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Generative Artificial Intelligence-Aided Image-Based Tuberculosis Diagnosis

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Abstract

Generative artificial intelligence systems such as large language models are coaxed via prompt engineering into generating suggestions for the development of an automated system for the diagnosis of tuberculosis on the basis of chest radiography image sequences. The recommendations of the generative artificial intelligence are followed through to construct artificial intelligence models and then these models are trained, tested and validated on suitably formatted data and harnessed for the automated detection of tuberculosis via the analysis or processing of chest radiography images. The performance of the trained artificial intelligence models could be enhanced with a view to fielding them in modules for the automated image-based diagnosis of tuberculosis as part of a comprehensive artificial intelligence-powered healthcare system that could provide clinical decision support to medical doctors and healthcare professionals.

Keywords: Tuberculosis, Artificial Intelligence (AI), Generative Artificial Intelligence, Large Language Model (LLM), Chat GPT, Deep seek, Convolutional Neural Network (CNN), Healthcare System, TensorFlow, Automated Disease Diagnosis and Prediction

1. Introduction

According to the World Health Organization (WHO), tuberculosis, a bacterial infection that affects the lungs, afflicts a significant fraction of the global population and causes over a million deaths a year, taking its place as one of the top single causes of mortality worldwide [1] – [2]. The disease is present in all regions of the world and in all populations and age groups. Worst affected are those in low- and middle-income countries (LMIC) who have to grapple with severe constraints in the resource pool for healthcare service delivery. Early detection, especially in resource-limited settings, can lead to improved health outcomes. The processing of chest radiography image sequences provides a viable pathway for the detection or diagnosis of tuberculosis.

In order to mitigate the effects of the resource constraints prevalent in LMICs by dramatically enhancing the productivity of medical doctors and other healthcare professionals and ameliorating the adverse consequences of the brain drain caused by the emigration of the already limited number of qualified healthcare professionals to more developed countries in search of greener pastures, as well as generally improve medical doctor productivity, save lives and improve living conditions in both developed and developing countries, Ekpar [3] – [6] introduced Scholar Medic, a comprehensive artificial intelligence-driven healthcare system with a modular design that accommodates a wide range of health conditions and permits the refinement of existing modules and addition of new modules on the basis of fresh data. Scholar Medic [3]– [6] uniquely facilitates the utilization of novel three-dimensional multilayer electroencephalography or Ekpar EEG [7] – [9] systems as well as support for the adaptation of traditional electroencephalography (EEG) systems to the advanced three-dimensional multilayer Ekpar EGG paradigm for greater insights and for enabling hitherto unattainable applications of EEG in myriads of domains ranging from computing to medicine.

Machine learning and artificial intelligence systems have been applied to the detection, diagnosis and prediction of health conditions [10] – [28]. Furthermore, large language models could also be utilized in this endeavor owing to their ability to learn knowledge representations and draw inferences from data [29] – [30]. Here, suggestions are extracted from generative artificial intelligence (AI) systems such as large language models (LLMs) and harnessed to develop two-dimensional convolutional neural network models for the automated diagnosis of tuberculosis on the basis of chest radiography (x-ray) image sequences.

2. Materials and Methods

Participant Recruitment

Individuals voluntarily participated in the research contributing to the development of the comprehensive AI-powered healthcare system. All participants provided informed consent before their involvement in the studies, ensuring their understanding of the research purpose, methods, and potential impacts.

Ethical Approval

The Health Research Ethics Committee at Rivers State University Teaching Hospital, located within Rivers State University, granted ethical clearance for the studies. The research complied with all relevant ethical and regulatory standards. Publicly available data were utilized in accordance with the licensing terms set by the original data creators.

3. Methodology

Publicly available healthcare datasets can be improved by incorporating data gathered from local experiments and data collection efforts. This combined dataset can then be used to train AI models to make actionable predictions based on new inputs. Examples of public healthcare data sources include the Centers for Disease Control, the University of California Irvine Machine Learning Repository, the American Epilepsy Society, and Kaggle.

