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Enhancing Diagnostic Accuracy of Drug-Resistant Tuberculosis on Chest X-rays Using Data-Efficient Image Transformers

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Abstract: Tuberculosis is an infectious disease with increasing fatalities around the world. The diagnosis of the disease is a major challenge to its control and management due to the lack of adequate diagnostic tools, contributing significantly to the prevalence of drug-resistant tuberculosis. Convolutional Neural Network (CNN) models have recently been developed to detect drug-resistant tuberculosis by analyzing chest radiograph images from the TB portal, but the classification results are low. This is because CNNs struggle to capture complex global and overlapping features in medical imaging, such as chest radiographs of drug-resistant tuberculosis. In contrast, transformers excel in these areas by utilizing self-attention mechanisms that detect inherent subtle and long-range dependencies across images. In this study, we used a pretrained data-efficient image transformer (DEiT) model to enhance the diagnosis of drug-resistant tuberculosis and differentiate it from drug-sensitive tuberculosis. The new model achieved an AUC of 80% in the detection of drug-resistant tuberculosis, an improvement of 13% in the AUC compared to current CNN models using data from the same source. The bootstrap significance test shows that the difference in AUCs is statistically significant. The results of the study can help healthcare providers improve drug-resistant tuberculosis diagnostic accuracy and treatment outcomes.

1 INTRODUCTION

Tuberculosis (TB) is commonly known as an airborne disease that causes a high global rate of severe illness and death. Despite TB being curable, drug-resistant tuberculosis (DR-TB) has recently emerged as the main public health challenge impeding the success of TB control worldwide (World Health Organization, 2023). This stems from a lack of adequate tools to diagnose drug-resistant TB for early treatment, especially in developing countries. Each year, it is estimated that 0.5 million TB cases out of 10 million cases worldwide are drug-resistant, which brings complications to treatment (Yang et al., 2022). DR-

TB occurs when *Mycobacterium tuberculosis* (MTB) in a patient develops resistance to one or more standard tuberculosis drugs (Sachan et al., 2023; Silva et al., 2023).

Drug-resistant TB is categorized into different types based on severity: Resistance to only one first-line anti-TB medication is known as mono DR-TB, whereas poly DR-TB is the resistance to two or more first-line anti-TB drugs. Multidrug DR-TB (MDR-TB) occurs when the MTB is non-reactive to the majority of first-line medicaments. On the other hand, extensive DR-TB (XDR-TB) is the term used for resistance to drugs of both the first and second line. Furthermore, pre extensively DR (Pre XDR) is more resistant than MDR-TB with the additional resistance to second-line drugs (Sethanan et al., 2023). In this regard, DR-TB is complicated, and its diagnosis and treatment are more challenging as it is costly and lasts for a long period, about 9 to 20 months. Compare this to drug-sensitive TB (DS-TB), which requires

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an individual to take a course of treatment for 6–9 months (Karki et al., 2022). The DS-TB commonly known as TB has been effectively cured by using standard initial anti-tuberculosis medicaments (Mnyambo and Barakabitze, 2023). Early tuberculosis and DR-TB diagnosis are crucial to improving treatment outcomes and reducing the transmission rate of TB in the community (Yang et al., 2022).

Health facilities must provide accurate and timely diagnosis alongside appropriate treatment to address the challenges posed by drug-resistant tuberculosis (Ereso et al., 2023; Vats et al., 2024). Achieving the end-tuberculosis strategy requires sensitive diagnostic tools to distinguish TB from DR-TB (Naidoo and Perumal, 2023). The World Health Organization (WHO) recommends chest X-rays (CXR) for diagnosing TB and identifying DR-TB (World Health Organization, 2023). However, implementation of this policy remains a challenge in resource-constrained countries that have a notable burden of tuberculosis, which increases disease transmission and drug-resistant TB (World Health Organization, 2023).

The size, form, and location of lung lesions on chest X-rays can be used to identify drug-resistant tuberculosis. Mediastinal lymphadenopathy, pleural effusions, cavities, infiltrates, collapse, and nodules are among the uncommon features in the lung regions that are diagnostic of DR-TB (Lv et al., 2023; Wáng et al., 2018). When bacteria cause tissue degradation in the lungs, cavities develop, while infiltrates and nodules represent the immune response, indicating areas of active inflammation or granulomatous lesions. Pleural effusions and mediastinal lymphadenopathy signify disease progression, and lung collapse may occur due to airway obstruction or chronic damage. These overlapping features are more pronounced in DR-TB compared to drug-sensitive TB, adding to the diagnostic complexity (Kuang et al., 2022; Libiseller-Egger et al., 2020). This highlights the need for computer-assisted diagnostic methods that can automate TB screening and identify DR-TB at a relatively low cost to facilitate early treatment (Jonathan and Barakabitze, 2023; Karki et al., 2022).

