# **Chapter 1:**

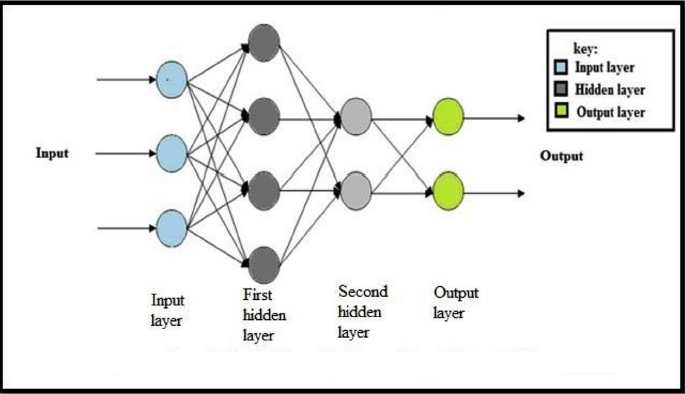
# **Introduction**

# **Background:**

Deep learning is a machine learning algorithm that teaches computers to perform tasks that humans typically perform: learning through examples and real-life experiences. Deep learning is a key component of the technology that allows driverless cars, among other things, to detect a stop sign or signal or to distinguish between a pedestrian and a lamppost. Deep learning is also used in the use of voice control in gadgets such as tablets, TVs, phones, and so on. [17]



**Signal transmission between two neurons [21]**



**Multiple Layer Feed Forward Neural Network [21]**

Machine Learning and Artificial Intelligence have made significant contributions in fields such as security and surveillance, healthcare, sports analytics, agriculture, retail shopping and fashion, and so on. In a disease like tuberculosis, where the majority of the risk factors are well known (examples: diabetes, kidney failure, HIV, immune-suppressant drugs, malnutrition), the addition of a few more input variables can aid in the development of a model for tuberculosis diagnosis. Artificial intelligence can be a useful tool in the early detection of tuberculosis. Artificial intelligence can assist in predicting patients who are at high risk of developing active tuberculosis. This will assist health officials in allocating health resources to a select few. Artificial intelligence can contribute to the ultimate goal of eliminating tuberculosis from the world. NLP and AI are being used by certain businesses to develop a universally available and reasonably priced health care system. The AI-powered bot assistant utilizes case notes that are dictated, photos, and files to automatically organize them and respond to clinical inquiries. Voice-activated digital assistants for doctors are made using AI. Additionally, computational genomics and AI work together to create sophisticated machine learning models that can speed up and reduce the cost of drug discovery for patients. In order to combat the novel coronavirus (COVID-19) pandemic, the most current use of AI in global healthcare is the prediction of emergent hotspots utilizing contact tracing and flight traveler data. Government officials use contact tracing as a disease control measure to limit disease spread. In order to prevent the disease from spreading further, contact tracing works by getting in touch with and informing those who have been exposed to someone who has the illness. Google and Apple have joined forces to develop a contact tracing platform that will employ artificial intelligence systems via application programming interfaces, or APIs, on smartphones. Users who choose to enroll in the platform will be able to report their lab results. The platform will then use location services to contact people who may have been in the vicinity of the infected person.

AI is capable of predicting and diagnosing disease faster than most medical professionals. In order to help care teams respond more rapidly, Viz.ai (business) uses AI-powered healthcare solutions. Delays in healthcare can be the difference between death and life. The business's AI technologies can swiftly identify issues and inform care teams, enabling professionals to discuss choices and decide on treatments earlier and ultimately save lives. To support radiology diagnostics, AI businesses are also creating deep learning medical solutions. To help doctors better comprehend a patient's needs in the present, the company's deep learning platform studies unstructured medical data, including genomes, blood tests, EKGs, radiology pictures, and patient medical histories. AI is also used in cancer screenings, diagnostic tests, and blood work by AI companies. Companies such as Free Nome are hoping to find novel treatments for cancer by implementing AI at routine checkups.

In 2021, 1.6 million people died from tuberculosis (including 187 000 people with HIV). TB is the 13th leading cause of death worldwide and the second leading infectious killer after COVID-19 (below HIV/AIDS). A deep learning model is a computer-trained model that learns how to perform classification, object detection, and segmentation from inputs such as images, videos, sounds, text, and so on. In most cases, deep learning models outperform humans in terms of accuracy. These models are trained using massive amounts of labelled data and multi-layered neural network architectures. [4]

Globally, an estimated 10.6 million people will contract tuberculosis (TB) by 2021. The population is made up of six million men, 3.4 million women, and 1.2 million children. Tuberculosis (TB) affects people of all ages and from all countries. Tuberculosis, on the other hand, is both curable and preventable. By 2021, 1.2 million children will be infected with tuberculosis worldwide. Tuberculosis (TB) in children and adolescents is frequently overlooked by healthcare providers and can be difficult to diagnose and treat. [4]

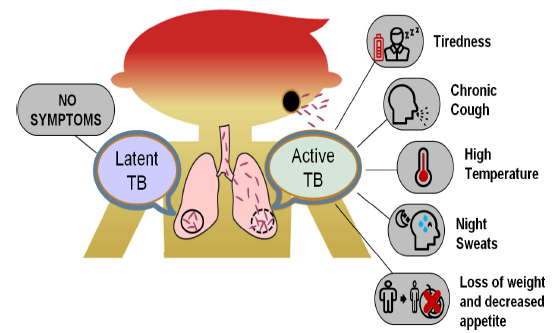
In 2021, the 30 high TB burden countries accounted for 87% of new TB cases. [4]

One of the United Nations Sustainable Development Goals' health targets is to end the TB epidemic by 2030. [4]

Tuberculosis (TB) is an infection caused by bacteria (Mycobacterium tuberculosis) that primarily affects the lungs. Tuberculosis is treatable as well as preventable.

Tuberculosis spreads from person to person through the air. TB germs are released into the air when people with lung tuberculosis cough, sneeze, or spit. In order to become infected, only a few of these germs must be inhaled.

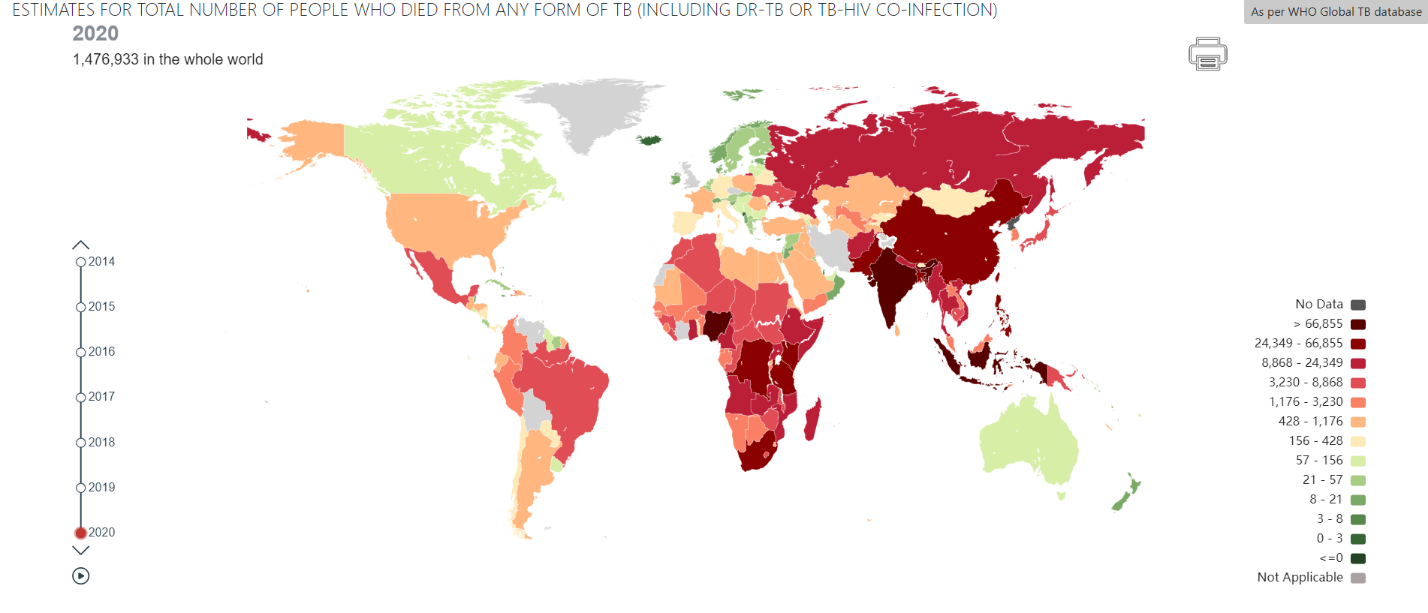
Approximately one-quarter of the world's population is tuberculosis (TB) infected, which means they have been infected by TB bacteria but are not (yet) ill and cannot transmit the disease. [4]



