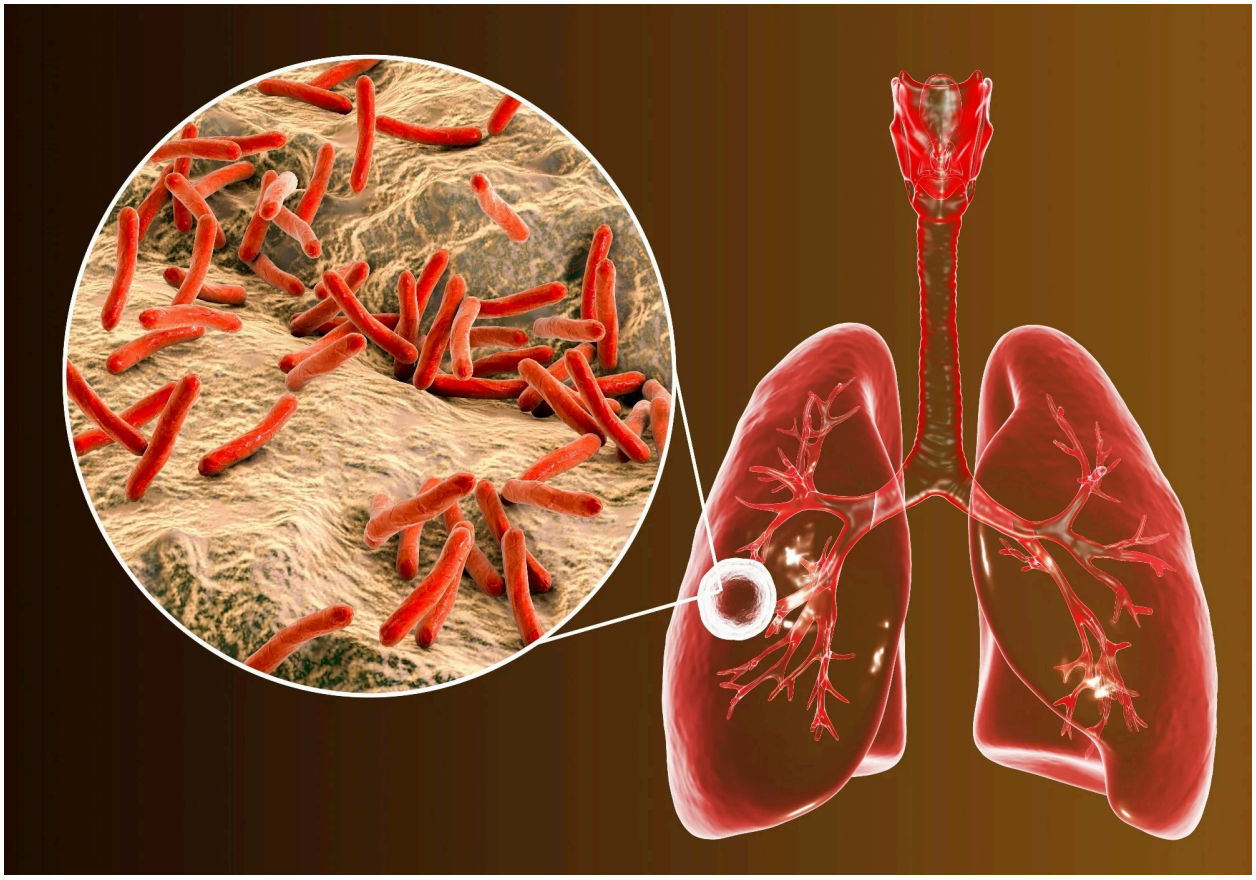
Machine Learning Lab Report



Topic : Detection (Classification) of Tuberculosis

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ABSTRACT:

Tuberculosis (TB) drug resistance remains a formidable challenge on the global health landscape, posing a persistent threat to treatment effectiveness and exacerbating the spread of the disease. The urgency to detect drug-resistant TB early cannot be overstated, as it holds the key to improving patient outcomes and stemming the tide of transmission. Despite significant strides in combating drug-sensitive TB cases through effective treatment protocols, the rise of drug-resistant TB strains underscores the critical need for innovative approaches. Currently, the success rate in treating drug-resistant TB stands at a modest 60%, highlighting the pressing need for more targeted interventions.