Artificial Intelligence (AI) has become a fascinating technology for the automated diagnosis of tuberculosis using publicly available medical images (Jonathan et al., 2024; Liang et al., 2022). For example, AI using deep learning methods, particularly CNN, has shown promising results in TB diagnosis by identifying the resistance to TB regimens from chest X-ray images (Ureta and Shrestha, 2021). The convolutional neural networks have been useful for radiologists to interpret results and to reduce the problems associated with false results and limited human resources (Naidoo and Perumal, 2023).

A customized CNN and pre-trained VGG16 models were trained to determine the presence of resistance to TB drugs using the CXR images from Belarus. The results show that the models can automatically discriminate tuberculosis between DR-TB and DS-TB (Jaeger et al., 2018). Additionally, a pre-trained VGG16 model to predict lung drug-resistant TB was developed using chest X-rays from Image-CLEF2017. After validation, the authors proposed that the model shows potential in identifying the type of resistance to TB drugs (Meshesha et al., 2024).

Furthermore, labeled X-ray images from a TB Portals dataset were employed to train and validate a specialized CNN to categorize drug-resistant TB and drug-sensitive TB. The AUC results indicate that the classifier effectively distinguishes between DR-TB and DS-TB, showing improvement over previous deep learning models for DR-TB identification (Ureta and Shrestha, 2021). Researchers, on the other hand, used CXR images from TB Portals to train a pre-trained InceptionV3 model with image augmentation to determine resistance to tuberculosis drugs. After model evaluation, the findings suggest that the model can be useful in detecting the occurrence of drug-resistant TB (Karki et al., 2022).

The need for further work is widely acknowledged to improve performance for the classification of drug-resistant and drug-sensitive TBs (Jaeger et al., 2018; Ureta and Shrestha, 2021; Karki et al., 2022; Meshesha et al., 2024). Potentially, transformer-based deep learning algorithms may be used to achieve this. A recent study compared the classification performance of CNN, residual networks (ResNet), and transformers using NIH X-ray images. The study found that the transformer model had higher classification accuracy than the other models in diagnosing lung conditions (Jain et al., 2024).

Transformer is a deep learning model architecture that was primarily developed for natural language processing (NLP) tasks. Several fields, such as computer vision, have made use of it. Vision Transformer (ViT) is a neural network that adapts transformer-based model processes to accomplish computer vision tasks (Dosovitskiy, 2020). The ViT is attracting interest because of its potential to outperform CNN in computer vision problems and to enhance performance. To maintain its usefulness, the Vision Transformer has been improved and has various types, including the Data-Efficient Image Transformer (DEiT). This model type was developed to address data efficiency and feature extraction capabilities, particularly for complex medical imaging tasks like DR-TB detection while maintaining computational costs (Jumphoo et al., 2024). Furthermore, the DEiT is particularly effective in tasks requiring both

fine-grained and global context interpretation, making it ideal for chest X-rays of DR-TB patients.

The DEiT has been designed in such a way that it utilizes data augmentation and distillation techniques for efficient training (Singh et al., 2024). This model analyses the input image as follows: The input image is split up into fixed-size patches using the patch embedding technique, which then simplifies the patches to form a sequence of vector patch embeddings. The positional encodings process adds information to the model about the position of each patch within the image to make it possible to understand patches spatial relationships (Imagawa and Shiimoto, 2024). Moreover, self-attention mechanisms ensure each patch attends to every other patch and captures global dependencies using the encoder-decoder structure (Sethanan et al., 2023).

For classification tasks during the training, an image representation is extracted and added to the final layer of the classifier. Then, it is passed through a Multi-Layer Perceptron (MLP) head to be transformed into the final classification output (Imagawa and Shiimoto, 2024). The ability of the network to capture global context and spatial relationships makes it suitable by enhancing classification performance more than CNN, which is local context-based (Jain et al., 2024). The application of ViT in healthcare using medical imaging has demonstrated a high potential for accurate diagnosis of different diseases, including Alzheimer's, COVID-19, pneumonia, and tuberculosis diseases.

Contributing to the decrease in the rate of life-threatening neurodegenerative disorders and Alzheimer's disease, the authors developed a novel vision transformer model, namely DEViT. The model was validated, and when tested on unseen data, the evaluation results indicated that the DEViT can identify dementia with higher accuracy (Sen et al., 2024). Additionally, an effective method for identifying pneumonia was implemented with the help of vision transformers and images of the chest X-ray. The results demonstrated that the model outperformed in detecting pneumonia from chest X-rays (Singh et al., 2024).