**Figure 1. Diagrammatic representation of symptoms of active and latent TB.**[25]

People exposed to tuberculosis bacteria have a 5- 10% lifetime risk of developing the disease. People with weakened immune systems, such as HIV, malnutrition, or diabetes, as well as smokers, are more likely to become ill. [4]

Active tuberculosis symptoms (cough, fever, night sweats, or weight loss) can be mild for months. This can result in treatment delays and the bacteria spreading to others. Over the course of a year, people with active tuberculosis can infect 5-15 other people through close contact. Without proper treatment, 45% of HIV-negative TB patients and nearly all HIV-positive TB patients will die. [[Tuberculosis (who.int)](https://www.who.int/news-room/fact-sheets/detail/tuberculosis)]



**Figure 2 Estimates for Total Number of People Who died from any form of TB**[16]

Due of its unique social and financial burden, tuberculosis continues to be a serious health issue in poor nations. Tuberculosis detection methods include methods such as nucleic acid magnification test (NAAT), polymerase chain reaction (PCR), as well as TB interferon gamma release (IGRA) assays.

Current diagnostic techniques, such as microscopic sputum analysis, tuberculosis chest X-ray testing, skin testing, as well as culture, are not only time-consuming but also inefficient. In an effort to control the condition and lower mortality rates, this has prompted substantial study into the development of new, efficient diagnostic tools and practices. [4]

Table 1.1 The number of new cases of active TB disease during a given time period is referred to as the TB incidence (usually a year) [15]

|  |  |  |
| --- | --- | --- |
| Estimates of TB Burden | Number | Rate per 100,000 Population |
| Incidence of TB cases (includes HIV + TB) | 2,590,000 | 188 |
| Incidence (HIV + TB only) | 53,000 | 3.8 |
| Laboratory confirmed MDR/RR-TB | 49,679 |  |

Because of the requirement and urgency to find modern and better methods, Artificial Neural Network as well as Convolutional Neural Network were developed.

Table 1.2 The biggest issues with TB diagnosis procedures [24]

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Test | Methodology | Interpretations | Shortcomings | References |
| 1)Chest X-Rays | Chest X-ray performed to check for lung inflammation | X-ray reveals an unusual shadow | Extrapulmonary tuberculosis cannot be ruled out. |  |
| 2) Skin test for TB | watching the swelling after injecting a little dose of tuberculin into the lower arm | The chance of TB infection increases with the size of the swelling's elevated region. | If the person is infected with another bacteria, the test may produce false results. Cannot distinguish between latent and active tuberculosis. |  |
| 3)TB interferon gamma | Mix blood sample with special  substances to identify  interferon gamma cytokine. | The likelihood of contracting TB increases with the size of the swelling's elevated region. | The likelihood of contracting TB increases with the size of the swelling's elevated region. |  |
| 4)Sputum smear test | A thin smear of the patient's sputum is stained with special stains and examined under a microscope for signs of tuberculosis bacteria. | Morphological characteristics  identification to detect  presence of M. Tuberculosis | In situations of HIV and TB co- infection, TB cannot be detected due to low levels of TB germs. |  |
| 5) Fluorescent microscopy | The patient's sputum smear is illuminated with a quartz/high pressure mercury lamp. | Identification of morphological characteristics to detect the presence of M. tuberculosis | Expensive and time consuming |  |
| 6) Culturing bacteria to test | A biological sample from a patient was used to cultivate bacteria on M. tuberculosis-specific media. | Detection of presence of  bacteria by observing colony  characteristics | Time Consuming |  |
| 7) observation of the characteristics of a colony to identify the presence of bacteria | The assay is concentrated on the KatG gene, which is unique to the TB bacterium. | The Mycobacterium tuberculosis complex must be present for the test to be considered positive. | Expensive |  |
| 8) GeneXpert evaluation | DNA found in tuberculosis bacteria has been identified. | If tuberculosis DNA is found, the patient is diagnosed. | Expensive |  |
| 9) Nucleic acid amplification test  Methodology | Nucleic acid amplification from biological samples of a suspected patient. | If nucleic acids are found, the patient has tuberculosis. | Sensitivity is lower for respiratory tract specimens. |  |

# Problem Statement:

Developing countries bear more than 95% of the Tuberculosis burden. Technologically advanced countries have made strides in tuberculosis early detection, resulting in low morbidity and mortality. Aside from a lack of technological resources, developing countries also lack expertise in the field of tuberculosis. In India's rural and semi-urban areas, there are not enough experts to diagnose tuberculosis early. [18]

In a disease like tuberculosis, where the majority of the risk factors are well known (for example, diabetes, kidney failure, HIV, immune-suppressant drugs, malnutrition), the addition of a few more input variables can aid in the development of a tuberculosis diagnosis model. [18]

CXR is more sensitive compared to verbal screening for detecting pulmonary tuberculosis. CXR has various drawbacks despite being a useful technique for TB detection. CXR image interpretation requires expert personnel for TB diagnosis. TB causes a variety of lung manifestations. Infiltrates, consolidation, and cavitation are common TB manifestations [4]. Figure 1 depicts examples of CXR images with various TB manifestations. [22]

In chest radiography image, tuberculosis affects the shape and texture of the lung. A qualified radiologist's job is to accurately determine the disease within CXR. Unfortunately, there aren't enough radiologists, particularly in high-TB-burden countries. [22]

A group of researchers from Dhaka, Bangladesh, compared 5 commercially available algorithms for detecting pulmonary tuberculosis in 23954 people's chest x-rays. They said:

Chest x-rays from 23 954 individuals were included in the analysis. All five AI algorithms significantly outperformed the radiologists. The areas under the receiver operating characteristic curve were 90·81% (95% CI 90·33–91·29) for qXR, 90·34% (89·81–90·87) for CAD4TB, 88·61% (88·03–89·20) for Lunit INSIGHT CXR, 84·90% (84·27–85·54) for Infer Read DR, and 84·89% (84·26–85·53) for JF CXR-1. Only qXR (74·3% specificity [95% CI 73·3–74·9]) and CAD4TB (72·9% specificity [72·3–73·5]) met the TPP at 90% sensitivity. All five AI algorithms reduced the number of Xpert tests required by 50% while maintaining a sensitivity above 90%. All AI algorithms performed worse among older age groups (>60 years) and people with a history of tuberculosis. (*A multiplatform evaluation of five AI products used for TB screening in a high TB-burden setting*, *Zhi Zhen Qin, Shahriar Ahmed, Mohammad Shahnewaz Sarkar*)

WHO consolidated guidelines on tuberculosis

Tool recommendations for systematic TB disease screening

Recommendations in the WHO consolidated tuberculosis guidelines 2021 suggest-

Screening of Tuberculosis in target specific populations

1. In regions with an estimated TB prevalence of 0.5% or higher, systematic tuberculosis disease screening is conducted among the general population.

2) In subpopulations with structural tuberculosis risk factors, systemic tuberculosis disease screening may be performed. These populations include those who live in impoverished urban areas, those who are homeless, those who live in remote or isolated areas, indigenous peoples, immigrants, refugees, people who have been internally displaced, along with other vulnerable or marginalized groups who have limited access to medical care.

1. People with HIV should have regular tuberculosis screenings at medical facilities (TB).
2. Testing for the disease should be done on family members and other close contacts of tuberculosis patients.
3. In prisons and penitentiary institutions, TB disease screening should be done on a regular basis.

6) People with TB risk factors who seek or are already receiving medical care in areas where the occurrence of TB in the general population is 0.001 or higher may be subjected to TB screening.

Screening tools for tuberculosis

1. In populations where TB screening is advised, systematic TB disease screening can be carried out among people 15 years of age and older help of a symptom screen, chest X-ray, or even a molecular WHO-recommended quick diagnostic assays, singly or in combination.
2. Computer-assisted detection software programs, in populations where TB screening is advised, rather than human readers, may be used to interpret digital chest X-rays for screening and triage for TB disease in individuals aged 15 and older.

