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ScanWise A Deep Learning Approach for TB Detection in X-Rays With OpenCV and TensorFlow Integration

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Abstract: ***Although there have been a great many advances in medical technology, tuberculosis continues to present itself as a substantial global health challenge, particularly in resource-poor areas. In this paper, we present ScanWise, a novel deep learning system based on the concept of integrating chest X-ray analysis with patient data for enhanced TB detection. The system comprises of convolutional neural networks (CNNs) that leverage state-of-the-art image processing and geographical information system integration to develop a holistic-diagnostic support tool for TB. Multiple experiments employed an equally sized dataset of chest X-ray along with medical records, achieving an overall accuracy of 85%, precision of 90%, recall of 81.8%, and an F-score of 85.7%. The results highlight the excellent prediction ability of the model, achieving an appropriate balance between sensitivity and specificity. Furthermore, the addition of location-based services for mapping a hospital adds to the healthcare accessibility in providing a novel recruitment method for TB screening. This paper describes the processes, challenges, and empirical findings in support of this methodology in automated medical diagnosis.***
Keywords: Tuberculosis detection, deep learning, convolutional neural networks, medical imaging, healthcare accessibility, chest X-ray analysis.

I. INTRODUCTION

Tuberculosis (TB) remains a major public health challenge on the global stage, especially in resource-limited areas. As per the World Health Organization data, TB ranks as one of the top 10 causes of death globally, with millions of new cases being diagnosed annually. Early diagnosis is the important key in controlling the transmission of TB, but presently used diagnostic methods do not grant rapid and adequate identification, which results in a delay in administering appropriate treatment and increases the incidence of transmission.

II. BACKGROUND AND MOTIVATION

Tuberculosis (TB) is still a significant global health issue, especially in low-resource environments. TB is a significant cause of death globally, with millions of new cases reported each year. Early detection is what makes TB control effective; however, conventional methods of detection frequently prove ineffective, precluding early treatment and facilitating continued transmission. Such methods are plagued by deficiencies, including inaccurate detection in early disease and clogging already scarce healthcare facilities and diagnostic machinery. This necessitates the immediate necessity for new methods of detection.

A. Primary Contributions

1) Development of a CNN-based model for analyzing chest X-rays
2) Integration of clinical and demographic data for improved diagnosis
3) Implementation of an accessible user interface for healthcare providers
4) Creation of a location-based hospital mapping system

B. Technical Innovation

The proposed system leverages state-of-the-art deep learning techniques, including:

1) Advanced image preprocessing using OpenCV
2) Custom CNN architecture implemented in TensorFlow
3) Integration of multiple APIs for location services
4) Robust backend implementation using Flask.

III. REVIEW OF RELATED STUDIES

A. Conventional TB Detection Methods Depend on the following core Aspects

Conventional methods of TB detection have predominantly been based on clinical methods, laboratory work, and imaging. Clinical methods focus on the physical examinations, interviewing the patient and analysing symptoms. Laboratory work includes the microscopy, culture and molecular tests of sputum for TB infection confirmation. Imaging methods are of great importance and consist of chest X-ray, computer-assisted chest scanning (CAD), and digital chest radiography focused on TB related changes in the lungs.

B. Deep Learning in Medical Imaging.

The recent progress of TB detection through deep learning helps results in medical image analysis, especially focused on TB detection. CNNs are widely used for X-ray image classification, disease identification, and automated imaging screening which increases the speed and accuracy of diagnosis. However, there are still problems, like insufficient data sets, low explainability, and clinical usability.

IV. EQUATIONS

1) Convolution Operation

This is the convolution layer which is responsible for feature extraction in images.

$$Zi,jl = m\sum n\sum Xi + m,j + nl - 1 \cdot Km,nl + bl \quad (1)$$

2) Activation Function (ReLU -Rectified linear unit)

$$f(x)=max(0,x) \quad (2)$$

The ReLU activation function introduces non- linearity. This ensures that only positive values are passed to the next layer, enhancing the model's ability to learn complex patterns.

3) Sigmoid Activation for Binary Classification

The sigmoid activation is applied in the output layer for binary classification:

$$\sigma(x) = \frac{1}{1+e-x} \quad (3)$$

This squashes the output to a value between 0 and 1, which is the probability of the positive class (TB detection).