Incorporating local data enhances the model, reduces bias, and ensures greater inclusivity and global applicability. A key feature of this project is the integration of diagnostic data (such as electrocardiographic results) from local experiments with EEG data, using both traditional and advanced three-dimensional multilayer EEG (Ekpar EEG) systems [7] – [9]. Ethical approval has been obtained for local data collection efforts from research ethics committees in the respective regions. Furthermore, partnerships have been established with licensed medical doctors who have direct access to patients and healthcare professionals within the community. These doctors are providing anonymized clinical data to help validate the AI models. Once trained, the AI models will be incorporated into a comprehensive healthcare system designed to support medical professionals in clinical decision-making and to generate Brain-Computer Interfaces (BCIs). This system will provide actionable insights and predictions based on new clinical data from healthcare providers, aiding in the early detection, diagnosis, treatment, prediction, and prevention of various conditions such as tuberculosis, chronic kidney disease, diabetes mellitus, heart disease, stroke, autism, and epilepsy.

This project is committed to promoting open science, reproducibility, and collaboration, and the resulting data will be shared on public platforms like GitHub.

System Design and Implementation

This paper presents a healthcare system with a modular design, where each health condition (e.g., tuberculosis, chronic kidney disease, liver disease, diabetes mellitus, heart disease, stroke, epilepsy, autism, etc.) is managed by its own dedicated module. This approach allows the system to be easily expanded in the future to include additional conditions, while also facilitating efficient updates to existing modules as new data becomes available. Modules tailored for Brain-Computer Interfaces (BCIs), including those that use the motor imagery paradigm, are capable of processing EEG data to generate actionable commands and appropriate responses.

The system also includes guidelines for upgrading traditional EEG systems to cutting-edge three-dimensional multilayer EEG (Ekpar EEG) systems. These innovative systems, developed by Ekpar [7] – [9], are based on a conceptual framework that uses approximations of key bio-signal features to analyze or influence the underlying biological systems. For each module, advanced AI models are developed and trained using well-structured data, as described in the paper. These models can integrate genetic, environmental, lifestyle, and other relevant factors to provide a more accurate understanding of the participants' circumstances.

Figure 1 represents selected key components of the system visually.

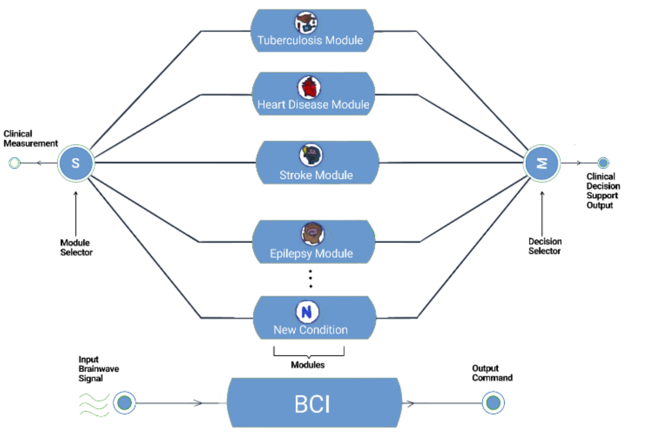

Fig. 1: System Schematic Design Diagram for the Comprehensive AI-Driven Healthcare Solution and Brain Computer Interface System. The New Conditions component represents additional health conditions that can be incorporated into the solution via new modules.

The development of AI models involves four primary approaches:

1. Leveraging Large Language Models (LLMs): This method utilizes models such as GPT-4 and Deepseek as inference engines, processing data formatted as multidimensional input vectors. Fine-tuning may also be applied to the LLM to optimize performance.
2. Prompt Engineering for LLMs: This approach applies prompt engineering to models like Deepseek, Bard, and GPT-4 (including future versions) to outline a sequence of actions for building the AI system. These steps are then executed with expertise in AI, neural networks, deep learning, Python, TensorFlow, Keras, and other machine learning tools such as Scikit-learn and Matplotlib.
3. Automated AI Model Generation: LLMs like Deepseek, Bard, and GPT-4 (and their future iterations) are used in an automated pipeline to generate specific AI models.
4. Custom AI Architecture Design: In this method, the AI system is designed directly by leveraging the creator's deep knowledge of AI, neural networks, deep learning, Python, TensorFlow, Keras, and additional ML tools such as Scikit-learn and Matplotlib.