WHO suggests in populations where TB screening is recommended, computer-aided detection software programs, rather than human readers, may be used to interpret digital chest X-rays for screening and triage for TB disease in individuals aged 15 and older (a new advice that is conditional and has little supporting evidence).

For decades, Chest X-Ray Screening screening for tuberculosis has been used.

In order to select the optimal clinical pathway for a thorough evaluation, chest X-rays are also frequently used to triage patients who present to treatment with TB-related signs, symptoms, or even risk factors. However, the use of CXR for TB screening and triage for TB disease is limited in many settings due to a shortage of educated health staff who can interpret radiography pictures as well as considerable inter- and intra-reader variability, and poor capacity to identify TB-related anomalies.

In order to assess the risk of TB disease, many software programs have been created that offer automated interpretation of digital CXR images or CAD. These programs represent a potential technical answer to the myriad implementation issues that come with human interpretation of CXRs.

[WHO EXPERTS] CAD software performance for screening and triaging use cases separately

Triaging refers to the process of selecting a person's diagnostic and care paths based on their symptoms, indications, risk factors, and test results. As a foundation for clinical decisions, triaging entails determining the likelihood of various differential diagnoses. It can be done in several steps and follow more or less standard protocols and algorithms. A TB triage test can be used to swiftly separate those who should be evaluated for non-TB diseases from those who need additional diagnostic testing for TB among persons who arrive at a health center (people with a positive or abnormal TB triage test).

When assessing the performance of Computer Aided Detected software, screening should be distinguished from triaging notwithstanding the possibility of overlap:

• The manner in which the disease screening populations could be different, where CXR findings of earlier TB are more likely than in triage populations. As a result, a different threshold score may be used to achieve the same specificity and sensitivity point.

• The prevalence of tuberculosis (TB) is often substantially lower in screening populations (5%) than in triage groups (10-20%), which has an impact on a test's predictive values and the proportion of patients who receive an accurate diagnosis as well as an incorrect one.

• There are different ethical implications for groups that seek and do not seek care when TB or other non-Tuberculosis-related chest x ray findings (nonetheless, clinically substantial deviations) are missed.

The WHO EXPERTS were given three independent assessments of the effectiveness of three various CAD programs for both the triage and screening use cases. For every digital image read, CAD programs produce a numerical anomaly score that can be used to compare to a user-defined threshold to decide whether to refer the patient for additional TB diagnostic testing. Because anomaly scores are created continuously, depending on the threshold, the specificity and sensitivity can be between 0 and 100%.

Each software program's sensitivity threshold for identifying pulmonary TB illness for GDG evaluation was set at 90% based on a microbiology reference standard. The software's associated specificity at that limit was then recorded, and in the same experiments, it was contrasted with the diagnostic precision of human readers analysing CXRs. The three evaluations included assessed the performance of each programme in various populations and settings.

Table 1.3. Ranges of CAD software as well as human readers evaluating computerized chest radiographs for detection of bacteriologically proved tb over 3 software applications, based on 3 different assessments of the software in a variety of populations and contexts. [31]

|  |  |  |
| --- | --- | --- |
| Type of case and type of reader | Accuracy estimate range | Accuracy estimate range |
| WHO target product profile | Sensitivity | Specificity |
| Screening use case |  |  |
| Computer Aided Detection software | 0.90-0.92 | 0.23-0.66 |
| Chest X Ray with human reader | 0.82-0.93 | 0.14-0.63 |
| Triage use case |  |  |
| Computer Aided Detection software | 0.90-0.91 | 0.25-0.79 |
| Chest X Ray with human reader | 0.89-0.96 | 0.36-0.63 |

The findings demonstrated the diversity of human observation and CAD applications across a broad range of contexts and population sizes. The data suggests that there is minimal difference between the range of accuracy of CAD and that of human readers interpreting CXRs when reader variability and large commonality between the two ranges are taken into consideration. Due to this, [WHO EXPERTS] came to the conclusion that CAD software programs perform better than human readers.

Given the lack of radiologists in many places, scaling up the technologies would likely be another desirable outcome in addition to their accuracy. This would enhance access to chest radiography. Furthermore, WHO EXPERTS pointed out that in many situations, general practitioners or other clinicians without specific radiology training are routinely faced with interpreting chest radiographs, and they might not be as skilled as the readers used for comparison in the evaluations evaluated, suggesting that the comparisons offered may underestimate the true comparative accuracy of CAD software for detecting TB.

The drawback of employing CAD interpretations for chest radiographs rather than human users is that it can only identify tuberculosis (TB) in the lung. Programs may be drawn to CAD technologies because of its capacity to test for numerous pulmonary or thoracic problems at once. In order to promote equality in the reach of TB screening initiatives and access to TB care, CAD technologies offer the ability to scale up radiography for triage and TB screening while also enhancing image interpretation.

The WHO guidelines may not always apply to other different types of tuberculosis. (e.g., TB that is only extrapulmonary, TB that has been medically diagnosed). These guidelines are only for adults and adolescents over the age of 15. The WHO advice is specifically in order to digital plain CXRs with posteroanterior or anteroposterior views for pulmonary TB; lateral or oblique views are not covered, and it is unknown if the suggestion applies to analogue CXRs.

Even when utilizing a similar technology which has the same threshold, the GDG [WHO EXPERTS] reviews of CAD programs showed a significant variance in diagnosis accuracy (sensitivity and specificity) among settings. In order to ensure that the overall yield, predictive values, accuracy and requirement for extra diagnostic testing are as anticipated, it is crucial to calibrate the threshold for each particular software for each context and population in which it will be utilized.

The environment, which includes assuring access to the essential tools for performing digital radiography, a continuous internet connection, and the compulsory software and hardware maintenance, has a significant impact on the practicality of CAD implementation. The environment, including the availability and pay of human readers, will determine the required resources and cost-effectiveness. [5]

# **1.3) Aims and Objectives:**

The aim of my research is to propose a CAD model for screening of pulmonary tuberculosis in the targeted high-risk population using chest x-rays. The model aims to shorten the time it takes to identify the deadly disease and streamline decision-making at the first point of care institution by modeling a system that will categorize X-rays into two categories, Tuberculosis or Normal.

The research objectives are as follows:

• To make a reliable deep learning model in order to detect pulmonary tuberculosis using chest x-rays.

• Access the dataset of x ray chest of Pulmonary Tuberculosis and Normal subjects from Kaggle which has a publicly available dataset

• The training, testing and validation dataset is created from the original dataset in the ratio 8:1:1.

• The dataset is trained by transfer learning methods such as DenseNet201, Inception V3, ResNet50 and XCeption , Mobile Net, depth based CNN, etc.

• Each model’s sensitivity, specificity, validation loss and accuracy will be compared side by side to decide which model would be best suited for screening of population of Pulmonary Tuberculosis.

• Deep learning is used to create a portable health gadget that will enhance TB diagnosis in high-burden nations like India.

* Lung field segmentation I, feature extraction II, and classification III make up a CAD model for TB detection. In order to extract the region of interest from Chest radiographs, lung segmentation is often carried out as a pre-processing step (ROI). These ROIs are prone to abnormalities and are often needed for further research. Clavicle segmentation can be crucial in the early detection of Tuberculosis and many other lung disorders because these conditions frequently present in the lung apex. Additionally, segmentation can help with area processing, such as bone suppression and contrast enhancement. Extraction of the visual elements which represent these ROIs comes after segmentation. Numerous texture features, such as wavelets and local binary patterns (LBP), shape features (such as ellipticity and circularity), and combinations of both are utilized to describe these lung areas [9–11]. In addition, in refs. [10, 12], various classifiers such as Support Vector Machine (SVM), Neural Network (NN), Random Forest (RF), and Bayesian network (BN) are investigated to classify CXR as normal or abnormal. Since the introduction of deep learning (DL) algorithms and their promising outcomes for different medical applications, significant progress has been made in building DL systems [13–21] to identify pulmonary tuberculosis and other lung abnormalities. Among all supervised machine learning techniques, deep convolutional neural network (DCNN) has shown to be a promising method for TB surveillance and detection. Many convolutional, pooling, and fully-connected layers make up a DCNN. Layers are connected to one another by kernels with a defined receptive field size. The weights are distributed among the layers in order to simplify computation and complexity. In order to extract the global and local characteristics inside the image that are more discriminative, convolutional neural network (CNN) models often use a huge dataset to learn the parameters. CNN models have great feature representation ability and do not require domain knowledge, in contrast to handwritten features. [22]

The goal is to make quick detection of pulmonary tuberculosis using x-rays chest.

