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Improved Tuberculosis Detection through Deep Learning

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Abstract

Tuberculosis (TB) is a significant public health challenge worldwide. Early and accurate diagnosis is crucial for effective treatment and containment of the disease. This research work addresses the problem by proposing a multi-model classification method for identifying TB cases from chest X-rays with high accuracy. It utilizes a dataset created from real-time patient data collected from TB hospitals. Additionally, a comparative analysis of two deep learning models is conducted for the accurate detection of TB from chest X-ray images. The models were assessed based on accuracy, precision, recall, and F1-score, with the one unconventional model demonstrating superior performance. This paper discusses the potential reasons for the observed discrepancies, including differences in model architecture, data handling, and training processes. Our findings suggest that the integration of the softmax activation function into binary classification models can have a beneficial impact on training efficiency, leading to improved performance in medical image analysis for Tuberculosis detection. Although softmax is mathematically equivalent to sigmoid in binary tasks, our results indicate a potential advantage in utilizing softmax that warrants further investigation. To further enhance the robustness of our approach, future research will focus on incorporating additional datasets from diverse populations and exploring the integration of ensemble learning techniques, aiming to increase the generalizability and reliability of TB detection in chest X-ray images across varied demographic groups.

Keywords: Deep Learning, Image Analysis, Tuberculosis, X-Ray Analysis.

Introduction

Tuberculosis (TB) remains a significant health issue, particularly in developing countries where it places a substantial burden on healthcare systems. The challenge of diagnosing TB is compounded by the global statistics from the WHO Global Tuberculosis Report 2023, which highlights that 7.5 million people were newly diagnosed with TB in 2022, the highest number recorded since WHO monitoring began in 1995. This high incidence rate, coupled with the fact that approximately 50% of TB patients and their households face catastrophic costs due to the disease, underscores the urgent need for more effective and accessible diagnostic methods (1-3). Furthermore, the burden on healthcare systems is increased by the large number of people undergoing TB testing for visa applications, increasing the demand for efficient and accurate diagnostic procedures (4, 5).

Diagnosing TB traditionally relies on chest X-ray examinations, where experts look for specific signs like lesions, cavities, and other abnormalities indicative of the disease (6, 7). These signs are often subtle and vary widely, making accurate diagnosis challenging without specialized radiological expertise, which may not be readily available in all healthcare settings (8, 9). In this work, tuberculosis detection refers to the automated process of identifying TB from chest X-ray images using deep learning models, which can significantly enhance the speed and accuracy of diagnosis compared to traditional methods (10, 11). The advent of deep learning offers a promising solution for enhancing TB detection by automating the analysis of chest X-ray images, a common and relatively affordable diagnostic tool (12-14). Various studies have underscored the importance of model architecture, data quality, and training strategies in the performance of these models (15-17).

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This study dives into the application of deep learning models for TB detection, focusing on two distinct approaches: one that employs a traditional binary classification using a sigmoid activation function in the output layer, and another that adopts a softmax activation function, typically used for multi-class classification, modified for binary classification. The sigmoid activation function outputs a probability score that describes the likelihood of an input belonging to a particular class, ideal for binary classification tasks. Softmax activation function extends sigmoid, outputting a probability distribution over 'n' different outcomes, and is typically used for multi-class classification. In our study, it's adapted for binary tasks to provide a comparative measure between 'Normal' and 'Tuberculosis' probabilities. We aim to compare these models to determine their effectiveness in identifying TB from X-ray images and discuss the reasons behind their performance. By leveraging a dataset of chest X-ray images verified by medical professionals, our research seeks to ensure the findings are both reliable and applicable in real-world scenarios. The broader impact of this study extends to the field of medical diagnostics, potentially influencing how deep learning models are applied in the detection of various diseases.

Methodology

Data Collection and Preparation

For this work, digital copies of chest X-ray images were obtained from Huma Specialist Hospital and Research Centre. The images used were part of routine diagnostics, and all patient identifiers were removed to maintain confidentiality and comply with ethical standards. The dataset comprised 499 X-ray images, each meticulously classified and labeled by experienced radiologists at the hospital to ensure accuracy in categorization. The images were divided into two distinct categories for this study: 'Normal' and 'Tuberculosis'.

