Tuberculosis detection in chest X-ray images using ResNet-18

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1. Introduction

Tuberculosis (TB) remains one of the leading causes of death worldwide, particularly in resource-limited regions.[1] Early detection and diagnosis are crucial for effective treatment and containment of the disease. Chest X-rays are one of the most commonly used tools for TB diagnosis due to their low cost and availability. However, their interpretation requires expert radiologists, and diagnostic accuracy can be inconsistent, with error rates varying based on expertise and workload.

The advent of deep learning has provided promising solutions to automate and enhance the diagnostic process. Convolutional neural networks (CNNs), specifically ResNet architectures, have demonstrated exceptional performance in medical imaging tasks.[2] This project explores the use of ResNet-18 for binary classification of chest X-rays, distinguishing between healthy lungs and those affected by tuberculosis.

2. Dataset and Methodology

2.1 Dataset

The dataset used in this project is the *Tuberculosis Chest X-ray Dataset* from Kaggle[3], comprising: **700 normal images** (healthy lungs fig. 1 and 2). **700 TB-positive images** (lungs diagnosed with tuberculosis fig. 3 and 4). Images are in PNG format with a resolution of 512x512 pixels. The dataset was split into training (70%), validation (15%), and test (15%) sets.

2.2 Data Preprocessing

To prepare the data for model training, the following preprocessing steps were applied: **Grayscale Conversion:** Original images were converted to grayscale to standardise input

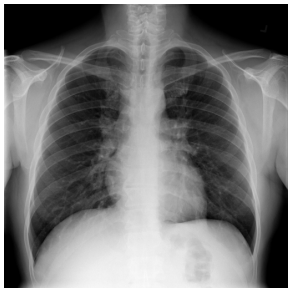


fig. 1

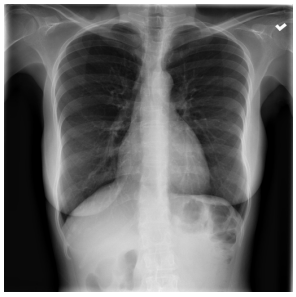


fig. 2

fig. 3

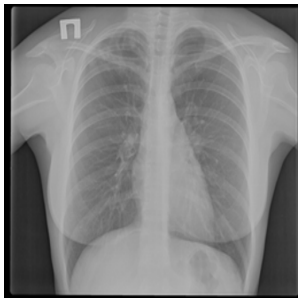


fig. 4

features. **CLAHE (Contrast Limited Adaptive Histogram Equalisation)**: Applied to enhance local contrast and improve feature visibility. **Gaussian Blurring**: Used to reduce noise. **Resizing**: Images were resized to 224x224 pixels to match the input requirements of ResNet-18. **Normalisation**: Pixel values were normalised to have a mean of 0 and a standard deviation of 1. **Data Augmentation**: Random rotations, flips, and translations were applied to improve model generalisation.

2.3 Model Architecture

ResNet-18[4] is a convolutional neural network designed to address the vanishing gradient problem using residual connections. It consists of 18 layers, including convolutional, batch normalisation, ReLU activations, and fully connected layers. Below is the structure of the network:

Initial Convolution Block: Input Layer: Processes RGB images with 3 channels. Conv1: 7x7 convolution with a stride of 2 and padding of 3, producing 64 feature maps. BatchNorm1: Normalises the feature maps to stabilise training. ReLU: Applies a non-linear