# **1.4) Significance of Study:**

For a number of aspects of infectious disease surveillance and detection, including tuberculosis, deep learning has shown potential. To evaluate the deep learning model's generalizability, I have built a deep convolutional neural network (CNN) model using a publicly available dataset on tuberculosis. Deep neural networks offer potential for fresh approaches to combat tuberculosis (TB). [6] The National Tuberculosis Elimination Program [NTEP] and WHO both propose using chest x-rays (CXR) for active case finding interventions and prevalence surveys in order to detect tuberculosis (TB) (NTEP). [7]

WHO’s recommendation is based on following evidence and rationale –X-Ray chest has been used for screening as well as triaging in tuberculosis control programs in various countries according to the population being studied and availability of X-Ray facility. However, the CXR usage for screening TB and TB triage is typically limited due to a shortage of medical professionals who are qualified to interpret radiography images as well as by a large amount of intra- and inter-reader variability in the accuracy of TB anomaly identification. A variety of specialized software programs offer CAD, interpret digital CXR images in an automated fashion, to determine the propensity of TB disease. These programs stand in as a potential technological response to the myriad implementation challenges that come up when radiologists or primary care doctors read chest X-rays. [7]

# **1.5) Scope of Study:**

# **1.5.1) In-Scope:**

The model will be prepared on dataset obtained from countries with high burden of pulmonary tuberculosis. In most cases Offline machine learning models is cheaper than online machine learning models as online machine learning models always have access to new data with different models and different parameters in real time and remains updated. Price, privacy and data-sharing, regulatory certifications of the product's operational characteristics, output format, input and machine compatibility choices for adaptation into the old system and current processes, deployment methodology, deployment mechanism (online and offline), and deployment methodology has been considered by health authorities (software, hardware, server requirement).

# **1.5.2 Out-Scope:**

It’s applicability to the countries with low and medium burden is limited. It’s applicability towards populations below 16 years of age or above 65 years of age as well as people with history of tuberculosis is limited. In most cases Offline machine learning models is cheaper than online machine learning models as online machine learning models always have access to new data with different models and different parameters in real time and remains updated. But on the other hand, online machine learning models also require constant internet accessibility. Price, privacy and data-sharing, regulatory certifications of the product's operational characteristics, input and machine compatibility, output format, choices for integration into the old system and current processes, deployment methodology, deployment mechanism (online and offline), and deployment methodology will also be considered by health authorities (software, hardware, server requirement). [8]

# **1.6 Structure of The Study:**

Chapter 1 discusses the Background of the Study which covers Tuberculosis and the number of people that have died due to it, the problem statement itself, the aims and objectives of this study and what we are try to achieve. The significance and contribution of this study towards achieving the goal of tuberculosis detection with deep learning. The Scope of the study, i.e., what parameters are taken into consideration and what are the drawbacks or hinderances to the study

Chapter 2 discusses the work done which is related to tuberculosis detection in some ways. It also discusses the deep learning techniques used as well as it’s preprocessing techniques, in which manner the data is split, in what ratio is it split, the evaluation metrics (are the models evaluated on sensitivity/specificity values or on precision/recall values, accuracy etc.). What are the advantages and disadvantages of each and every research.

Chapter 3 discusses Research Methodology where the details of the Dataset, the preprocessing of the data, how the data is transformed, what were the models used , and what were the evaluation techniques used.

Chapter 4 discusses the Analysis of the Dataset, univariate analysis of the model, bivariate analysis between two models.

Chapter 5 discusses experimenting by modifying the current model by changing hyperparameters, showing the converging graphs as well as their outputs. The modified transfer learning techniques and its comparisons with our current model are made.

Chapter 6 discusses the what we conclude from the analysis of the dataset and the techniques we use for tuberculosis detection and solutions to the objectives of our Study and what are the Future scopes of the study and our contribution to the knowledge of Tuberculosis Detection.

# **Chapter 2.**

# 

# **Related Work/Literature Review:**

# **2.1 Machine learning based research:**

# **2.1.1 Comparison of literature based on techniques, preprocessing techniques, evaluation metrics, pros and cons for ML research:**

**Research 1:**

On a sizable dataset, like ImageNet, which has 1.2 million photos categorized into 1000 classes [8], the model is built using pre-trained CNN models. The initial weight values for the network are provided by the pre-trained models. Even on comparatively tiny datasets, Deep CNN can be successfully trained with such precise initial weights. Transfer learning is what we call this. The CNN is trained with help of architecture shown in the above table using training and validation datasets, and all layer weights are initialized at random. Training loss decreases gradually when validation accuracy performance is not satisfactorily converged. To lessen the impact of random split, the tests were carried out three times. The resulting datasets are designated as Dataset 1, 2, 3, accordingly. Considering the lowest convolutional layers, frequently extract low-level details from incoming images, we used previously learnt convolutional parameters to recreate edges and/or curves. (filters from first along with second convolution layers in CNN which were trained in ImageNet) (C1 and C2). [10 including tables and figures].

**Table 2.1 Training Data Testing Data Graph [21]**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Not utilising transfer learning | Not utilising transfer learning | Not utilising transfer learning | s | Through Transfer Learning | Through Transfer Learning | Through Transfer Learning | Through Transfer Learning |
|  | Area Under Curve | Accuracy | AP (pos) | AP (neg) | AUC | Accuracy | AP (pos) | AP (neg) |
| First Dataset | 0.824 | 0.773 | 0.750 | 0.884 | 0.963 | 0.902 | 0.951 | 0.973 |
| Second Dataset | 0.828 | 0.788 | 0.759 | 0.879 | 0.963 | 0.905 | 0.950 | 0.974 |
| Third Dataset | 0.796 | 0.758 | 0.721 | 0.868 | 0.967 | 0.903 | 0.957 | 0.976 |
| Average | 0.816 | 0.773 | 0.743 | 0.877 | 0.964 | 0.903 | 0.953 | 0.974 |

The public can access two sets of postero-anterior chest radiographs from Shenzhen, China, and Montgomery County, Maryland. To categories TB and normal patients from CXR pictures, a CNN-based transfer learning strategy was utilized using 5 different pre-trained models, including Xception, ResNet50, Inception v3, VGG16, and VGG19. 5 performance metrics were used to assess the accuracy, sensitivity/recall, precision, area under curve (AUC), and F1-score of models for testing datasets. All suggested models offered two-class classification with reasonable accuracy. The precision, sensitivity, F1-score, accuracy, and AUC of our suggested CNN architecture (ConvNet), which was 87.0% lower than the pre-trained models, were all slightly higher.

The best automatic TB classification performance was achieved by Exception, ResNet50, and VGG16, with, sensitivity, F1-score, precision and AUC 90.0%, 90.0%, and 91.0%, respectively. [10]

**Research 2:**

The proposed method has been created. KERAS is used to extract image characteristics that will be used as classification attributes. KERAS is a Python-based open-source neural network library that includes the ResNet50 architecture, which will aid in the extraction of image characteristics through arrays. [20]

Three classification methods were used in this study:

1. Support vector machines (SVMs) are supervised learning models with data analysis and pattern recognition algorithms. The data points or data set components that, if removed, would cause the dividing hyperplane to move are known as support vectors. They could therefore be viewed as crucial elements of data gathering. [20]
2. In order to forecast the chance of a dichotomous categorical-dependent variable, or data that can be categorized into one of two potential categories, one uses the machine learning classification process known as logistic regression (LR) (alive or dead, healthy or sick, no or yes, etc.). The logistic model is one of the most significant statistical models for estimating the probability of a particulars event or category, such as failure or success. On the other hand, logistic regression uses a particular quantity of predicted variables that might be either numerical or categorical. Each recognized object or thing in the image will be given a probability value between 0 and 1, up to 1. [20]
3. The third method uses a supervised type machine learning method called nearest neighbors (KNN, K-Neighbors Classifier). Closest neighbor tactics have remained common in practice due to their empirical success throughout time.