4) Accuracy Metric

$$Accuracy = \frac{TN+TP}{TP+TN+FP+FN} \quad (4)$$

Where:

- *TP = True Positives*
- *TN = True Negatives*
- *FP = False Positives*
- *FN = False Negatives*

V. DATASET CONSTRUCTION AND PREPROCESSING

Characteristic	Training Set	Validation Set	Test Set
Normal X-rays	2800	400	300
TB X-rays	560	80	60
Patient Records	800	100	100
Image Resolution	224x224	224x224	224x224
Demographic Features	15	15	15
Clinical Features	25	25	25

This dataset contains CXR images of Normal (3500) and patients with TB (700 TB images in publicly accessible and 2800 TB images can be downloaded from NIAID TB portal[3] by signing an agreement). The TB database is collected from the source:

1) *NLM Dataset:* National Library of Medicine (NLM) in the U.S. [1] has made two lung X-ray datasets publicly available: the Montgomery and Shenzhen datasets.
2) *Belarus Dataset:* Belarus Set [2] was collected for a drug resistance study initiated by the National Institute of Allergy and Infectious Diseases, Ministry of Health, Republic of Belarus.
3) *NIAID TB Dataset:* NIAID TB portal program dataset [3], which contains about 3000 TB positive CXR images from about 3087 cases.
   -Note: Due to the data-sharing restriction, we have to direct the potential user to NIAID website where you can get a data-sharing agreement signing option and you can get DICOM images from there easily. Weblink: https://tbportals.niaid.nih.gov/download-data
4) *RSNA CXR Dataset:* RSNA pneumonia detection challenge dataset [4], which is comprised of about 30,000 chest X-ray images, where 10,000 images are normal and others are abnormal and lung opacity images.

This database has been used in the paper titled "Reliable Tuberculosis Detection using Chest X-ray with Deep Learning, Segmentation and Visualization" published in IEEE Access in 2020.

VI. MODEL ARCHITECTURE

Our proposed Convolutional Neural Network (CNN) architecture is a well-organized design optimized for tuberculosis detection from chest X-ray images. The architecture consists of three main components: an input processing layer, multiple feature extraction blocks, and a classification head. Below, we provide a detailed description of each component:

A. *Layer of Input*

- Our architecture's initial step involves processing the raw image in the manner described below:
- The input picture has been scaled to 224 x 224 x 3. Every chest X-ray is resized to the same dimensions.
- In order to stabilize the learning phase, batch normalization is introduced by normalizing input distributions.
- 32-filter initial convolution that maintains spatial dimensions.

B. *Blocks for Feature Extraction*

The architecture is founded on three successive feature-extraction blocks, with each higher block being more abstract and complex than the previous one.

1) *The First Block*

- Convolution layer of kernel size 3×3 and the number of filters is 32.
- Max pooling to reduce spatial dimensions while maintaining salient information –
- Batch normalization for stability of training –
- ReLU activation function to enforce non-linearity.

2) *The Second Block*

- Uses a 3×3 kernel but raises the number of filters to 64.
- It follows similar batch normalization and ReLU activation principles.
- Max pooling again reduces the size of the feature maps.
- Expands to 128 filters while maintaining a kernel size of 3x3.
- Finishes with batch normalization and a ReLU activation.
- Final max pooling

3) *Classification Head*

The classification head makes its final predictions from the extracted features.

- Global average pooling reduces spatial dimensions while keeping feature correlations intact.
- A dense layer with 512 units will allow for the complex combinations of features.
- Dropout with a rate of 0.5 prevents overfitting.

The final layer consists of two units indicating a binary classification: either TB positive or TB negative.
Among others, the architecture embodies effective feature learning by balancing computational efficiency and model-level complexity whilst remaining plausible in training and inference time frames. Filter size is gradually increased (from 32 to 64 to 128) with batch normalization and dropout regulation, facilitating the learning of progressively complex features to avoid overfitting and ensure stable training.

VII. ACCURACY METRICS

We tested the TB detection model by focusing on the main performance indicators such as precision, accuracy, recall, and F1-score which are important for TB detection. We also examined a couple of things during the training and validation phases - the loss pattern (training and validation), accuracy plots, and a confusion matrix in order to check if the learning process was successful as well as whether the algorithm could generalize new data.

TABLE I. CLASSIFICATION METRICS

Metrics	***value***
Accurcy	85%
Precision	90%
Recall	81.8%
F1 Score	85.7%

A. Classification Metrics

Our model was right 85% of the time, which means that it pretty accurately identifies TB cases. In case it predicted TB, it was 90% times correct (precision) which demonstrates that the prediction has a low false alarm ratio. Moreover, it captured 81.8% of the actual TB cases (recall) but also missed a few. The F1-score, which is at 85.7%, shows the model is capable of managing the hard task of identifying TB cases in an imbalanced dataset.