Thorough documentation of the methodologies and tools used in developing the solution is carried out, ensuring seamless transfer and reuse of the system.

The generated AI models are then assessed and compared based on performance metrics (e.g., specificity, sensitivity) and their effectiveness in addressing the challenges at hand.

4. Automated Image-Based Tuberculosis Diagnosis Module

The second method of the four methods outlined above is adopted to get generative artificial intelligence tools such as large language models and in particular, ChatGPT, to generate instructions for the construction of convolutional neural networks for the automated diagnosis of tuberculosis on the basis of chest radiography image sequences.

A generalized prompt is utilized to generate recommendations for the overall design of the system for automated image-based diagnosis of tuberculosis. Then a more refined prompt follows for more precise steps and actual source code for the actual convolutional neural network models to be constructed in light of the dimensions of the input and/or pre-processed image datasets.

5. Dataset

Chest radiography image sequences in datasets provided by Rahman et al [31] were employed for the training, testing and validation of the AI models developed herein. Data augmentation, possibly through local data collection drives could enhance the original datasets, improve the performance, stability and robustness of the AI models and pave the way for incorporation into the comprehensive AI-powered healthcare system created by Ekpar [3] – [6] as a module for the automated diagnosis of tuberculosis based on image processing.

Figure 2 shows a set of randomly selected images from the dataset with their corresponding classes, that is, normal or with tuberculosis present. The original images had dimensions of 512 pixels by 512 pixels and were pre-processed to 180 pixels by 180 pixels for faster processing.

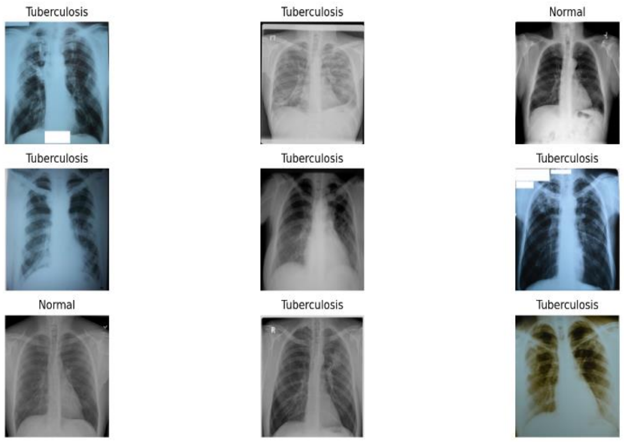

Fig. 2: Sample images from dataset indicating the presence or absence of tuberculosis.

Data Availability

The data collections that support the conclusions of this study are contained in the chest radiography image dataset publicly available from the Kaggle dataset repository at https://www.kaggle.com/datasets/tawsifurrahman/tuberculosis-tb-chest-xray-dataset.

First Chatgpt Prompt

Design a system for automated image-based diagnosis of tuberculosis.

First Chatgpt Response

Designing a system for automated image-based diagnosis of tuberculosis (TB) involves creating a pipeline that processes chest X-ray (CXR) images, analyzes them using machine learning algorithms, and provides diagnostic results. The goal is to identify signs of tuberculosis in the images with high accuracy and efficiency, supporting healthcare providers with a fast and reliable diagnosis.

Here's a step-by-step approach to designing such a system:

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1. Data Collection and Preprocessing

The system needs a diverse dataset of chest X-rays, including both TB-positive and TB-negative cases. The quality and diversity of the dataset will directly impact the system's performance.

Data Sources:

- Public datasets such as NIH Chest X-ray Dataset, Kaggle's Chest X-ray Images (Pneumonia), or TBX11K.
- Medical institutions could also provide anonymized X-ray data.

Preprocessing:

- Normalization: Standardize the image size and resolution (e.g., 224x224 pixels).
- Data Augmentation: Use techniques like rotation, flipping, and scaling to increase dataset diversity and make the model more robust.
- Image Enhancement: Apply contrast enhancement or edge detection to improve the visibility of lung areas and abnormal regions.

- Normalization: Standardize pixel values (e.g., to a range of 0-1 or -1 to 1).
- Segmentation: Apply lung segmentation techniques to focus the analysis on lung areas, ignoring irrelevant parts of the image.