The images that were used were preprocessed. Preprocessing is divided into two parts: (1) padding and (2) resizing are both options. After the images have been extracted, both stages produce a matrix with dimensions of 224 by 224 and numbers ranging from 0 to 255 for each input image. In order to give the network a matrix with these dimensions, this method generates a 224 224 image in RGB base 3 channels.

They integrate into the ResNet50 network once they have finished these processes. To ensure that the training set never saw the test images, 80% of the images were used for training and 20% for testing. The accuracy, precision, recall, and F-Measure evaluation metrics for each classification that was made and noted.

These metrics are commonly referred to by their English names in the current state of the art. [20]

**Table 2.2 Joint training and testing results [20]**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Classification | Accuracy | Precision | Recall | F1 Score |
| Support Vector Machine | 0.879 | 0.859 | 0.859 | 0.84 |
| Regression Logistic | 0.808 | 0.818 | 0.808 | 0.79 |
| Classifier for K-neighbors | 0.758 | 0.778 | 0.758 | 0.74 |

**Research 3:**

The Shenzhen Data and the Montgomery County X Ray Dataset are the two most often utilized input datasets for diagnosing tuberculosis. Nonetheless, these datasets have limitations that are inherent in them. These datasets are small in comparison to the size of the training model, requiring more computational memory and time. Google Net and Alex Net are two of the most popular transfer learning models. Furthermore, evaluation with many parameters is error-prone (overfitting). To overcome these problems, a number of enhanced dataset models—including the shufflenetV2 model for tuberculosis diagnosis—have been developed.

This dataset model is more specific, accurate, and faster to predict, thanks to the use of a lightweight neural network. Another limitation is the difficulty in distinguishing multidrug-resistant tuberculosis from other types of tuberculosis. The adoption of an Artificial intelligence - based model trained to identify multidrug-resistant TB early on is therefore required. Transfer learning was used to create a ResNeXt 50 CNN classifier that can distinguish between MDR-TB and DS-TB. ResNet 50 is a highly modular image classification Convolutional neural network model with Fifty hidden deep layers. [19]

A two-stage classification method (TSCM) was developed using the CNN model to classify tuberculosis culture. On the non-negative class, the model improved recall and precision by 98% and 99%, indicating successful detection of cultural anomalies. The input image's features were extracted using a range of pre-train Convolutional networks, notably Mobile Net, ResNet, Xception, Efficient Net, and Inception. A straightforward, quicker, and highly accurate CNN model that is simple to set up in mobile devices was suggested as a solution to the overfitting problem. The model had an 86% accuracy rate and detected tuberculosis using a grad-CAM visualization technique.

Similar to this, a deep learning model based on segmentation, image data augmentation, picture preposing followed by DL classification algorithms, was presented to accurately diagnose TB from CXR images. Transfer learning was used in pre-trained deep CNN models to distinguish between non-TB and TB cases. Furthermore, the Score-CAM visualization method was used to demonstrate the fact that models learn from the segmented lung areas and produce tuberculosis diagnosis results with high precision, accuracy, and sensitivity, namely 97.34%, 97.07%, and 97.07%, respectively. [19]

**Research 4:**

I used unidentified x-ray chest images from the following two places: First is the Set from Hospital of Shenzhen, second Montgomery Collection There are a sum of 662 X-Rays in the Shenzhen Dataset. A total 326 normal images and 336 abnormal images among them. There are 138 CXRs in the Montgomery Country X-ray Set. There are 80 normal x-ray images and 58 abnormal x ray images [14]. Each image has three color channels.

The Montgomery X-ray Set has images that are 4892\*4020 in size. However, the sizes of the photos from the Shenzhen X-ray Set differ. [23]

All images have been scaled down to 224\*224. The images were then normalized by dividing all pixel values by 255, which is the highest pixel value, to effectively reduce the pixel range while preserving the relative difference between them. We only had 800 records after combining two datasets. As a result, we only tested our model with 15% of the data. So, 680 images were chosen at random to train our model, as well as the remaining 120 images were used to test the trained model. Because we only have 680 pieces of training data, which makes the training process of our model becomes difficult.

Once the special data has been set aside for model testing, data was augmented to constructively train the current model. Data augmentation is a reliable method for increasing the accuracy of data classification. We obtained a total of 3020 images after the augmentation, 1530 of which are infection free and 1490 of which are abnormal x-rays. The table below shows the in-depth information of data arrangement. [23]

**Table 2.3 VALIDATION AND TRAINING IMAGE DISTRIBUTION AFTER AND BEFORE DATA AUGMENTATION [23]**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Class | Before Data Augmentation | Before Data Augmentation | After Data Augmentation | After Data Augmentation |
|  | Set of Training | Set Of Validation | Set of Training | Set Of Validation |
| Normal | 345 | 61 | 1530 | 61 |
| Tuberculosis | 335 | 59 | 1490 | 59 |
| Total | 680 | 120 | 3020 | 120 |

[23]

Dense Net 169, Mobile Net, Xception, InceptionV3, and pre-trained architectures were the four models we employed for our comparison. Using the Keras TensorFlow Application Programming Interface, the models were created [21]. In all of the models, GlobalAveragePooling2D, Batch Normalization, Dropout, Dense layers with ‘sigmoid' activation functions were used. The Adam optimizer which has a learning rate of 0.0001 is used. With help of a training set, each model was trained over 90 epochs. The train batch size has been set to ten, along with batch size of validation. As the loss function, binary cross-entropy is chosen. The accuracy metric is used to assess overall model performance. The model is evaluated by calculating the average of F1-score, Recall, AUC as well as Precision. [23]

**PERFORMANCE REPORT Table 2.4**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Model | Class | Precision | Recall | F1-Score | Support | Validation Accuracy |
| DenseNet169 | Normal | 0.90 | 0.93 | 0.92 | 61 | 0.916 |
| DenseNet169 | Tuberculosis | 0.93 | 0.90 | 0.91 | 59 | 0.916 |
| DenseNet169 | Average | 0.92 | 0.92 | 0.92 | 120 | 0.916 |
| Mobile Net | Normal | 0.95 | 0.85 | 0.90 | 61 | 0.899 |
| Mobile Net | Tuberculosis | 0.86 | 0.95 | 0.90 | 59 | 0.899 |
| Mobile Net | Average | 0.90 | 0.90 | 0.90 | 120 | 0.899 |
| XCeption | Normal | 0.88 | 0.85 | 0.87 | 61 | 0.871 |
| XCeption | Tuberculosis | 0.85 | 0.88 | 0.87 | 59 | 0.871 |
| XCeption | Average | 0.87 | 0.87 | 0.87 | 120 | 0.871 |
| Inception V3 | Normal | 0.89 | 0.92 | 0.90 | 61 | 0.899 |
| Inception V3 | Tuberculosis | 0.91 | 0.88 | 0.90 | 59 | 0.899 |
| Inception V3 | Average | 0.90 | 0.90 | 0.90 | 120 | 0.899 |

[23]

According to the table above, DenseNet-169 is the best model for training the data set. The accuracy of the DenseNet-169 validation is 91.67%. The lowest accuracy which is obtained using the Xception architecture from the validation set comes as 87.08%. Although both InceptionV3 and Mobile Net provided 90% accuracy for dataset, however, their precision and recall values were different. The AUC for Mobile Net and Inception-v3 architecture was 0.907.

The Area Under Curve for the Xception architecture was 0.879, while the AUC for DenseNet-169 was 0.915. The classifier in Dense Net makes use of feature maps at various levels. It contributes to more even decision boundaries in general. This is one of the primary reasons that dense networks perform well when data is scarce. The detailed results obtained with DenseNet-169 are discussed because it performed the best of the four architectures.[23]

**Research 5:**

The dataset used in this study is a collection of publicly available chest radiographs or X-rays created by a team of Qatar University researchers in Doha, Qatar, and the University of Dhaka in Bangladesh, along with Malaysian collaborators and medical doctors from Hamad Medical Corporation and Bangladesh. Both normal and abnormal chest radiographs with TB manifestations are included in the datasets. The dataset includes 700 TB images as well as 3500 normal images. [26]

The models used here are InceptionV-3, VGG-19, ResNet50, and XCeption.