Furthermore, vision transformers were employed to create models using chest X-ray images for a multiclass COVID-19 classification problem. Subsequently, it was proposed that these models can accurately detect COVID-19 with high AUC performance (Chetoui and Akhloufi, 2022). Additionally, a ViT model, pretrained using FastViT, was fine-tuned to screen for tuberculosis by analyzing chest X-rays, achieving high accuracy in predicting the tuberculosis class (Ko et al., 2024). Another ViT model, trained on the TBX11K dataset, was used to

identify TB-related bacteria from chest X-rays. As a result, the model demonstrated exceptional effectiveness with notable diagnostic accuracy (Kotei and Thirunavukarasu, 2024).

The studies have revealed the usefulness of vision transformer models in addressing tuberculosis challenges (Ko et al., 2024; Kotei and Thirunavukarasu, 2024). However, there is a need to enhance the effectiveness of diagnosing anti-drug TB using variations of vision transformers. To this end, this paper intends to use a DEiT, a vision transformer-based transfer learning method, to locate tuberculosis resistant to medications from chest X-ray imaging. DEiT is particularly suitable for this task due to its ability to handle complex CXR patterns and effectively capture the fine-grained details and global context of the subtle and overlapping features characteristic of DR-TB (Jumphoo et al., 2024). The following are the unique contributions to this study:

- We present a DEiT model architecture for the detection of drug-resistant tuberculosis using chest X-rays.
- We evaluate the performance of the DEiT model using metrics such as recall, precision, F1 score, and AUC, utilizing a CXR dataset from TB Portals.
- We provide a comprehensive comparison between the DEiT model and existing CNN approaches.

The following sections make up this paper: Section (2) introduces the methodology we followed in this research, Section (3) presents the analysis and findings, Section (4) addresses the results of the study, Section (5) provides ethical considerations, and Section (6) concludes the paper.

2 METHODOLOGY

This section presents the ViT deep learning model for detecting TB bacteria that have developed resistance to standard anti-TB drugs using chest X-rays from TB Portals. The model was trained using a pre-trained DEiT base model, a basic vision transformer.

2.1 Dataset

This study used anonymized clinical data and grayscale CXR images in DICOM format from the TB Portals of the National Institute of Allergy and Infectious Diseases (NIAID)¹, which were collected over a period of 10 years. These portals offer open

¹<https://tbportals.niaid.nih.gov>

access to anonymized multi-domain TB data from diverse domains of international TB patient cases, such as diagnosis and treatment, for analysis and to improve TB research. The portals are regularly updated, and the data was publicly available in August 2023 and extracted on December 20, 2023. Radiologists added clinical information and radiological features based on manual annotations, ensuring that each patient record was associated with the corresponding CXR image.

Figure (1) shows the distribution of TB drug resistance cases by country and the overall proportion of different drug resistance types. Initially, the dataset consisted of 8,846 cases from 13 countries with a high burden of drug-resistant TB. These cases were classified into six categories of drug resistance, with the MDR non-XDR category being significantly more prevalent than the others, leading to a class imbalance. A positive class, DR-TB, was created by combining all cases from the resistant classes (MDR non-XDR, XDR, Mono DR, Pre-XDR, and Poly DR) (Ureta and Shrestha, 2021). Therefore, this study focused on analyzing both resistant and sensitive class cases.

2.2 Pre-processing

The variance of the Laplacian metric was computed to ensure that high-quality images were used for model performance and generalization. As a result, the study relied on a comprehensive set of clear images, as summarized in Table (1). The positive class, DR-TB, contained the majority of the images, while the negative class, DS-TB, consisted of fewer. The data were randomly split into three sets: the majority were used for training, with smaller portions allocated for validation and testing. This distribution ensures that the model has sufficient data to learn meaningful patterns, prevents overfitting, and provides robust generalization to unseen data (Jaamour et al., 2023). The clear grayscale images were transformed to RGB format, resized to 224x224 pixels, and converted into tensors to ensure uniform dimensions compatible with the vision transformer. The RGB values were normalized to standardize the data, ensuring consistent mean and standard deviation values across the dataset.