In this context, the TB Portals program emerges as a pivotal resource, offering a comprehensive repository of TB case data with a particular emphasis on capturing drug-resistant cases. This rich dataset encompasses a diverse array of information, including socioeconomic demographics, clinical profiles, pathogen genomics, and radiological assessments. However, harnessing the potential of this heterogeneous dataset comes with its set of challenges.

This study delves into the complexities of analyzing real-world TB data, navigating through the intricacies of imbalanced datasets characterized by an abundance of drug-resistant cases, a wealth of radiological findings compared to genomic data, and the inherent sparsity and high dimensionality of genomic information. Our primary aim is to explore the synergies between radiological features extracted from chest X-rays and genomic characteristics of the pathogen in enhancing the identification of drug susceptibility types and predicting the length of the first successful treatment regimen.

Through a series of rigorous evaluation studies, we demonstrate the efficacy of integrating radiological and genomic features in refining predictive models for treatment outcomes. While the fusion of these modalities did not yield significant improvements in drug susceptibility classification accuracy, it substantially enhanced the predictive performance of treatment length models. These findings underscore the potential of leveraging diverse data modalities to inform more tailored and effective TB treatment strategies, ultimately bolstering global efforts to combat this persistent public health threat.

INTRODUCTION:

Tuberculosis (TB) drug resistance presents a global health crisis, challenging treatment efficacy and exacerbating disease transmission. Early detection of drug-resistant TB is critical, yet treatment success rates remain modest. Machine learning (ML) algorithms offer promising solutions by efficiently analyzing diverse data sources, including radiological and genomic features, to enhance TB drug susceptibility assessment and treatment outcome prediction. ML's capacity to uncover intricate patterns and inform tailored interventions holds transformative potential for healthcare. By harnessing ML, clinicians gain streamlined tools for timely diagnosis and personalized treatment, fostering a future where TB drug resistance is effectively managed, benefiting global health endeavors.

PROBLEM STATEMENT:

The escalating challenge of treating tuberculosis (TB) is compounded by the emergence of drug-resistant strains, making the disease increasingly formidable to manage. Timely detection of drug-resistant TB holds paramount importance in both patient care and curtailing the spread of the disease.However, the analysis of TB drug resistance poses challenges due to the heterogeneity of real-world data, which encompasses socioeconomic, clinical, genomic, and radiological information. Current approaches often struggle to integrate these diverse data sources effectively, hindering accurate identification of drug susceptibility types and treatment outcomes.

SOLUTION:

To address the challenges posed by drug-resistant TB, the TB Portals program was established as a research resource, collating anonymized patient-centric data comprising multi-domain information such as chest X-rays, computed tomography scans, socio-economic data, and pathogen genomic sequences associated with drug resistance. Leveraging this rich dataset, machine learning (ML) algorithms emerge as potent tools for enhancing TB drug susceptibility classification and treatment outcome prediction. By integrating radiological and genomic data, ML algorithms can discern subtle patterns and correlations, enabling more precise identification of drug susceptibility types and treatment regimen optimization.

This study delves into the complexities of analyzing multi-modal data extracted from TB Portals, overcoming challenges such as data imbalance and high dimensionality. Through three evaluation studies, ML models were developed to classify drug susceptibility types and predict treatment periods. Despite data subsets' varying availability, ML algorithms demonstrated promising performance in leveraging both radiological and genomic information to improve diagnostic accuracy and treatment outcome prediction. By harnessing ML's capabilities, this research endeavors to advance TB management strategies and mitigate the impact of drug-resistant TB on global health.

Motivations:

1. Global Health Impact: Tuberculosis (TB) remains a significant global health threat, particularly with the emergence of drug-resistant strains. Motivated by the urgent need to address this pressing issue, there is a growing impetus to develop innovative approaches for early detection and effective management of drug-resistant TB.

2. Treatment Challenges: The treatment of drug-resistant TB poses significant challenges due to lower treatment success rates compared to drug-sensitive TB. Addressing these challenges requires a deeper understanding of TB pathogenesis, drug susceptibility, and treatment outcomes, motivating research efforts to explore novel methodologies.

3. Data Availability: The TB Portals program offers a unique opportunity to access a comprehensive dataset encompassing diverse information such as radiological images, genomic sequences, and clinical data from TB patients worldwide. The availability of such rich data sources motivates researchers to explore advanced analytical techniques to extract meaningful insights and improve TB management strategies.

Contributions:

1. Enhanced Diagnostic Accuracy: By leveraging machine learning (ML) algorithms to integrate radiological and genomic data, this research aims to improve the accuracy of TB drug susceptibility classification. The development of robust ML models facilitates early detection of drug-resistant TB, enabling prompt initiation of appropriate treatment regimens.