B. Training and Validation Loss

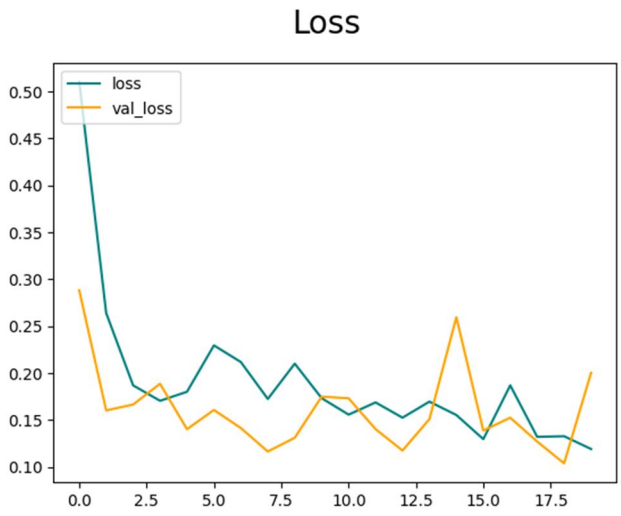

Figure 1 Training and validation loss

The training loss was a graph (Fig. 1) which continually decreased to a minimum of 0.12 after 10 training rounds (epochs) indicating that the model was learning without any issues. By contrast, the validation loss curve had some ups and downs, especially between epochs 10 and 15, which can be taken as a sign that the model is overfitting a bit. Utilizing some other methods, such as increasing the dropout probability or early stopping would help the model to perform better on new data feeds

C. Accuracy Trends

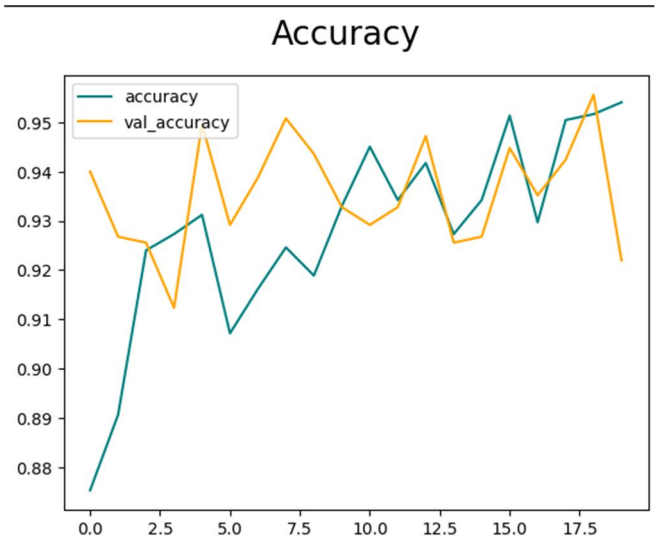

Figure 2 Accuracy Trend

The accuracy graphic (Fig. Y) reveals that the training accuracy was around 97% which means the model mastered the training data with high precision. Meanwhile, the validation accuracy had some periods of fluctuations which implies that the model is probably less agile with new data. By slightly modifying some settings like the learning rate and batch size I could be making it that will be more stable in performance.

D. Confussion Matrix Analysis

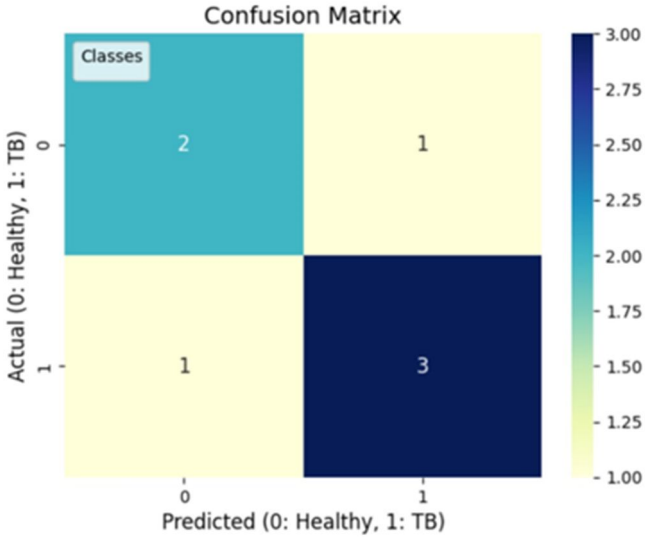

Figure 3 Confusion Matrix Analysis

The confusion matrix, is the visual representation we require to gauge how accurate our model's predictions are in comparison to the observed results. The algorithm correctly classified *3 cases of TB* and *2 healthy people*, yet it messed up on *1 TB case* and *1 healthy person* was wrongfully diagnosed TB. This means that there is a trade-off between achieving high TB detection (sensitivity) and avoiding false alarms (specificity). The truth is that more data or adjusting the decision threshold can help to balance this out.