activation function. MaxPooling: 3x3 pooling with stride 2 to downsample the feature maps. Residual Layers: The network is divided into 4 main layers, each containing two Basic Blocks. Each block has two 3x3 convolutional layers and batch normalisation. The output of each block is added to its input (skip connection) to form the residual connection. Details of Residual Layers: Layer 1: Input: 64 channels → Output: 64 channels. Consists of 2 Basic Blocks without downsampling.
Layer 2: Input: 64 channels → Output: 128 channels. Downsampling occurs at the first block using a 1x1 convolution in the shortcut connection.
Layer 3: Input: 128 channels → Output: 256 channels. Downsampling occurs at the first block using a 1x1 convolution in the shortcut connection.
Layer 4: Input: 256 channels → Output: 512 channels. Downsampling occurs at the first block using a 1x1 convolution in the shortcut connection.
Final Layers: Average Pooling: Adaptive average pooling reduces the spatial dimensions to 1x1.
Fully Connected Layer (FC): A linear layer maps the 512 features to the number of output classes (2 in this case: Normal and Tuberculosis).

Parameters and Highlights

- Residual Connections: Help prevent the vanishing gradient problem by directly passing the input to later layers.
- Number of Weights: The model contains approximately 11.7 million trainable parameters.
- Layers:
  - Convolutional Layers: 18 layers including residual connections.
  - Fully Connected Layer: 1 linear layer at the end.

2.4 Training Setup

- **Optimiser:** SGD (Stochastic Gradient Descent) with a learning rate of 0.01.
- **Loss Function**: CrossEntropyLoss, suitable for multi-class classification.
- **Batch Size**: 30
- **Epochs**: 5 (due to computational limits or convergence observed in early experiments.)
- **Framework: PyTorch.**

3. Results

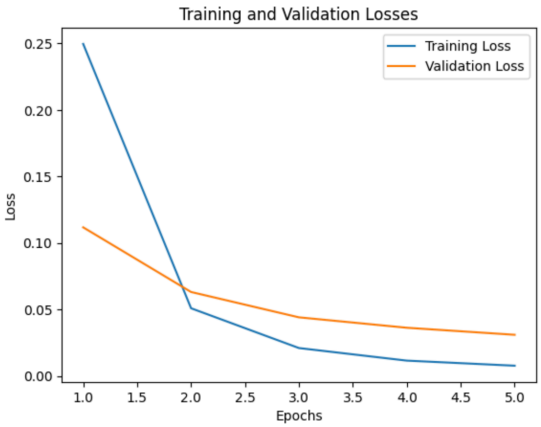
3.1 Classification Report:

Precision, Recall, and F1-Score: Both classes (0: Normal, 1: Tuberculosis) show extremely high precision, recall, and F1-score, nearly at 1.00. This indicates the model is highly accurate in predicting both classes.
Accuracy: 99% accuracy is achieved on the test dataset, which is very high.
Support: The number of samples per class is balanced (73 for Normal and 67 for Tuberculosis), which avoids bias towards a particular class. The exceptionally high scores might indicate that the dataset is relatively simple for the model, or that the model is overfitting due to the small dataset size. Such high scores on a small dataset can sometimes be misleading if the model has merely memorised the data rather than learning generalisable patterns.

	precision	recall	f1 score	support
0	0,99	1,00	0,99	73
1	1,00	0,99	0,99	67
accuracy			0,99	140
macro avg	0,99	0,99	0,99	140
weighted	0,99	0,99	0,99	140

3.2 Training and Validation Loss

The training loss decreases steadily and approaches near zero after 5 epochs, indicating that the model is learning the training data effectively. The validation loss also decreases initially and flattens, showing no signs of divergence. This indicates that the model generalises well to unseen validation data and is not significantly overfitting within these epochs. The near-zero training loss might suggest that the model has memorised the training data to a great extent. This could be due to the relatively small dataset size, making it easier for the model to overfit. Since the validation loss is not increasing, overfitting seems limited, but more testing on different datasets is recommended for better evaluation.



4. Discussion and Conclusion

4.1 Findings

The ResNet-18 model successfully classified chest X-rays with high accuracy, demonstrating the potential of deep learning in automating TB diagnosis. The use of transfer learning significantly accelerated the training process and improved performance on a relatively small dataset.