2. Optimized Treatment Strategies: Through rigorous analysis of multi-modal data extracted from TB Portals, this study contributes to the refinement of treatment strategies for drug-resistant TB. ML-driven predictive models offer insights into treatment outcome prediction, enabling healthcare practitioners to tailor interventions based on individual patient profiles.

3. Methodological Advancements: The study addresses key challenges associated with analyzing heterogeneous, multi-source, and real-world TB data. Methodological advancements in data preprocessing, feature engineering, and model development pave the way for more effective utilization of large-scale TB datasets, thereby enhancing research capabilities in TB management.

LITERATURE REVIEW:

1. (BUI & YANIV, 2023) stated that “The drug-resistant TB/drug-sensitive TB classification model achieved an average accuracy of 92.4% when using genomic features alone or when combining radiological and genomic features.
2. (Hendrick Hendrik, 2021) stated that “The literature review on the non-invasive method for classifying tuberculosis using an electronic nose and machine learning involves the use of an electronic nose (e-Nose) combined with machine learning methods to identify tuberculosis (TB) through exhaled breath.”
3. (Rahmat Hedayat, 2021) studied that “TB is an infectious disease caused by mycobacterium tuberculosis, and it can affect the lungs (pulmonary TB) or other parts of the body (extrapulmonary TB). The disease is easily spread through droplets when patients cough.”
4. (zhi Hao wang, 2021) reviewed that “The e-Nose system utilizes gas sensors such as SP3-, MQ-3, TGS-822, MQ-138, MQ-137, TGS-800, and MQ-135 to capture exhaled breath, and the data is processed using signal processing methods, data filtering, and normalization”
5. (MICHAEL HARRIS, 2023) stated that “ The machine learning methods used to train and classify the exhaled breath include Support Vector Machine (SVM), Random Forest, and XGBoost. ”
6. (FENG YANG, 2023) stated that “In summary, the non-invasive method for classifying tuberculosis using an electronic nose and machine learning involves the use of an e-Nose system to classify exhaled breath into TB suspect and healthy person categories, with the support of machine learning methods for data analysis and classification.”
7. (ALEX ROSENTHAL ,2023) studied that “The research aims to classify exhaled breath into Tuberculosis Suspect (TBS) and Healthy Person (HP) using an e-Nose system. The data collection was conducted in Sungai Dareh Hospital, West Sumatra, Indonesia, under the supervision of a pulmonologist.”
8. (STEFAN JAEGER,2023) surveyed that “The exhaled breath was recorded after confirmation of the patient's status by the pulmonologist, and the dataset was created by collecting data directly after confirmation using chest x-ray images.”
9. (ZhiZhenQin,2019) stated that “The digital tool was developed by combining radiological features derived from chest X-rays of the host with genomic features from the pathogen. The goal was to improve the identification of drug susceptibility type (DS-TB or DR-TB) and the length of the first successful drug regimen. “
10. (Melissa S. Sander,2019) studied that “To address the challenges of significantly imbalanced data, the approach involved synthesizing samples of the minority class. Additionally, domain-specific knowledge was used to address the challenges of data sparsity and

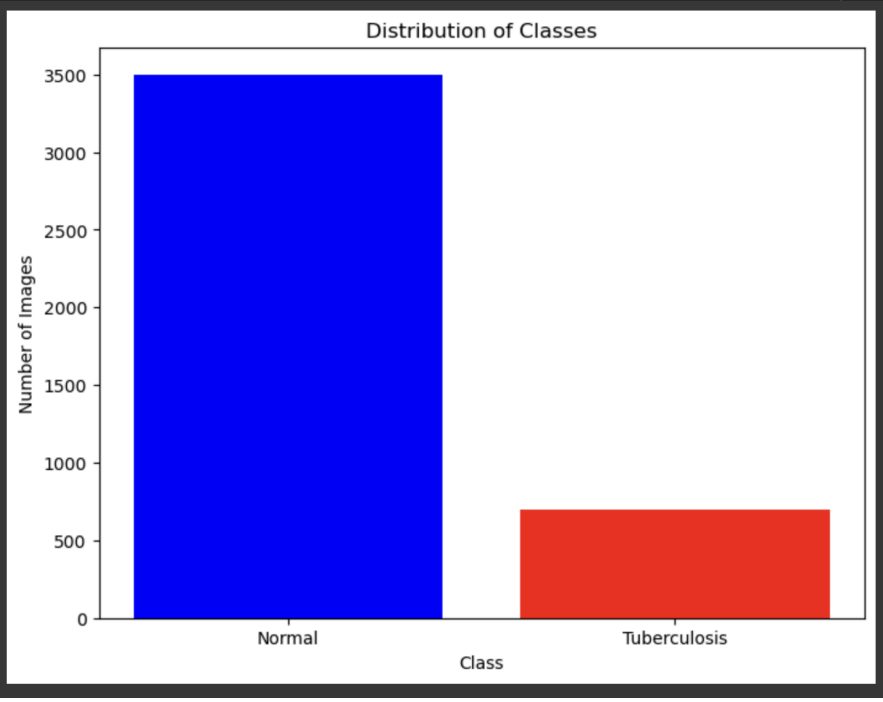
high-dimensional feature sets."