2.3 DEiT Model Training and Development

The experiments were conducted using Python 3.9.19 and involved data augmentation techniques, such as random horizontal flips, random vertical flips, and random rotations (up to 20 degrees), applied to the

Table 1: Dataset overview and split

Category	Number of Images
Total	7,961
Class Distribution	
DR-TB	5,386
DS-TB	2,575
Dataset Split	
Training Set	4,777
Validation Set	1,592
Testing Set	1,592

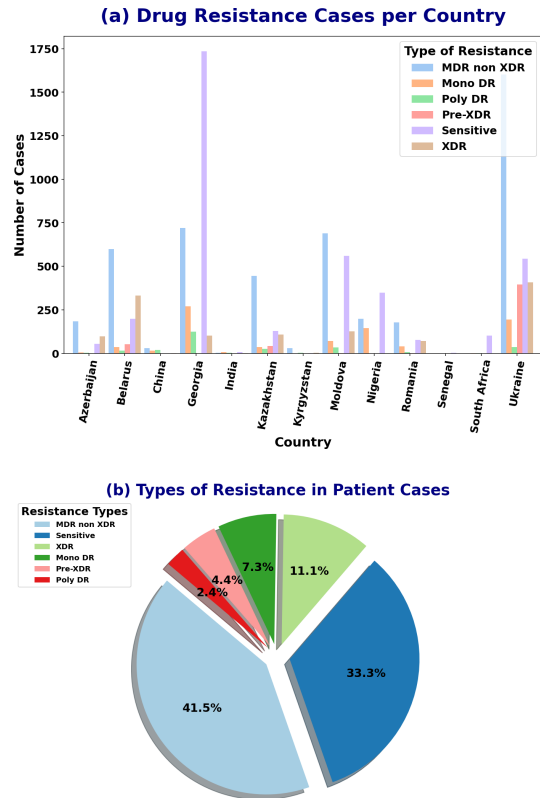


Figure 1: Distribution of TB drug resistance types across countries and overall proportions of drug resistance types

training dataset. The primary goal of these augmentations was to increase dataset diversity and prevent overfitting, thereby improving classification performance. No data augmentation was applied to the test and validation datasets. The study employed the ViT framework, specifically using the pre-trained DEiT-B/16 model weights, which were trained on ImageNet. DEiT, a type of Vision Transformer, incorporates knowledge distillation to enhance data efficiency and training practicality, improving transformer performance for image classification tasks (Jumphoo et al., 2024). The DEiT model's self-attention mechanism overcomes the limitations of CNNs by enabling the model to capture both local and global patterns,

making it well-suited for extracting complex features from medical images, such as DR-TB chest X-rays. To predict a single output from a fixed set of classes, an encoder-only model, based on the standard transformer encoder structure, was utilized, as shown in Figure (2).

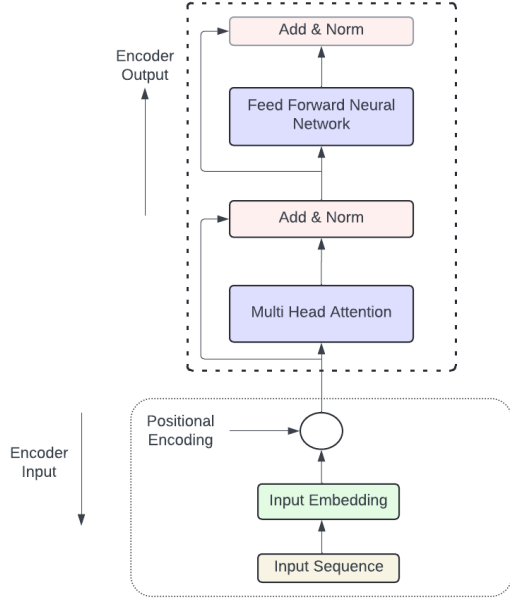


Figure 2: Transformer-encoder architecture

During training the pre-trained DEiT-B/16, each input image was first split into 16x16 non-overlapping patches. These patches were then flattened into single-dimensional vectors, and a sequence of patch embeddings was produced. Afterward, the positional embeddings were added to the sequence of patch embeddings to maintain the position information of each patch. The transformer encoder receives the series of patch embeddings, each with positional encoding, as input and uses its layers to process the input. Multi-head attention is one of the layers that allows a model to perform multiple self-attention operations concurrently and concatenate the results. Moreover, the Add and Norm layer plays a critical role in stabilizing and improving training by combining residual connections with layer normalization. Adding non-linearity to the model, non-linear activation functions are used between the fully connected layers of the feedforward neural network (FFNN) layer. The fully connected layers, namely MLP, contain multiple layers of neurons, which are essential to helping a model learn complicated patterns. This training mechanism is explained in Figure (2) and Section 2.5.