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2. Model Development (Deep Learning-Based Approach)

2.1 Convolutional Neural Network (CNN)

A CNN can be used for feature extraction from chest X-ray images. Transfer learning from pre-trained models such as ResNet, DenseNet, or VGG19 can be a good approach, as they have been trained on large datasets and can recognize complex patterns.

Model Architecture:

- Input Layer: The chest X-ray image (224x224 pixels, 1 or 3 channels depending on grayscale or color input).
- Convolutional Layers: Extract low-level features such as edges, textures, and shapes.
- Pooling Layers: Reduce dimensionality and retain important features.
- Fully Connected Layers: Combine features from convolutional layers to classify the image as TB-positive or TB-negative.
- Softmax Output Layer: Outputs the probabilities for TB-positive and TB-negative.

Example CNN Models:

- ResNet50: Known for its residual blocks, allowing deep networks to avoid vanishing gradient problems.
- EfficientNet: A model designed to be efficient in terms of parameters and computational resources.
- 2.2 Pre-trained Model & Fine-tuning

Start with a model like ResNet or EfficientNet, pre-trained on ImageNet, and fine-tune it on the chest X-ray dataset. Fine-tuning allows the model to leverage learned features and specialize in TB diagnosis.

2.3 Data Augmentation & Regularization

- Augmentation: Rotate, scale, and crop X-ray images to create more training data.
- Dropout: Prevent overfitting in the fully connected layers.

2.4 Transfer Learning (optional)

For more robust performance, a hybrid model could use a pre-trained architecture and fine-tune it using a TB-specific dataset. This approach helps improve accuracy, especially with limited TB datasets.

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3. Model Evaluation and Validation

3.1 Performance Metrics

To evaluate the model’s accuracy, use metrics such as:

- Accuracy: Percentage of correct classifications.
- Precision: Measure of positive prediction correctness (important in a medical context).
- Recall (Sensitivity): Measure of detecting actual TB cases (important for patient safety).
- F1-Score: Harmonic mean of precision and recall, balancing both metrics.
- ROC-AUC Curve: To evaluate the classification thresholds.

3.2 Cross-validation

Use cross-validation techniques like k-fold cross-validation to assess the model's generalizability and avoid overfitting.

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4. Post-Processing & Result Explanation

4.1 Heatmap Generation (Grad-CAM)

To explain the model’s decision, use Grad-CAM (Gradient-weighted Class Activation Mapping) to generate heatmaps that highlight areas in the chest X-ray where the model detected signs of TB.

4.2 Risk Score

In addition to a binary classification (TB-positive or TB-negative), the system can generate a risk score that quantifies the probability of TB being present, helping healthcare professionals make more informed decisions.

4.3 Multiclass Classification (Optional)

For further categorization, the system can classify TB severity or types (e.g., active TB, latent TB, or no TB).

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5. User Interface and Integration

5.1 Web or Mobile Application

- Upload: The user uploads chest X-ray images through a web or mobile interface.
- Prediction: The system processes the image and returns the TB diagnosis, along with the heatmap and risk score.
- Feedback: Healthcare professionals can provide feedback on the results to further fine-tune the model.
- 5.2 Cloud Integration
- The system could be cloud-based to allow access from remote clinics and hospitals with minimal infrastructure.
- Provide an API for integration with existing hospital management systems (HMS) for seamless patient data flow.

5.3 Error Handling and Confidence Scores

- Provide users with confidence scores to indicate the certainty of the diagnosis.
- In cases of low confidence or ambiguous results, the system should request a second opinion from a human radiologist.

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6. Deployment and Monitoring

6.1 Deployment

The trained model can be deployed on a cloud server or edge device, depending on infrastructure needs. Cloud servers are scalable, while edge devices (e.g., mobile phones or local servers) are more suitable for remote areas with limited internet connectivity.

6.2 Continuous Learning

The system can be designed to continuously learn from new annotated X-ray images, retraining periodically to improve performance as more data becomes available.

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7. Ethical Considerations & Regulations

- Privacy & Security: Ensure compliance with medical data privacy laws like HIPAA (Health Insurance Portability and Accountability Act) or GDPR (General Data Protection Regulation).
- Bias Mitigation: Use a diverse dataset to minimize demographic bias in TB diagnosis.
- Clinical Validation: Before full deployment, conduct clinical trials and obtain regulatory approval (e.g., from the FDA or CE certification) to ensure the system meets medical standards.