Despite the fact that models like InceptionV3, ResNet50, and Xception produced nearly identical accuracy, ResNet50 outperformed others in terms of time consumption, loss rate, and accuracy (98%). We used 3360 images for training and the remaining images for validation and testing for each model. Sensitivity=0.93, Specificity=0.89 [26]

**Research 6:**

The Shenzhen Public Dataset served as the basis for each experiment conducted for this study [34]. The Guangdong, China-based Shenzhen Hospital collected the Shenzhen data set. 662 frontal CXR are included in the sample, 336 of which have tuberculosis and 326 do not. The resolution of each image is roughly 3K pixels. [27]

Since the input is a grayscale image, we will utilize a height, width, and depth pixel array (e.g., 224 224 1). Models from ResNet-18, ResNet-50, and EfficientNet-B4 were applied in the transfer learning experiment.

**Table 2.5 Parameter Used in the Training Stage**

|  |  |  |
| --- | --- | --- |
| Parameter | ResNet | EfficientNet-B4 |
| Batch Size | 6 | 2 |
| Num of workers | 10 | 10 |
| Max Epoch | 10 | 10 |
| Learning Rate | 0.01 | 0.01 |
| Learning Rate Decay | 0.5 | 0.5 |
| Learning Rate Step Size | 3 | 3 |
| Weight Decay | 1 \* 10^-5 | 1 \* 10^-5 |
| Crop Scale | 3.5 | 3.5 |
| Image Size | 224 | 224 |

The pre-trained EfficientNet-B4 model can generate more stable outcomes in enhanced images when employing the HEF and UM approaches. The result accuracy of the pre-trained EfficientNet-B4 is 89.92. [27]

**Research 7:**

In our experiments, we used three publicly available datasets courtesy of the NLM which stands for National Library of Medicine, the National Institute of health, ChestX-ray14, Montgomery, Maryland, and Shenzhen, China. Sets of external tests from Montgomery and Shenzhen were used to assess the efficacy of our models. [28]

Three models—ResNet152, Inception-ResNet, and DenseNet121—were applied. Internal ChestX-ray14, the Montgomery testing dataset, and the Shenzhen testing dataset show that DenseNet121 has the greatest AUC, followed by 0.9139 and 0.9384 respectively. [28]

**Table 2.6 Three separate testing sets' AUC results**

|  |  |  |  |
| --- | --- | --- | --- |
| trained model before | 14th Internal Chest X-ray | Montgomery | Shenzhen |
| ResNet152 | 0.8675 | 0.7002 | 0.7496 |
| Inception-ResNet | 0.9606 | 0.8552 | 0.9179 |
| DenseNet121 | 0.9872 | 0.9139 | 0.9384 |

**Research 8:**

In our study, we used the "China-Shenzhen set Chest X-ray Database," "Montgomery County Chest X-ray Database," and "NIH Chest X-ray Dataset of 14 Common Thorax Diseases" datasets [3,9,13]. The model used in this case is ResNet 50. The training-to-validation ratio was kept at the widely accepted 80:20 percent. Dropout is 0.25, image batch size is 16, image size is 299\*299, learning rate is 0.01 and the last fully connected layers were trained over three epochs (FCL). The specificity is 90% and the sensitivity is 95%. The accuracy of the model is 94.8%. [29]

**Research 9:**

The Montgomery along with Shenzhen datasets [5,] the Shenzhen Dataset [5,], and the NIH-14 dataset [6] are examples of hospital-scale datasets. Additionally, we go over benchmarks for the classification and localization of typical thoracic illnesses under inadequate supervision along with data of chest x-rays. Several tried-and-true architectures that serve as the basis are VGG16, VGG19, DenseNet-121, ResNet-50, and Inception ResNet. The models undergo 100 iterations of training after being given ImageNet weights as initialization. [30]

**Table 2.7 VARIOUS ARCHITECTURES AUCS**

|  |  |  |  |
| --- | --- | --- | --- |
| Model | Initialized Weights | Shenzhen AUC | Montgomery AUC |
| ResNet-50 | ImageNet | 0.99 | 0.70 |
| VGG-16 | ImageNet | 0.50 | 0.50 |
| VGG-19 | ImageNet | 0.50 | 0.50 |
| Inception ResNetV2 | ImageNet | 0.99 | 0.80 |
| Dense Net | ImageNet | 0.99 | 0.80 |

# **2.1.2 Hybrid techniques in literature:**

This research is distinctive in that it pulls characteristics from deep learning models and combines them with texture, form, and geometry features retrieved by DWT, GLCM, and LBP algorithms before categorizing them using hybrid techniques for precise and successful tuberculosis diagnosis. We will look at several studies that use deep learning to diagnose tuberculosis in this section. On a different dataset, Seelwan et al. presented and evaluated a Deep convolutional neural model for classifying chest X-rays. They discovered that deep learning algorithms do not perform consistently when applied to diverse datasets after being constructed on a training dataset.

The fact that this technology has been developed is an advantage; The drawback is that it is limited to one dataset and cannot be used to another. Three machine learning algorithms were created by Rubinder et al. [10] utilizing data from numerous hospitals in Punjab, India, to predict tuberculosis. With a 95% accuracy rate, the decision tree had the best performance when diagnosing tuberculosis. This method has the advantage of using many classification algorithms, but all approaches have the drawback of relying only on machine learning. The Haar and LBP approaches were used by Ram et al. [11] to extract features from chest X-ray images in order to create a ResNet model to diagnose tuberculosis.

A pipeline built on intuitive characteristics was utilized to enhance the dataset. An SVM technique was suggested by Zhiheng et al. [12] to discriminate between lung disease and pulmonary tuberculosis. Based on these identifying characteristics, the system classifies the photos. With an accuracy of 85percent and a sensitivity of 88%, the algorithm's performance indicates that bronchiectasis can be utilized to identify two crucial traits. This technique has the advantage of extracting representative features; however, it does not achieve satisfactory accuracy. Olfa et al[13] .'s enhanced SVM algorithms for categorizing chest X-rays by using texture information derived by the WT technique. The representative traits were chosen by a genetic algorithm.

The SVM algorithm was used to classify the selected features. The advantage of utilizing an algorithm to choose features is a drawback of this method, as it does not evaluate the features on several classifiers. Two detection datasets were used in the development of an Efficient Nets model by Mustapha et al. [14] to identify TB. Five different types of efficient nets were employed, with efficientNet-b4 attaining the best accuracy (92.33%).

While this method can diagnose tuberculosis using many Efficient Nets, it does not do so with great accuracy. Chirath et al [15].'s demonstration of a deep convolutional network for chest X-ray picture optimization, generation, segmentation, and classification made use of a generative adversarial network, with 3 distinct architectures. To enhance diagnostic outcomes, data augmentation and parameter adjustment depending on a genetic algorithm were applied; this approach produced an accuracy of 97.1%.

The two X-ray dataset’s contrast and noise were optimized. In this study, two datasets—the first (Shenzhen) dataset and the second dataset—were used to assess the proposed systems (TB Chest Radiography Database). The first Shenzhen dataset was produced by the US Medicine National Library in association with Shenzhen No. 3 People's Hospital and Guangdong Medical College China. Using a Philips DR Digital Diagnose system, chest X-rays were taken at outpatient clinics in September 2012. 662 PNG chest X-rays are included in the dataset.

Each chest X-ray has a somewhat different dimension, although the standard size of the image is 3000 3000 pixels. Normal X-rays (326) and tuberculosis X-rays (336) were separated from the dataset. The set of data also contains 138 X-ray images from Montgomery County, Maryland, USA's tuberculosis control programme. Blurry spots appear in X-rays with abnormal distortions. Figure 2a depicts a subset of the Shenzhen dataset. Scientists from Qatar University, Doha, and Dhaka University Bangladesh, in cooperation with a group of Hamad Medical Corporation physicians, describe the 2nd dataset, which consists of tuberculosis X-ray data, in this section.

Data from the Republic of Belarus, the National Institute of Allergy and Infectious Diseases (NIAID), the US National Library of Medicine (NLM), and the NIAID website were used to create the dataset. 4200 chest X-rays in PNG format with a resolution of 512 512 pixels are included in the dataset. The information was split into 3500 regular X-rays and 700 X-rays for tuberculosis. In this work, data preprocessing was utilized to modify the average grayscale and color scaling for all chest X-rays. The contrast of chest X-rays was enhanced using the contrast limited adaptive histogram equalization (CLAHE) technique.