We extracted features by freezing all pre-trained layers and training only the final layers, modifying the classification head for binary classification with a

customized dataset. The pre-trained model was run with a batch size of 64 for 50 epochs, shuffling the dataset before each epoch. We used the AdamW optimizer with a weight decay of 1e-1 and a learning rate of 1e-3, along with a Cosine Annealing Learning Rate Scheduler to adjust the learning rate based on a cosine function. The rate scheduler was used to help the model converge more effectively with the following parameters: $T_{\max} = 10$, $\eta_{\min} = 1 \times 10^{-6}$, which are the maximum number of iterations for one cycle and the minimum learning rate, respectively.

BCEWithLogitsLoss was used as the loss function for the binary classification task, combined with pos_weight to address the issue of data imbalance. The pos_weight was useful to change the weight of positive cases in the loss calculation, allowing for greater emphasis on that class and balancing the impact of both classes on the loss. Thereafter, the training set was used to train the model, which was then evaluated on the testing set. Early stopping was also systematically implemented to determine the optimal number of epochs and prevent overfitting.

2.4 DEiT Model Architecture

Only the encoder part of a typical transformer is present in the recommended DEiT model architecture. Further details regarding the process of generating the encoder input and the encoded output, which serves as the MLP head's input, can be found in Section 2.3 and Figure 2. The MLP head processes the output of the transformer encoder to produce the final classification prediction. Given that the study used the pre-trained weights of DEiT, only modifications to the classification head for binary classification using the custom dataset were made, and the layers not to be fine-tuned were frozen.

This architecture consists of two fully connected linear layers. The first layer takes the input features from the output of the transformer encoder and maps them to 64 units (hidden layer), reducing the dimensionality to 64 features. The ReLU activation function is applied to introduce non-linearity, which enhances the model's learning capabilities and adaptability in the classification head. Dropout is applied to reduce overfitting by randomly deactivating neurons during training, helping to improve generalization. The second linear layer projects the 64 features to a single output for binary classification. The BCEWithLogitsLoss is used, which combines the sigmoid activation and binary cross-entropy loss with a positive weight adjustment, addressing data imbalance. Figure (3) illustrates the complete architecture of the DEiT model.

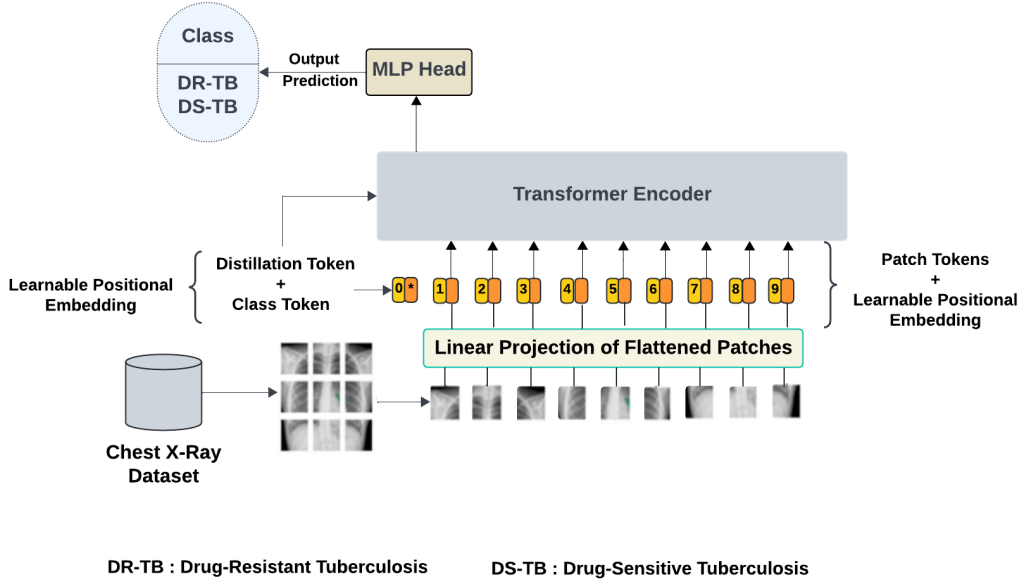


Figure 3: DEiT model architecture for detecting drug-resistant tuberculosis using chest X-rays