Training set: 247 ‘Normal' images and 62 ‘Tuberculosis' images.

Testing set: 152 'Normal' images and 38 'Tuberculosis' images.

This division and unbalance of data was due to the availability of X-rays as 'Normal' cases are more prevalent than 'Tuberculosis' cases. All images were standardized by resizing to 224x224 pixels and converting to grayscale. This pre-processing was done to maintain consistency across the dataset and ensure compatibility with our convolutional neural network models.

Model Development

Binary classification refers to the task of classifying the elements of a given set into two groups based on a classification rule. In the context of our study, it involves distinguishing between 'Normal' and 'Tuberculosis' classes from chest X-ray images. Two CNN-based deep learning models were created for the binary classification of medical images. Model 1 employs a conventional approach with a sigmoid activation function in the output layer. Model 2 utilizes a softmax activation function in the output layer, a method commonly reserved for multi-class classification. This unconventional application of softmax is tested in binary classification. The utilization of softmax activation in Model 2, traditionally reserved for multi-class classification, offers a distinctive advantage in binary classification scenarios such as tuberculosis detection from chest X-rays. Unlike the sigmoid function that outputs a probability score for a single class, softmax provides a probability distribution across both classes. This is particularly effective in medical imaging where distinguishing between subtle variations is critical. The probabilistic output of softmax allows for a more nuanced interpretation of the X-ray images, potentially increasing the model's sensitivity to tuberculosis features compared to traditional binary classifiers. Both models were trained and validated using an 80-20 split of the dataset.

Evaluation Metrics

To assess the performance of our models, a range of evaluation metrics, including accuracy, precision, recall, and F1-score were compared. These metrics are crucial in medical diagnostic applications, where the cost of false negatives and positives can be significant. The goal was to develop models that not

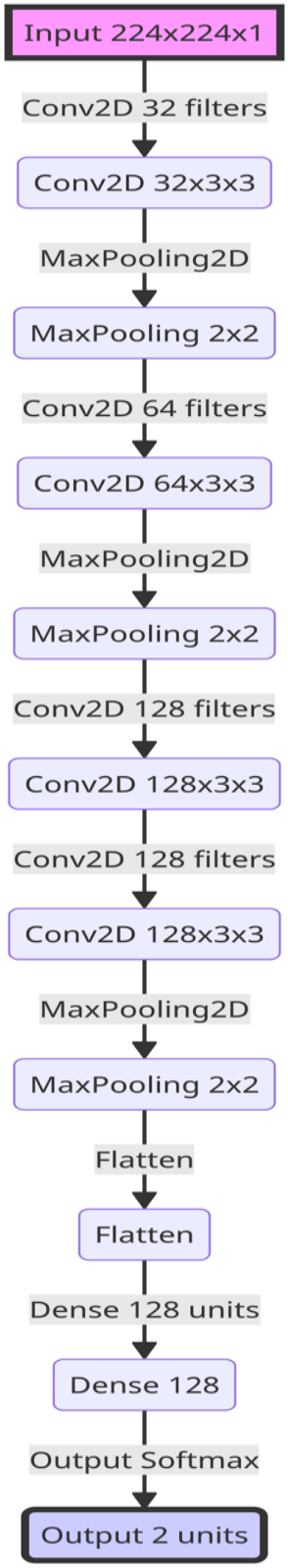

Figure 1: Flow diagram of CNN-based binary classification

only accurately identify TB from chest X-rays but also minimize the rate of misdiagnosis.

Architecture Overview and Algorithm

Common Structure for Both the Models

Input: Both models process single-channel (grayscale) chest X-ray images with a resolution of 224x224 pixels.

Convolutional Base

Layer 1: Features 32 filters of size 3x3 with ReLU activation, followed by a 2x2 max-pooling layer.

Layer 2: Increases to 64 filters of size 3x3 with ReLU activation, followed by another 2x2 max-pooling layer.