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8. Future Enhancements

- Multimodal Diagnosis: Combine X-ray images with other medical data (e.g., patient history, lab results) for a more comprehensive diagnosis.
- Mobile Deployment: Adapt the system for use in low-resource settings, enabling healthcare workers in remote areas to conduct diagnoses.
- Integration with AI-Assisted Tools: Use AI to automate the reporting process, such as automatically generating diagnostic reports and suggestions for treatment.

This system can greatly enhance early detection of tuberculosis, particularly in resource-limited settings where radiologists may not be readily available. By automating the image-based diagnostic process, the system helps increase efficiency, reduce diagnostic errors, and improve overall TB care outcomes.

Second Chatgpt Prompt

Design a two-dimensional convolutional neural network for classification of images into two classes where each image is 180 pixels by 180 pixels.

Second Chatgpt Response

Designing a two-dimensional convolutional neural network (CNN) for image classification into two classes (binary classification) with input images of size 180×180180 \times 180 pixels involves the following layers:

1. Input Layer:

- Input shape is (180,180,3) (180, 180, 3) because the images are colored (RGB), so there are three channels.

2. Convolutional Layers:

- Convolutional layers are used to extract features from the image.
- We use several filters (kernels) that slide over the image to detect patterns like edges, textures, and more complex features in deeper layers.

3. Pooling Layers:

- After convolutional layers, pooling layers (usually max-pooling) are used to reduce the spatial dimensions (height and width) while retaining important information.

4. Flattening Layer:

- After applying convolution and pooling layers, the resulting feature maps are flattened into a one-dimensional vector to feed into the fully connected layers (dense layers).

5. Fully Connected Layers (Dense Layers):

- These layers are used to make final predictions based on the extracted features.
- Typically, we use one dense layer followed by a final output layer.
- Output Layer:
- The output layer is a sigmoid activation function, which gives us a probability of belonging to one of the two classes.

Here's an example design in Keras:

```
import tensor flow as tf
from tensor flow. keras import layers, models
# Define the model
model = models. Sequential ()
# First Convolutional Layer
model. add (layers. Conv2D (32, (3, 3), activation='relu', input_shape= (180, 180, 3)))
model. Add (layers. MaxPooling2D ((2, 2)))
# Second Convolutional Layer
model. Add (layers. Conv2D (64, (3, 3), activation='relu'))
model. Add (layers. MaxPooling2D ((2, 2)))
# Third Convolutional Layer
model. Add (layers. Conv2D (128, (3, 3), activation='relu'))
model. Add (layers. MaxPooling2D ((2, 2)))
# Flattening Layer
model. Add (layers. Flatten ())
# Fully Connected Layer
model. Add (layers. Dense (128, activation='relu'))
# Output Layer
model. add (layers. Dense (1, activation='sigmoid')) # For binary classification
# Compile the model
model. compile (optimizer='adam',
          loss='binary_crossentropy',
          metrics=['accuracy'])
# Model summary
model. Summary ()
```

Explanation:

1. Conv2D Layers:

- The first Conv2D layer has 32 filters with a kernel size of 3×33 \times 3, and the activation function is ReLU (Rectified Linear Unit).

- Each subsequent Conv2D layer increases the number of filters (64 and 128) to capture more complex features as the network deepens.

2. MaxPooling2D Layers:

- These layers reduce the spatial dimensions by pooling over a 2×22 \times 2 region. This helps reduce the computational complexity and control overfitting.

3. Flatten Layer:

- This layer flattens the 3D output (from the convolutional and pooling layers) into a 1D vector to be passed to the dense layers.

4. Dense Layer:

- A fully connected layer with 128 neurons and ReLU activation to learn complex patterns.

5. Output Layer:

- A single neuron with a sigmoid activation function for binary classification (output between 0 and 1).
- Model Compilation:
- The model is compiled with the Adam optimizer and binary cross-entropy loss function, which is typically used for binary classification tasks.
- Accuracy is used as the evaluation metric.