2.5 DEiT Theoretical Framework

This section outlines the key mathematical concepts behind DEiT, enabling efficient image processing and analysis by capturing complex relationships and patterns within the input images. The patch embedding process transforms an input image with dimensions $224 \times 224 \times 3$ by partitioning it into patches that are independent of size 16×16 . This leads to $N = \left(\frac{224}{16}\right) \times \left(\frac{224}{16}\right) = 14 \times 14 = 196$ patches, where the height, width, and number of channels are represented by the dimensions 224, 224, and 3, respectively. After being flattened into a 1D vector, each of the 196 patches containing $16 \times 16 \times 3 = 768$ pixel values has a vector size of 768. A learnable linear transformation is then used to project these patch vectors onto a lower-dimensional space, mapping the 768-dimensional patch vector to a d -dimensional vector of size 512. The transformer’s dimensionality reduction improves the model’s efficiency while also lowering computational costs and memory usage. After projection, we obtain a sequence of 196 patch vectors, each with a dimension of 512. These vectors collectively form a matrix X with dimensions 196×512 (i.e., $N \times d$). The output of the matrix can be represented as:

$$\mathbf{X} = [\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_N] \quad \mathbf{X} \in \mathbb{R}^{N \times d} \quad (1)$$

Then, a distinct class token, denoted as $\mathbf{x}_{cls} \in \mathbb{R}^d$, is added at the beginning of the sequence of patch embeddings, mainly for classification in the output layer.

The updated input sequence is as follows:

$$\mathbf{X}' = [\mathbf{x}_{cls}, \mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_N] \quad \mathbf{X}' \in \mathbb{R}^{(N+1) \times d} \quad (2)$$

Subsequently, positional encodings (PE) are incorporated into the sequence of patch embeddings to provide spatial information. The input to the transformer after adding positional encodings is:

$$\mathbf{Z}_0 = \mathbf{X}' + \mathbf{PE} \quad (3)$$

Later, Multi-Head Self-Attention (MHSA²) enables the model to utilize multiple heads to capture various relationships between patches. The self-attention mechanism calculates the attention scores for every pair of patch vectors, X_i .

The learned linear projections are then used to convert each patch vector X_i into *Query* (Q)³, *Key* (K)⁴, and *Value* (V)⁵. The dot product of the query and key vectors is then used to measure the attention scores between patches. The attention scores are then normalized using a softmax function to ensure that

²MHSA enhances the self-attention mechanism by introducing multiple independent attention heads that each focus on different aspects or relationships within the input data.

³ Q refers to the input for which the model is intended to extract relevant information.

⁴ K represents the possible attributes or data that can be handled.

⁵ V indicates the actual information utilized in the output, determined by the attention scores.

they total up to 1. Finally, the output representation of each patch is computed as a weighted sum of the value vectors from all patches using the attention weights. In terms of mathematics, it is expressed as:

$$\text{Output}(i) = \sum_{j=1}^N \text{Attention Weights}(i, j) \cdot V_j \quad (4)$$

This mechanism allows self-attention to dynamically adjust which patches influence each other based on their content, thereby capturing dependencies between patches.

Following the self-attention block, the output is processed by a feed-forward neural network, referred to as the MLP block, which consists of two layers and incorporates a GELU non-linearity function:

$$\text{MLP}(x) = \text{GELU}(xW_1 + b_1)W_2 + b_2 \quad (5)$$

Here, W_1 and W_2 are the weight matrices, while b_1 and b_2 are the bias vectors for the layers.

Non-linearity is applied to help the model capture more complex relationships and patterns in the data through feedforward neural networks and enhance performance. Each block incorporates layer normalization⁶ for stabilizing and enhancing the training process before both the MHSA and MLP⁷. After each sub-layer, a residual connection is applied, adding the input to the output.

In the attention sub-layer, this is formulated as:

$$Z' = \text{LayerNorm}(Z_0 + \text{MultiHead}(Q, K, V))$$

In the case of the MLP sub-layer:

$$Z_{\text{out}} = \text{LayerNorm}(Z' + \text{MLP}(Z'))$$

At the end of the transformer layers, the class token, which has been processed through the attention and feed-forward layers, is input into a linear layer to predict class probabilities. This linear transformation of the class token produces the final output:

$$\text{output} = \text{softmax}(W_{\text{cls}}x_{\text{cls}}) \quad (6)$$

Where W_{cls} is a weight matrix that has been learned to transform the final class token into the class space.

⁶Layer normalization stabilizes and enhances the training process by maintaining the mean and variance of feature distributions, resulting in faster convergence and improved performance.

⁷MLP improves transformer capabilities by enabling powerful feature transformations, non-linear mapping, and essential architectural components.

3 RESULTS AND ANALYSIS

This section presents and analyzes the results obtained from the DEiT model for binary classification. We first assess the model's performance using metrics, followed by its significance test.

3.1 DEiT Model Classification Performance

After training and validating the DEiT model for the classification of DR-TB and DS-TB on the training and validation sets. We subjected the model to the unseen data to evaluate the results. This study used recall, precision, F1-score, and AUC scores to measure the model classification performance when dealing with imbalanced data. Table (2) shows the metric results of the model when evaluated on the unseen data. Comparative results of different deep learning models with the DEiT are summarized in Table (3).