4.2 Approaches and limitations

I explored different network architectures, including simple CNNs, and tested various numbers of training epochs to find an optimal configuration. While ResNet demonstrated high accuracy, I believe the results might be overly optimistic due to the dataset size and potential overfitting. A larger and more diverse dataset would have likely led to more realistic evaluation metrics by testing the model's generalisability. The current dataset may allow the model to overfit, learning specific patterns rather than generalising to unseen data. I had planned to implement techniques like data augmentation to artificially expand the dataset and Grad-CAM for model interpretability. However, time constraints and my limited programming experience prevented me from fully integrating these features. Without Grad-CAM or similar techniques, it is challenging to interpret what the model is learning. This limits the ability to assess whether the model is making decisions based on medically relevant features.
The dataset used consisted of 1400 X-ray images equally split between tuberculosis-positive and healthy cases. While this dataset was sufficient to achieve a high accuracy (99%), the limited amount of data likely contributed to the model's strong performance due to its ability to memorise rather than generalise the patterns in the data.

Conclusion

This project highlights the potential of deep learning in improving TB diagnostics through automated image classification. The ResNet-18 model, combined with rigorous preprocessing and augmentation techniques, provides a strong baseline for future research in medical imaging.

Future Directions

Given the challenges and limitations, I see several opportunities to improve this work:

1. Use a larger dataset with more diverse examples to better evaluate the model's performance.
2. Integrate data augmentation techniques to simulate variability in the training data.

3. Apply Grad-CAM or similar visualization tools to better understand the decision-making process of the model.
4. Transition to a more robust computational environment for longer experiments and additional model iterations.

4.3 Personal challenges and limitations

As someone with a non-programming background, embarking on this project to train a model for tuberculosis detection using chest X-ray images has been a challenging yet rewarding experience. The journey required not only understanding the technical aspects of machine learning but also managing practical limitations, such as computational resources and time constraints. This section reflects on the key challenges faced, the approaches attempted, and the limitations encountered.

The process of debugging and addressing errors turned into an unexpected learning opportunity. While errors often stalled progress, they helped me better understand the functionality of machine learning pipelines, preprocessing, and data loaders.

This project has been both demanding and enriching. Despite the challenges, I am proud of having achieved a functioning model with high performance metrics, aware of its potential limitations. This journey has significantly expanded my understanding of machine learning and inspired me to continue learning and improving.

References

1. https://www.who.int/teams/global-tuberculosis-programme/data
2. Tawsifur Rahman et al., "Reliable Tuberculosis Detection using Chest X-ray with Deep Learning, Segmentation and Visualization," *IEEE Access*, 2020. DOI: 10.1109/ACCESS.2020.3031384.
3. Kaggle Tuberculosis Chest X-ray Dataset: https://www.kaggle.com/datasets/kmader/pulmonary-chest-xray-abnormalities
4. He, K., Zhang, X., Ren, S., & Sun, J. (2016). "Deep Residual Learning for Image Recognition." Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition (CVPR), 770–778. DOI: 10.1109/CVPR.2016.90.

The following software and libraries were utilised to implement and evaluate the ResNet-18 model for tuberculosis detection using chest X-ray images:

Programming Language: Python 3.10
Frameworks and Libraries:
PyTorch (torch==2.0, torchvision==0.15): For building and training the ResNet-18 model.
NumPy (numpy==1.26): For numerical operations and data preprocessing.
Matplotlib (matplotlib==3.8): For plotting training/validation losses and visualizing Grad-CAM results.
Scikit-learn (scikit-learn==1.5): For generating classification reports and metrics.
OpenCV (opencv-python==4.8): For preprocessing X-ray images (e.g., resizing, grayscale conversion).
Platform: Google Colab (free version)
- Used for running experiments and training the model. The free version was subject to computational resource limits. Hardware: NVIDIA Tesla K80 GPU (when available via Google Colab) or CPU.

The code: https://github.com/DajanaKolarova/AI_TB_model/tree/main