Layers 3 and 4: Each applies 128 filters with a 3x3 kernel, using ReLU activation, followed by a final 2x2 max-pooling layer.

Flattening Layer: Converts the 3D feature maps into a 1D feature vector.

Fully Connected Layer: A dense layer with 128 neurons and ReLU activation.

Model 1 - CNN with Sigmoid Activation

Output Layer: Utilizes a single neuron with a sigmoid activation function, outputting a probability score for the 'Tuberculosis' class.

Loss Function: Binary cross-entropy, suitable for binary classification tasks.

Pseudo-code

```
def model_1(input_image):
    x = apply_conv_layers(input_image)
    x = flatten(x)
    x = apply_dense_layer(x)
    output = sigmoid(x)
    return output
```

Model 2 - CNN with Softmax Activation

Output Layer: Features two neurons, each corresponding to one of the classes ('Normal' and 'Tuberculosis'), with a softmax activation function providing a probability distribution over these classes.

Loss Function: Categorical cross-entropy, typically used for multi-class classification but applied here in a binary setting.

Pseudo-code

```
def model_2(input_image):
  x = apply_conv_layers(input_image)
  x = flatten(x)
  x = apply_dense_layer(x)
  output = softmax(x)
  return output
```

Key Differences

Output Layer and Activation Function: Model 1 employs a sigmoid function for a binary outcome, while Model 2 uses a softmax function for probabilistic outputs over two classes.

Loss Function: Aligned with the activation functions, Model 1 uses binary cross-entropy, and Model 2 uses categorical cross-entropy.

Both models are designed for binary classification but adopt different approaches in the output layer to explore their efficacy in the context of medical image analysis.

Proof of equivalence between Softmax and Sigmoid function in Binary classification

Softmax function: In binary classification, the softmax function for a pair of inputs z_1 and z_2 is defined as shown in eq 1 and 2:

$$softmax\ (z_1) = \frac{e^{z_1}}{e^{z_1}+e^{z_2}} \quad [1]$$

$$softmax\ (z_2) = \frac{e^{z_2}}{e^{z_1}+e^{z_2}} \quad [2]$$

The softmax function outputs probabilities that sum to 1. For binary classification, these probabilities can be interpreted as the likelihood of the data belonging to either of the two classes.

Sigmoid function: The sigmoid function for an input z is defined as shown in eq 3:

$$sigmoid\ (z) = \frac{1}{1+e^{-z}} \quad [3]$$

The sigmoid function maps a real-valued number to a value between 0 and 1, making it suitable for binary classification to represent the probability of a single class.

Simplifying the softmax function: In binary classification, we can simplify the softmax function by setting one of the inputs to zero (i.e., $z_2 = 0$). This is valid because, in binary classification, one class can be considered the baseline. Thus, we have

$$softmax\ (z_1) = \frac{e^{z_1}}{e^{z_1}+e^{0}} = \frac{e^{z_1}}{e^{z_1}+1}$$

$$softmax\ (z_2) = \frac{e^{0}}{e^{z_1}+e^{0}} = \frac{1}{e^{z_1}+1}$$

Demonstrating the equivalence: We can observe the similarity between the softmax and the sigmoid function.

$$softmax\ (z_1) = \frac{e^{z_1}}{e^{x_1}+1} = \frac{1}{1+e^{-z_1}} = sigmoid\ (z_1)$$

This shows that the softmax function for z_1 is equivalent to the sigmoid function (16, 17).

Similarly, softmax(z_2) represents the probability of the negative class.

$$softmax\ (z_2) = \frac{1}{e^{z_1}+1} = 1 - sigmoid\ (z_1)$$

The softmax function in a binary classification scenario is thus equivalent to the sigmoid function for the positive class. The probability of the negative class in softmax is simply one minus the sigmoid function's output. This equivalence demonstrates that both softmax (in a binary setting) and sigmoid functions provide the same probabilistic output, validating their interchangeability in binary classification tasks.

Results and Discussion

Model 1 (CNN with Sigmoid Activation)

Confusion Matrix

True Negatives (Normal): 152 cases were correctly identified as normal.

True Positives (Tuberculosis): 27 cases were correctly identified as tuberculosis.