Table 2: Classification performance of the DEiT model

Our model	Recall	Precision	F1 Score	AUC
DEiT	82.8%	82.6%	82.7%	80%

In medical diagnosis, particularly when dealing with imbalanced data, recall plays a critical role in ensuring that true positive cases are identified, as missing these cases can have serious consequences. For this study, detecting drug-resistant tuberculosis as the target class was prioritised. As shown in Table (2), the model demonstrates strong performance in recall, effectively identifying a large portion of actual DR-TB cases. Furthermore, precision is vital for evaluating the reliability of positive predictions guaranteeing that the detected cases of drug-resistant tuberculosis are accurate. The results confirm that the model achieves a balance between detecting DR-TB and minimising false positives. Previous work, such as (Ureta and Shrestha, 2021), highlights the importance of precision for addressing class imbalance and improving the identification of drug-resistant tuberculosis, which is resistant to standard treatments.

In addition, to balance the identification of positive cases (recall) and maintain the accuracy of positive predictions (precision), the F1 score was used as a unified metric to assess this trade-off. The results demonstrate that the model achieves an optimal balance between recall and precision, which makes it effective in distinguishing between drug-resistant TB and drug-sensitive TB. Previous studies (Scholz et al., 2024) have shown that the F1 score is particularly reliable for binary classification tasks with class

imbalance, as observed in this study. Furthermore, the model exhibits strong performance in terms of the area under the curve (AUC), successfully differentiating DR-TB from DS-TB across various threshold settings. As illustrated in Figure (4), the AUC score highlights the model’s superior accuracy compared to other deep learning approaches reported in related research (Singh et al., 2024).

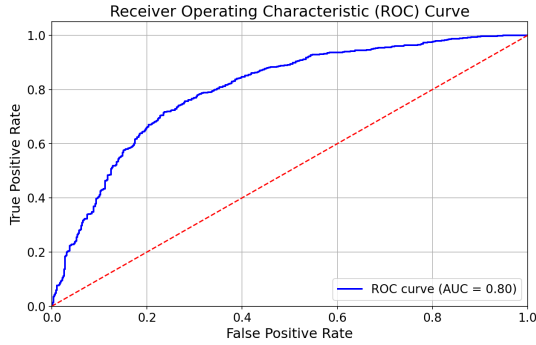


Figure 4: ROC curve showing the AUC of the DEiT model

The confusion matrix in Figure (5) demonstrates the classification performance of the DEiT model. The model identifies a large majority of drug-resistant TB and drug-sensitive TB cases, with relatively low misclassification rates. This performance translates into a test accuracy of 76.5%. Compared to the pre-trained VGG16 model, which achieved an accuracy of 64%, our DEiT model shows a significant improvement in classification accuracy (Meshesha et al., 2024).

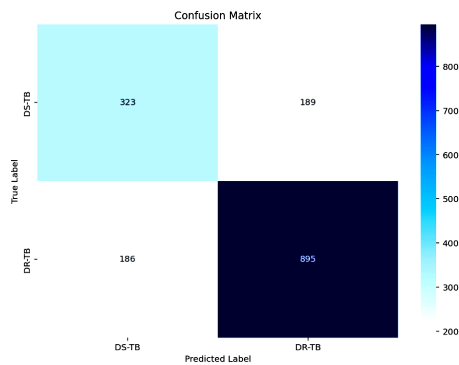


Figure 5: Confusion matrix derived from the test data for the DEiT model

3.2 Bootstrap Significance Test

We applied the bootstrap significance test to estimate the confidence interval (CI) of the AUC for the DEiT model. This interval helps assess whether the performance difference in AUCs between our model and existing models is statistically significant. Using the bootstrap algorithm (Noma et al., 2021), the test data were randomly resampled with replacement, and the AUC for each resampled dataset was computed. The average AUC, along with the 2.5 and 97.5 percentiles of the AUC distribution, was then calculated. Figure (6) shows that the model achieved a mean AUC, and the confidence interval suggests that with 95% confidence, the true AUC of the model lies within a certain range.