Example Training Code:

Assuming you have your dataset loaded into X_train, Y_train, X_val, Y_val

X_train and X_val should have shape (num_samples, 180, 180, 3), Y_train and Y_val should have shape (num_samples, 1)

history = model. Fit (X_train, Y_train,

epochs=10,

batch_size=32,

validation_data=(X_val, Y_val))

Key Considerations:

- Data Augmentation: If your dataset is small, using data augmentation (e.g., rotations, flips, and zooms) can help improve the model's ability to generalize.
- Regularization: Techniques like dropout or L2 regularization can be added to the dense layers to prevent overfitting, especially if you have a small dataset.
- Training: The number of epochs and batch size should be tuned based on the specific dataset and hardware.

This architecture can be a good starting point, and you can adjust the number of filters, layers, and other hyperparameters based on the performance and the size of your dataset.

Two-Dimensional (2d) Convolutional Neural Network (Cnn) Architecture

Based on the recommended of ChatGPT reproduced above, the 2D CNN was designed. The detailed architecture is contained in the recommendations above.

Figure 3 illustrates the graphical representation of a 2D CNN along the lines of the architecture suggested by ChatGPT.

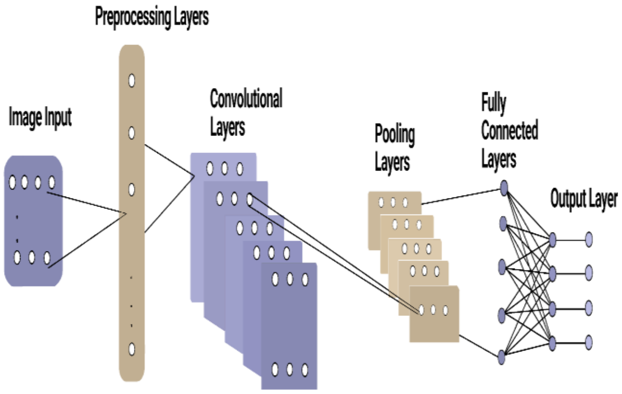

Fig. 3: Schematic Graphical Representation of Two-dimensional (2D) Convolutional Neural Network (2D CNN) Architecture.

5. Results

This study implemented the suggested 2D CNN architecture using the source code generated by the generative artificial intelligence system or large language model (ChatGPT) in the Python programming language by leveraging the

TensorFlow platform and the associated Keras Application Programming Interface (API) [32] – [33]. Partitioning of the dataset resulted in a split into a training dataset with 80% of the data and a testing/validation dataset with 20% of the data. Training proceeded for 10 epochs with the Adam Optimizer [34] – [35] and binary cross-entropy loss function with a batch size of 32.

Figure 4 depicts a plot of the traces of the training and validation accuracy and training and validation loss pairs over the training cycles.

The performance of the model can be gleaned from the plot which demonstrates convergence of the training and validation performance metrics over the epochs.

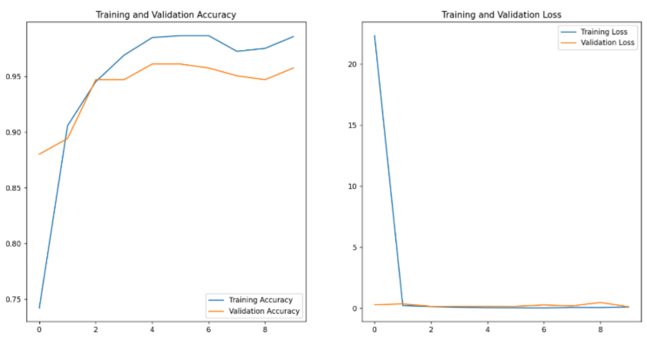

Fig. 4: Performance Metrics – Training and Validation Accuracy and Loss Traces.

6. Conclusion

The work reported in this paper relied on the recommendations of generative artificial intelligence tools such as large language models to develop artificial intelligence models, and more specifically, convolutional neural networks for the automated diagnosis of tuberculosis by examining chest radiography image sequences. Enhancement of the resulting artificial intelligence models could permit their inclusion in modules for the automated chest radiography image-based detection of tuberculosis within the framework of a comprehensive artificial intelligence-driven healthcare system capable of proffering insights for clinical decision support in actual healthcare settings including those with limited resources.

Conflicts of Interest

There are no conflicts of interest to disclose.

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