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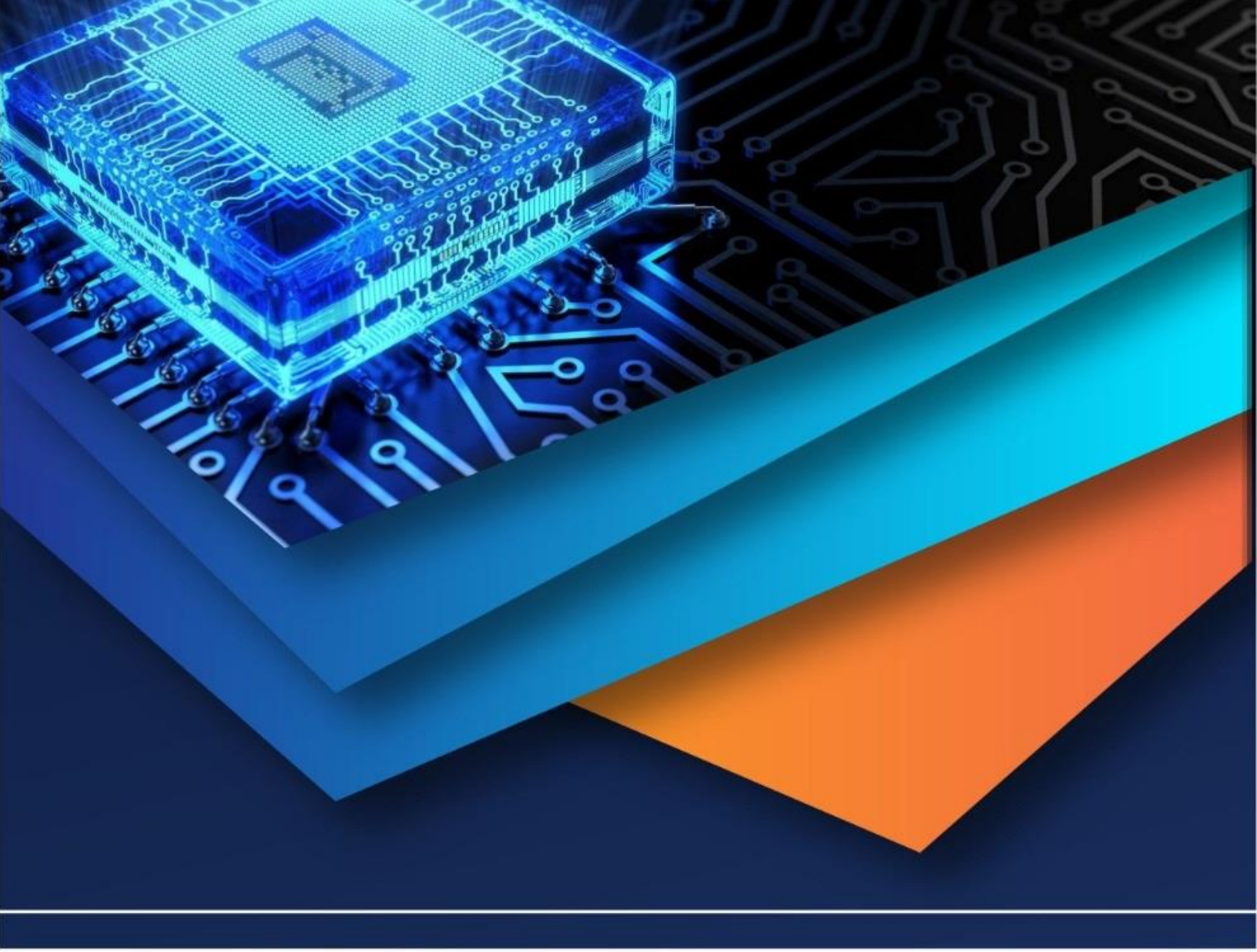

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