On chest X-rays, the CLAHE enhances the visibility of edges and local contrast by ensuring a uniform distribution of light values. The derivative of the transformation function based on nearby pixels transforms each central pixel. Depending on the contrast of the image, the number of adjacent pixels is altered. When the central (target) pixel is smaller than the surrounding pixels, the image is improved and the contrast is increased; when the central pixel is larger than the surrounding pixels, the image is deteriorated and the contrast is decreased.

As a result, the resulting pixels are proportional to their neighbors, resulting in better images.

This section offers a novel approach for classifying X-ray pictures using an ANN in order to diagnose tuberculosis utilizing characteristics taken from deep learning models (ResNet-50 and Google Net) and methods (GLCM, DWT, and LBP) [40]. The steps for implementing the suggested method are as follows: The ResNet-50 and Google Net models receive the improved X-ray images first. These models employ convolutional, pooling, and auxiliary layers to extract deep features.

ResNet-50 and Google Net produce 2048 deep features, which are stored in 662 2048 feature vectors in the first dataset and 4200 2048 feature vectors in the second.

The two datasets are then reduced in size while preserving the most crucial properties using the PCA technique. Following PCA, the first dataset's feature size is 662 512, and the second dataset's feature size is 4200 512.

The texture and shape features are then extracted using the DWT, LBP and GLCM algorithms. In order to extract texture features from a grey level matrix, the gray level co - occurrence algorithm represents the region of interest in the matrix. The algorithm distinguishes between smooth and coarse regions because they have almost similar pixel values, whereas smooth and coarse regions have very different pixel values.

By collecting spatial data, the algorithm produces 13 statistical measures. Chest X-ray pictures from two datasets were used to evaluate the suggested systems in this study in order to meet the study's objectives. First dataset (Shenzhen) includes 662 chest X-rays with tuberculosis (326) and normal (326) classifications (326). (336). The second dataset is made up of 4200 chest X-rays, which are separated into 3,500 normal X-rays and 700 X-rays for tuberculosis. The two datasets were split in half, with 20% being used to test the suggested systems and 80percent being utilized for training and validation. [11]

**Table 2.8 Splitting the two X-ray datasets for TB.[11]**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Datasets | First Dataset | First Dataset | First Dataset | Second Dataset | Second Dataset | Second Dataset |
| Phase | Training and Validation | Training and Validation | Training and Validation | Training and Validation | Training and Validation | Training and Validation |
| Classes | Training (80%) | Validation (20%) | Testing (20%) | Training (80%) | Validation (20%) | Testing (20%) |
| Normal | 209 | 52 | 65 | 2240 | 560 | 700 |
| Tuberculosis | 215 | 54 | 67 | 448 | 112 | 140 |

**Table 2.9 Results of the performance of hybrid systems on the two tuberculosis datasets. [11]**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Datasets | First Dataset | First Dataset | Second Dataset | Second Dataset |
| Measure | ResNet50 + SVM | Google Net + SVM | ResNet50 + SVM | Google Net + SVM |
| Accuracy % | 95.5 | 97 | 98.1 | 97.1 |
| Sensitivity | 96.14 | 97.21 | 95.52 | 95 |
| Precision % | 95.72 | 97.45 | 97.11 | 94.5 |
| Specificity % | 95.84 | 97.38 | 95.61 | 94.85 |
| AUC % | 97.28 | 98.13 | 98.43 | 97.63 |

# **2.3 Summary:**

In this chapter, we discussed several research papers, which methods they used for building machine learning models to detect Tuberculosis, how they preprocessed data, what kind of evaluation Metrix they used to evaluate their models etc. as well as using hybrid techniques for making a tuberculosis detection model.

# **Chapter 3:**

# **Research Methodology:**

# **3.1 Dataset Details:**

In collaboration with medical doctors from Hamad Medical Corporation and Bangladesh, a team of researchers from Qatar University, Doha, Qatar, and the University of Dhaka, Bangladesh, as well as collaborators from Malaysia, have created a database of chest X-ray images for Tuberculosis (TB) positive cases as well as normal images. In the current release, there are 700 publicly accessible TB images, 2800 TB images that can be downloaded from the NIAID TB portal by signing an agreement, and 3500 normal images. [12]

# **3.2 Data Preprocessing:**

# The data was divided into training, testing, and validation datasets in the ratio of 8:1:1 using a split folder. Each training, testing, and validation folder contains two folders: Normal and Tuberculosis Images.

# **3.3 Data Transformation:**

Using Image Augmentation, I artificially increased the size of the image training dataset.

*Image Augmentation increases the size of the dataset by creating a modified version of the existing training set images, which increases dataset variation and, as a result, improves the model's ability to predict new images.*

I created an Image Data Generator for the Train Set that randomly applies defined parameters to the train set using the tensor flow. keras. preprocessing. image library, and for the Test & Validation set, I am simply rescaling them to avoid manipulating the test data beforehand. Due to the varying sizes of the input images, the image height and width were both set to 500 \* 500 pixels. There will be sixteen in the batch.

It has been claimed that adding more data to deep learning systems can increase their classification accuracy. The number of samples in training datasets can also be greatly increased via data augmentation. [13]

Shear and zoom ranges are both set to 0.2, and horizontal flip is set to TRUE. Convolutional layers are viewed as the essential component of CNN. Convolution is used in CNNs as opposed to conventional matrix multiplication. Instead of standard matrix multiplication, CNNs use convolution. Kernels are used in convolutional layers to extract particular information from an input image. A well-liked activation layer for deep learning is the rectified linear unit (ReLU). ReLU is used in this scenario. In order to reduce the spatial scale of the input data, a pooling or down sampling layer may be added after the convolutional layer. This reduces the quantity of parameters in the network. The most popular pooling method is called Max Pooling. Other pooling strategies include L2-norm pooling and average pooling.

**3.4 Modelling:**

The model is made up of 5 Convolutional 2D layers (3 of which extract 32 features and the other two extract 64 features, with all 5 activation layers activating as 'relu'), 5 Max-Pooling Layers with pooling size of (2,2). After Flattening the last layer, 3 Dense Layers are activated with activation as 'relu', with units 128, 64, 1units.

The input image has a size of 500 500 pixels. Our model is made up of five different blocks. In the first block, a single convolutional layer with 32 filters in a ReLU activation function and three dimensions was employed. After that, we down sampled using a Max Pooling layer which had a pool size of (2, 2). This factor was utilized to shrink the size of the images, minimizing model requirements while maintaining image quality. Alternating the second as well as third blocks is possible. The fourth as well as fifth blocks, however, employed 64 filters of size 3\*3.

The third block recovered tensor was converted into a one-dimensional vector using a flatten layer. Following that, three dense layers with 128,64, and 1 node or neurons, as well as a ReLU activation function, were used. In this problem, the classification model produced a two-class classification.

This study made use of datasets containing TB CXR images. After splitting and pre-processing the dataset, training was conducted using image augmentation techniques. As a result of data augmentation, over-fitting is avoided.

# We trained the suggested models with the Adam optimizer and categorical cross-entropy loss function to reduce the dimension of the retrieved features. For training, the following solver parameters were used: epoch of 25, minimum learning rate of 0.00001, batch size of 16.

# **3.5 Evaluation Metrics:**

Accuracy, recall, precision, f1 score, sensitivity, and specificity were used to evaluate the model.

Accuracy = (TP + TN)

(TP + FP + TN + FN)

Recall = (TP)

(TP+FN)

Precision = (TP)

(TP+FP)

F1 – score = 2 \* (Precision \* Recall)

Precision \* Recall

My model has the following statistics:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | precision | recall | F1-score | Support |
| NORMAL | 0.96 | 0.98 | 0.97 | 350 |
| TUBERCULOSIS | 0.90 | 0.77 | 0.83 | 70 |
| Accuracy |  |  | 0.95 | 420 |
| Marco avg | 0.93 | 0.88 | 0.90 | 420 |
| Weighted avg | 0.95 | 0.95 | 0.95 | 420 |

Below is the confusion Matrix of My Model

Actual Normal

|  |  |
| --- | --- |
| 344 | 6 |
| 16 | 54 |

Actual Tuberculosis

Predicted Normal Predicted Tuberculosis

Sensitivity = TP

(TP + FN)

Specificity = TN

(FP + TN)

Sensitivity of my model is: 0.95

Specificity of my model is: 0.90

Accuracy of my model is: 0.94

Both sensitivity and specificity are above the WHO standards of having at least 90% sensitivity and at least 70% specificity.