False Negatives (Tuberculosis): 11 cases were incorrectly classified as normal.

False Positives (Normal): 10 cases were incorrectly classified as tuberculosis.

Classification Report

Precision (Normal): High precision for the 'Normal' class at 93%, suggesting a high accuracy when the model predicts an image as normal.

Recall (Tuberculosis): The recall for 'Tuberculosis' is 71%, indicating that the model missed 29% of the actual tuberculosis cases.

F1-Score: The F1-score is 0.81 for 'Normal' and 0.76 for 'Tuberculosis', balancing precision and recall.

Overall Accuracy: The overall accuracy of Model 1 is 80%.

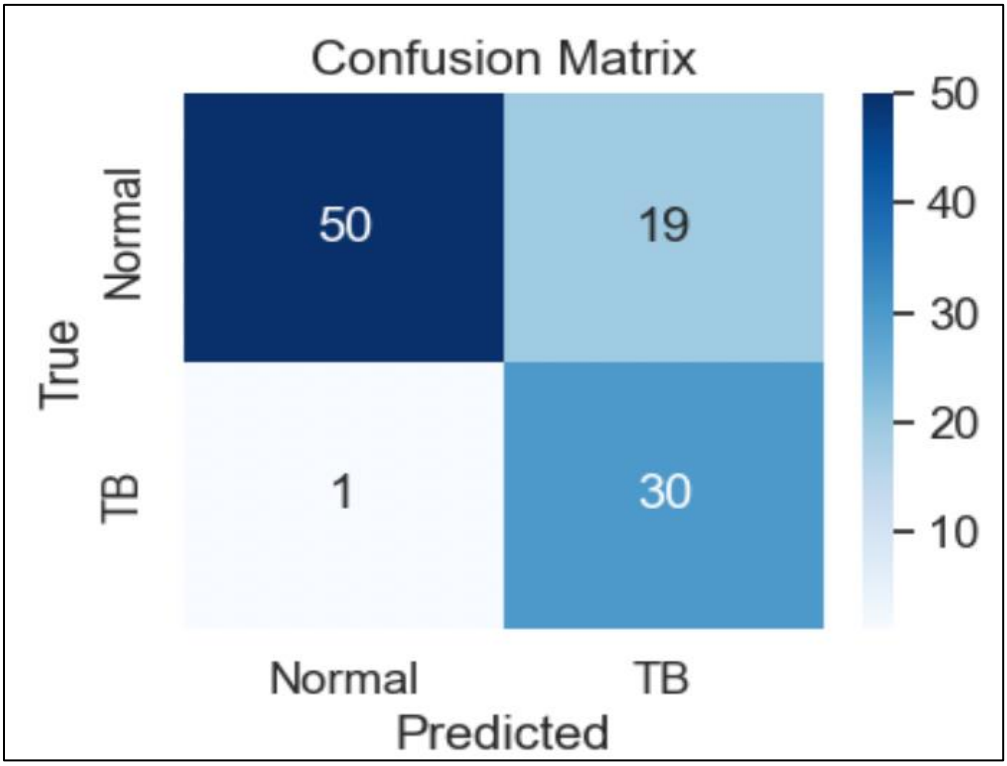

Figure 2: Confusion matrix for model 1

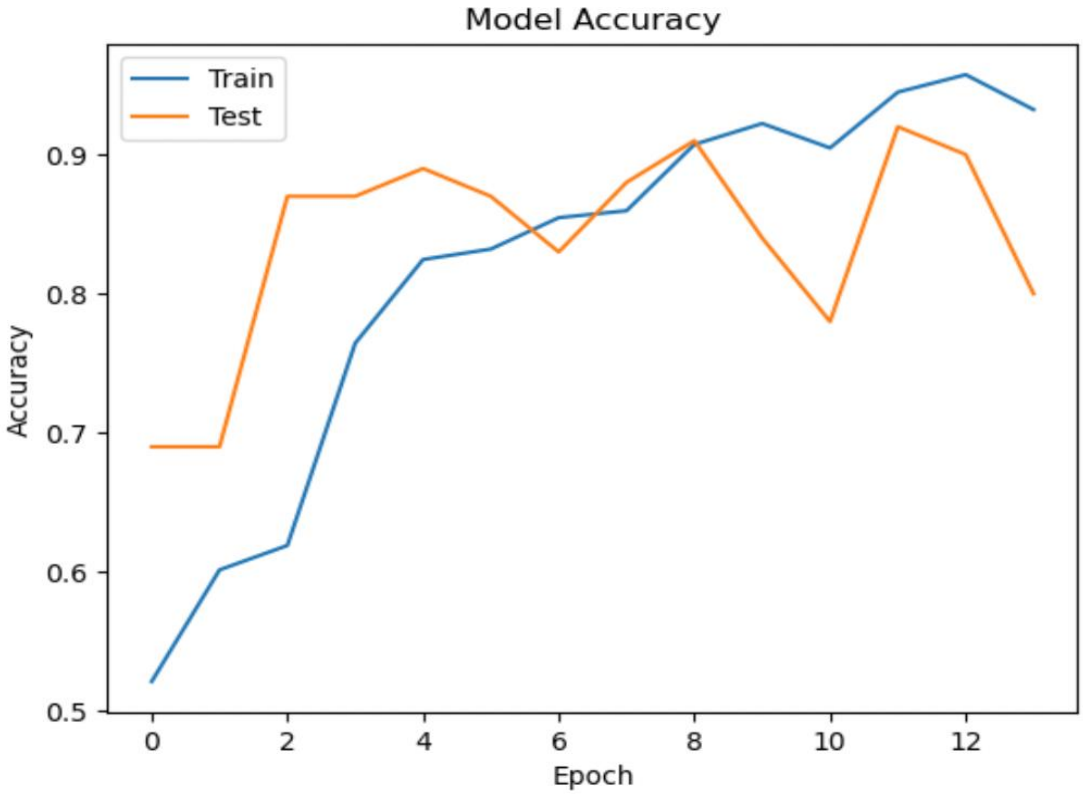

Figure 3: Accuracy comparison for model 1

Classification Report:

	precision	recall	f1-score	support
Normal	0.98	0.72	0.83	69
TB	0.61	0.97	0.75	31
accuracy			0.80	100
macro avg	0.80	0.85	0.79	100
weighted avg	0.87	0.80	0.81	100

Figure 4: Classification report for model 1

The confusion matrix, accuracy comparison, and classification report for model 1 are shown in Fig. 2, 3, and 4 respectively.

Model 2 (CNN with Softmax Activation)

Confusion Matrix

True Negatives (Normal): 138 cases were correctly identified as normal.

True Positives (Tuberculosis): 32 cases were correctly identified as tuberculosis.

False Negatives (Tuberculosis): 6 cases were incorrectly classified as normal.

False Positives (Normal): 14 cases were incorrectly classified as tuberculosis.

Classification Report

Precision (Normal): Precision for 'Normal' is 96%, showing a high level of accuracy in identifying normal cases.

Recall (Tuberculosis): The recall for 'Tuberculosis' is 84%, indicating that the model successfully identified most tuberculosis cases.

F1-Score: The F1-score is 0.95 for 'Normal' and 0.88 for 'Tuberculosis', indicating a good balance between precision and recall.

Overall Accuracy: The overall accuracy of Model 2 is 90%.