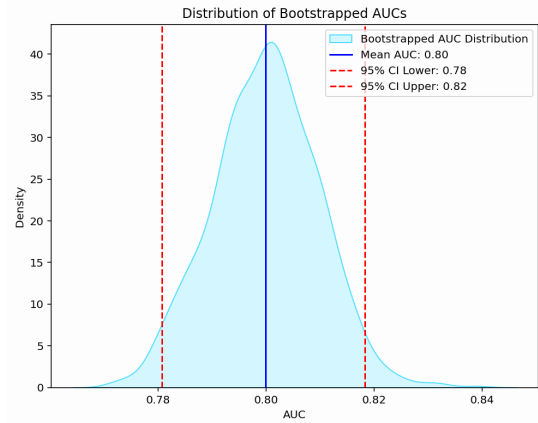


Figure 6: The AUC distribution of the DEiT model highlights its performance and robustness across different data subsets

4 DISCUSSION

To evaluate the performance of the DEiT model, we compared our results with those from other studies that used chest X-ray images from TB Portals and Belarus for deep learning-based classification. Table (3) presents this comparison. A customized CNN and a pre-trained VGG16 model were developed to distinguish between drug-sensitive and drug-resistant tuberculosis using the Belarusian dataset. These models achieved lower classification performance compared to our DEiT model, which can be attributed to the limited dataset size, which likely impacted their ability to generalize effectively to unseen data.

Additionally, a specialized CNN model was created using a dataset from TB Portals, achieving notable performance in distinguishing between drug-resistant and drug-sensitive tuberculosis (Ureta and Shrestha, 2021). The use of data augmentation tech-

Table 3: Comparison of classification performance across different models

Authors	Dataset	Images	Method	AUC
Jaeger et al. (2018)	Belarus	135	Customized CNN	62%
			Pre-trained VGG16	57%
Ureta and Shrestha (2021)	TB Portals	2,973	Specialized CNN	66% - 67%
Karki et al. (2022)	TB Portals	3,642	Pre-trained InceptionV3	66%
Our model	TB Portals	7,961	Pre-trained DEiT	80%

niques enhanced the model’s performance by generating synthetic variations of the existing data. Similarly, a pre-trained InceptionV3 model was fine-tuned using a larger dataset of chest X-rays, which demonstrated improved performance in classifying DR-TB and DS-TB after evaluation (Karki et al., 2022).

When comparing the performance of the DEiT model to existing deep learning models for classifying tuberculosis as drug-resistant or drug-sensitive, the DEiT model showed significant improvement. As illustrated in Figure (6), the confidence interval for the DEiT model’s performance does not overlap with those of previous models, indicating a statistically significant difference. DEiT’s capacity to efficiently capture intricate chest X-ray patterns, especially the subtle and overlapping characteristics of drug-resistant tuberculosis, is responsible for this improvement. In order to overcome the difficulties in precisely identifying drug-resistant tuberculosis, the model’s self-attention mechanism allows it to concentrate on minute features as well as the larger environment.

5 ETHICAL CONSIDERATIONS

The University of Plymouth Faculty of Science and Engineering Research Ethics and Integrity Committee (IRAS ID 5029), Medical Research Coordinating Committee of Tanzania (NIMR/HQ/R.8a/Vol.1X/4645), and Tanzania Mission for Science and Technology authorized the study (CST00000774-2024-2024-00781). The National Institute of Allergy and Infectious Diseases (NIAID) TB Portals approved the use of TB Portal data (B92A8156-AD1A-4035-9DA5-E8C09F755F).

6 CONCLUSIONS

This study investigates a DEiT model along with its architecture to discriminate drug-resistant TB from drug-sensitive TB using the CXR from the TB Portal. In pre-processing, we used methods including resizing, normalization, and the variance of the Laplacian metric to obtain the required format and improve the quality of the data. To prevent the model from overfitting and increase diversity in the training data, data augmentation techniques, such as horizontal flipping, vertical flipping, and rotation, were utilised. The model was trained, validated, and tested with the customised preprocessed dataset, demonstrating strong performance across various evaluation metrics, including recall, precision, F1 score, and AUC. This demonstrates the ability of the model to effectively address the challenges of DR-TB detection by uncovering complex patterns in chest X-rays. Ultimately distinguishing between drug-resistant and drug-sensitive tuberculosis.

In our work, the DEiT model surpasses existing deep learning models, such as customized CNN, VGG-16, and InceptionV3, in terms of AUC. The experimental results show a significant improvement in classification performance, with a statistically significant difference. This model shows promise in assisting radiologists in interpreting results in regions with limited resources and a high prevalence of drug-resistant tuberculosis. For future work, we anticipate focusing on the interpretability of the classification results with the additional radiological features to provide more insights into the performance of the model. Shapley Additive exPlanations (SHAP) will be used to determine the extent to which every feature contributes to the model output. Moreover, we will train the model with a balanced class dataset to address the challenge of an imbalanced dataset.

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