# **3.6 Summary:**

In this chapter, I have managed to make a model that has a sensitivity of 95%, specificity of 90%. My model’s precision in predicting Normal is 0.96 and it is 0.90 in Predicting Tuberculosis. The recall for normal is 0.98 and 0.77 in case of Tuberculosis. The f1-score for Normal is 0.97 and 0.83 for Tuberculosis. The support for Normal is 350 and 70 for Tuberculosis.

# **Chapter 4:**

# **Experimentation and results**

## **4.1 Modified Machine Learning Technique:**

### **4.1.1 Hyperparameter Tuning:**

In this case, I have added a Batch-Normalization layer along with Dropout layer to my CNN model. Batch Normalization – commonly abbreviated as Batch Norm – is one of these methods. Currently, it is a widely used technique in the field of Deep Learning. It improves the learning speed of Neural Networks and provides regularization, avoiding overfitting. **Batch Norm is a normalization technique done between the layers of a Neural Network instead of in the raw data.** It is done along mini-batches instead of the full data set. It serves to speed up training and use higher learning rates, making learning easier.

**Batch Norm reduces the internal covariate shift of the network.** The internal covariate shift is a change in the input distribution of an internal layer of a Neural Network. For the neurons in an internal layer, the inputs received (from the previous layer) are constantly changing. This is due to the multiple computations done before it and the weights over the training process.

Applying Batch Norm ensures that the mean and standard deviation of the layer inputs will always remain the same;  and , respectively. Thus, the amount of change in the distribution of the input of layers is reduced. The deeper layers have a more robust ground on what the input values are going to be, which helps during the learning process.

Lastly, it seems that **Batch Norm has a regularization effect**.  Because it is computed over mini-batches and not the entire data set, the model’s data distribution sees each time has some noise. This can act as a regularizer, which can help overcome overfitting and help learn better. However, the noise added is quite small. Thus, it generally is not enough to properly regularize on its own and is normally used along with Dropout.

**The Dropout layer is a mask that nullifies the contribution of some neurons towards the next layer and leaves unmodified all others.** We can apply a Dropout layer to the input vector, in which case it nullifies some of its features; but we can also apply it to a hidden layer, in which case it nullifies some hidden neurons.

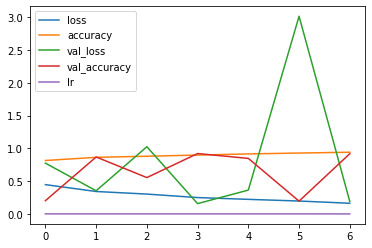
Dropout layers are important in training CNNs because they prevent overfitting on the training data. If they aren’t present, the first batch of training samples influences the learning in a disproportionately high manner.

I have added a Dropout with parameter of 0.3 alongside Batch Normalization.

I have achieved a Sensitivity of 94% and a Specificity of 82%, both parameters surpass the WHO guidelines of having greater than or equal to 90% Sensitivity and having greater than or equal to 70% Specificity. [32] [33]

### **4.1.2 Convergence Graphs:**

Below are the convergence graphs of modifications done through Hyperparameter tuning



As seen above, the validation accuracy after rising rapidly, ends up having a steep decline.

The Accuracy of the model has a not so steep increase.

The loss decrease as the model training approaches its end.

The learning rate just like the accuracy of the model has a not so steep increase.

### **4.1.3 Outputs - Classification Report:**

The Output of the Model with Modified Parameters are:

Sensitivity = 94 %

Specificity = 82%

## **4.2 Modified Transfer Learning Technique:**

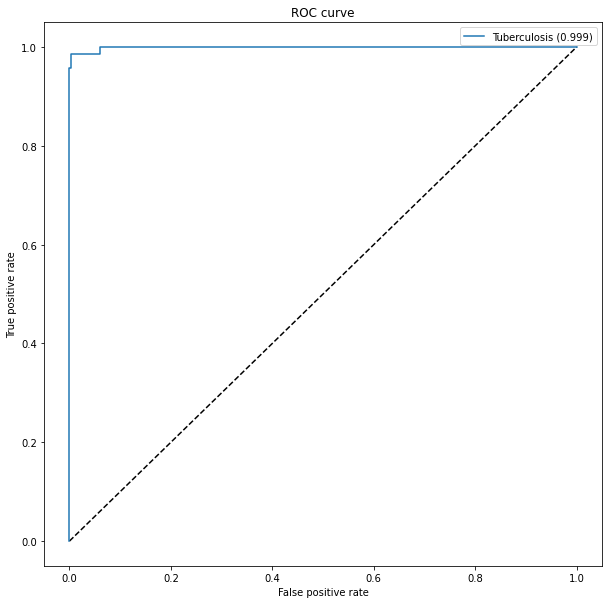
### **4.2.1 Hyperparameter Tuning:**

Many transfer learning models were successful in terms of predicting Tuberculosis with Deep Learning. The most effective model in terms of predicting Tuberculosis as well as fitting the WHO guidelines is the transfer learning method of XCeption.

A Global Average Pooling Layer alongside a Dense Layer with activation type sigmoid was added into it thus putting the last layer as false. The Area Under Curve was 0.995. The accuracy of the model was calculated as 94%. It achieved a sensitivity of 97% and a specificity of 100%.

### **4.2.2 Convergence Graphs:**

Below is the Area Under Curve of the XCeption model is 0.99 as shown below



### **4.2.3 Outputs - Classification Report:**

I achieved a sensitivity of 97 % and a specificity of 100%.

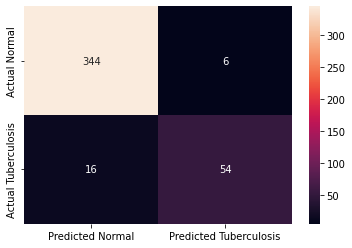
The accuracy of the model is 97%

## **4.3 Comparison with SOTA:**

My model achieved an accuracy of 94.76% and a sensitivity of 98.28% and a specificity of 77.14% which exceeds ResNet50(sensitivity 93.11%, specificity 93.16%, accuracy 93.11%), Inception V3(sensitivity 95.73%, specificity 95.92%, 95.72% accuracy), DenseNet-201 (sensitivity 95.07, specificity 95.12, accuracy 95.07%), ResNet-101 (sensitivity 94.55%, specificity 94.59%, accuracy 94.55%), ResNet-18(sensitivity 93.85%, specificity 93.91%, accuracy 93.85%).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | My model | ResNet-50 | ResNet-101 | ResNet-18 | DenseNet-201 | Inception V3 |
| Accuracy | 94.76% | 93.11% | 94.55% | 93.85% | 95.07% | 95.72% |
| Sensitivity | 98.28% | 93.11% | 94.55% | 93.85% | 95.07% | 95.73% |
| Specificity | 77.14% | 93.16% | 94.59% | 93.91% | 95.12% | 95.92% |
| Precision | 95.55% | 93.4% | 94.74% | 94.08% | 95.27% | 95.92% |
| F1-Score | 96.47% | 93.09% | 94.54% | 93.84% | 95.07% | 95.73% |

**Confusion Matrix:**



## **4.4 Summary:**

In this module we discussed how I modified my machine learning technique to improve my model in some ways as well as use transfer learning to achieve different results as well as comparing my model to some of the best models used in Tuberculosis Detection.

# **Chapter 5**

# **Conclusion and Future Scope:**

## **5.1 Conclusion and Discussion:**

I have come to the conclusion that the models I have made either with hyperparameter tuning or with transfer learning are of great use. Either of them can work incredibly depending on what the person is looking for. For example, if the aim is to get more accurate prediction on patients who are Normal then then model (without hyperparameter tuning) which achieved a sensitivity of 98% would be the best pick. If the aim is to get more accurate prediction on specificity, then the XCeption model would be the best pick.

## **5.2 Contribution to Knowledge:**

I made a CNN model with 4 pairs of Convolutional Layers alongside Max-pooling. I made the decision to insert Early Stopping so that my model would stop training if the loss would increase after 3 epochs, otherwise training would be extremely time consuming and the model trained would be highly insufficient. The learning rate would change and adjust itself if the learning has stopped improving.

## **5.3 Future Scope:**

In my opinion, given the fact that Artificial Intelligence and Machine Learning is such a fast growing and innovative field, the improvements would help doctors immensely in detection and cure of Tuberculosis and other diseases such as pneumonia, arthritis etc.

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