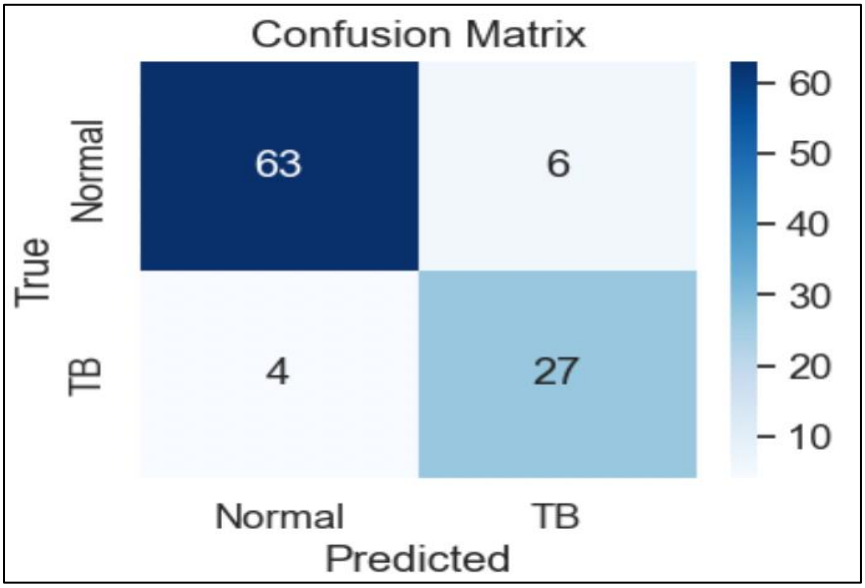

Figure 5: Confusion matrix for model 2

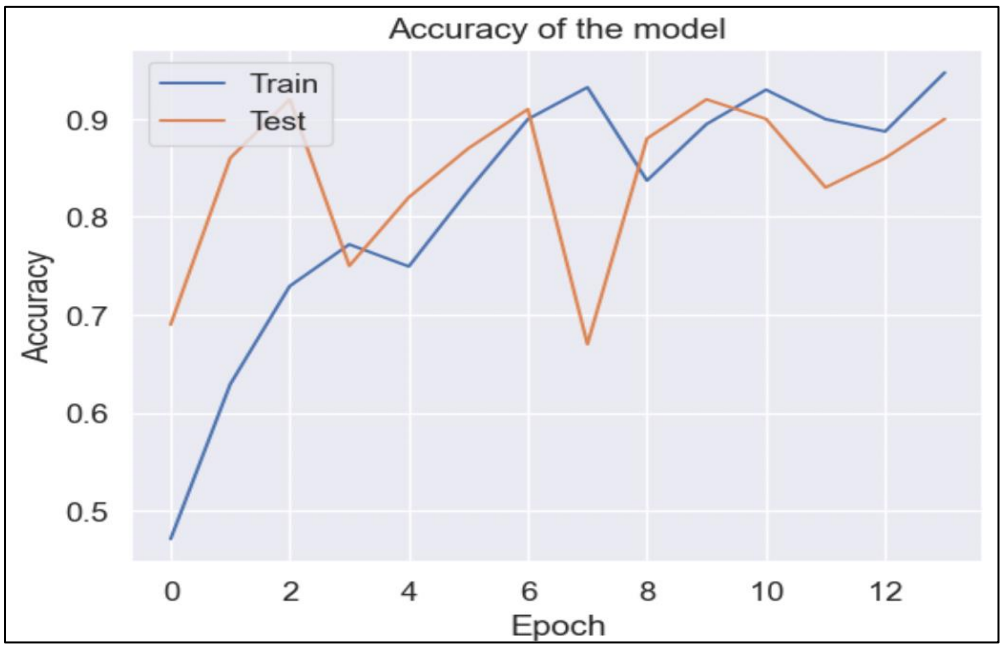

Figure 6: Accuracy comparison for Model 2

Classification Report:

	precision	recall	f1-score	support
Normal	0.94	0.91	0.93	69
TB	0.82	0.87	0.84	31
accuracy			0.90	100
macro avg	0.88	0.89	0.89	100
weighted avg	0.90	0.90	0.90	100

Figure 7: Classification report for Model 2

The confusion matrix, accuracy comparison, and classification report for model 1 are shown in Fig. 5, 6, and 7 respectively.

Comparative Analysis between Model 1 and Model 2

Model Performance: Model 2 outperforms Model 1 in terms of overall accuracy, precision, recall, and F1 score for both classes. Model 2 shows more consistent learning and generalization capabilities as evidenced by higher accuracy and better balance between precision and recall.

Confusion Matrix: Model 1 has a higher number of false negatives and false positives for the 'Tuberculosis' class compared to Model 2, which is critical in medical diagnostics, as missing or incorrectly identifying a case of tuberculosis can have significant consequences.

Although the sigmoid and softmax functions are mathematically equivalent in binary classification, several factors can lead to performance differences between Model 1 (with sigmoid) and Model 2 (with softmax).

Loss Function Sensitivity: Model 1 uses binary cross-entropy, while Model 2 uses categorical cross-entropy. These loss functions, while similar, can respond differently to the training process, affecting model learning.

Numerical Stability and Precision: The implementation of softmax can offer better

numerical stability and precision, particularly in handling class imbalances or borderline cases.

Model Training and Optimization: Variations in training dynamics, such as initialization and optimization techniques, can lead to different learning outcomes even with theoretically equivalent activation functions.

Data Representation and Handling: The way each model handles data during the training process, including any preprocessing steps, can influence their ability to learn and generalize.

Class Imbalance Handling: Softmax's probabilistic distribution over classes might offer a subtle advantage in datasets with imbalanced classes.

These factors collectively contribute to the observed differences in the performance of your deep learning models for TB detection in chest X-ray images.

Conclusion

This research work concludes that contrary to conventional practice, the CNN model with softmax activation (Model 2) can demonstrate superior performance in binary classification in certain scenarios. This outcome challenges the standard use of sigmoid activation in binary classification tasks. The distinctive choice of a softmax output layer in Model 2, typically associated with multi-class scenarios, appears to offer a more nuanced and effective approach for handling binary classification, especially in datasets with imbalanced class distributions.

The insights gained from this comparative study suggest that the application of softmax activation in binary classification tasks, particularly in medical image analysis, can potentially enhance diagnostic accuracy and efficiency. While Model 1, with its traditional sigmoid activation, follows a well-established approach, Model 2's unconventional use of softmax activation paves the way for rethinking binary classification strategies in CNN architectures.

The integration of deep learning through convolutional neural networks significantly advances the detection capabilities for tuberculosis. By automating the analysis of chest X-ray images, these models reduce reliance on human expertise, which can vary and be limited in resource-constrained settings. The deep learning approach not only enhances the accuracy of detecting TB but also speeds up the diagnostic process, allowing for quicker intervention and potentially reducing transmission rates. The ability of these models to learn from vast amounts of data and identify patterns undetectable to the human eye marks a substantial improvement over conventional diagnostic method.

The interpretability of our deep learning models is implicitly supported by the high accuracy and clarity of the outputs provided to end-users, which include detailed probability scores for both 'Normal' and 'Tuberculosis' classifications. These scores help clinicians assess the confidence level of the model's predictions, facilitating informed decision-making in medical diagnostics. Although specific visualization techniques like Grad-CAM were not employed in this initial research, the model’s architecture and training processes are designed to be transparent and understandable. To ensure the reproducibility of our findings, we have meticulously documented the dataset preparation, model architecture, and training parameters. The dataset, consisting of 499 labeled chest X-ray images, was split into 80% for training and 20% for testing, with images preprocessed to uniform dimensions and grayscale to maintain consistency. Our models were developed using a convolutional neural network framework, optimized with the Adam optimizer, and evaluated using standard metrics such as accuracy, precision, recall, and F1-score. These details, combined with the availability of our code and model parameters in a public repository, support the robustness and reliability of our research, allowing other scientists to replicate our work or extend it in future studies.

Future research can focus on further optimizing the architecture and parameters of both models, exploring the impact of various activation functions across different types of datasets, and investigating the role of data characteristics in model performance. The exploration of these models with larger and more diverse datasets could provide additional insights and reinforce the conclusions drawn from this study.

The findings from our analysis contribute to a deeper understanding of CNN applications in medical imaging and open new avenues for enhancing

machine learning models in clinical diagnostics. The broader implications of these findings underscore the importance of continual experimentation and innovation in the field of AI-driven medical image analysis.

Abbreviation

TB: Tuberculosis (TB); World Health Organization (WHO); Convolutional Neural Network (CNN).

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Author Contributions

Nil

Conflict of Interest

The authors declare that they have no known competing interests or personal relationships that could have appeared to influence the work reported in this paper.

Ethics Approval

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