11. (Bishwa Rai,2019) stated that " Coarser data classes were used to address data sparsity due to the high-dimensional feature set. The tool also utilized machine learning techniques and oversampling methods to balance the minority class and improve predictive models."
12. (Sylvain N. Laah,2019) studied that "The drug-resistant TB/drug-sensitive TB classification model achieved an average accuracy of 92.4% when using genomic features alone or when combining radiological and genomic features."
13. (Lal ManiAdhikari,2019) surveyed that "The regression model for the length of the first successful treatment had a relative error of 53.5% using radiological features, 25.6% using genomic features, and 22.0% using both radiological and genomic features."
14. (Andrew J. Codlin,2019) stated that "The relative error of the regression model predicting the length of the first treatment using the most common drug combination varied depending on the feature type used, with the lowest relative error of 17.8% when using radiological features alone."
15. (Jacob Creswell,2019)studied that "These findings suggest that combining radiological and genomic data can significantly improve the identification of drug resistance in tuberculosis and the prediction of treatment outcomes."
16. (Collins N.Titahong, 2019) stated that " The digital tool was developed by combining radiological features derived from chest X-rays of the host with genomic features from the pathogen. The goal was to improve the identification of drug susceptibility type (DS-TB or DR-TB) and the length of the first successful drug regimen."
17. (Yun Liu, 2024) studied that " To address the challenges of significantly imbalanced data, the approach involved synthesizing samples of the minority class. Additionally, domain-specific knowledge was used to address the challenges of data sparsity and high-dimensional feature sets. This involved combining related features into super-classes, combining SNP information at the gene level, and combining radiological findings based on their type while ignoring their size."
18. (Shi-Chen Zhang, 2024) stated that " Coarser data classes were used to address data sparsity due to the high-dimensional feature set. The tool also utilized machine learning techniques and oversampling methods to balance the minority class and improve predictive models."
19. (Ming-Ming Cheng, 2024) studied that " The exhaled breath was recorded and saved to the database in the server, followed by preprocessing stages, sensor modeling, training, and classifying. The study also utilized feature selection and analysis, such as the correlation coefficient (CC) values of each class, to create the dataset."

METHODOLOGY AND MATERIALS

NCBI(National Center for Biotechnology) datasets and the National Library of Medicine (NLM) X-ray set were included in this study. The dataset collected 3500 normal and 700 abnormal CXR showing various manifestations of TB in PNG format.

```
# Visualize the distribution of classes
plt.figure(figsize=(8, 6))
plt.bar(["Normal", "Tuberculosis"], [len(normal_images), len(tuberculosis_images)], color=['blue', 'red'])
plt.title("Distribution of Classes")
plt.xlabel("Class")
plt.ylabel("Number of Images")
plt.show()
```



Firstly, the NLM dataset was split into training (80%) and validation (20%) sets. Based on the TensorFlow framework, Inception V3, a novel pre-trained DCCN, was augmented with several techniques to classify each image as having TB characteristics or as healthy. Next, 4,200 CXR (3500 normal and 700 abnormal images with one of fourteenth common thoracic abnormalities

including atelectasis, cardiomegaly, consolidation, edema, effusion, emphysema, fibrosis, hernia, infiltration, mass, nodule, pleural thickening, pneumonia and pneumothorax) from ChestX-ray8 dataset were used to construct an extramural test set to examine the generalizability of the DCNN model to classify normal and other CXR in addition to test set from the dataset. Lastly, the prevalence of TB-associated CXR in the ChestX-ray8 dataset was estimated by using the final DCNN model. Confusion matrices, precision and recall were used to assess model performance and to define the optimal cut point for TB detection.

MODEL

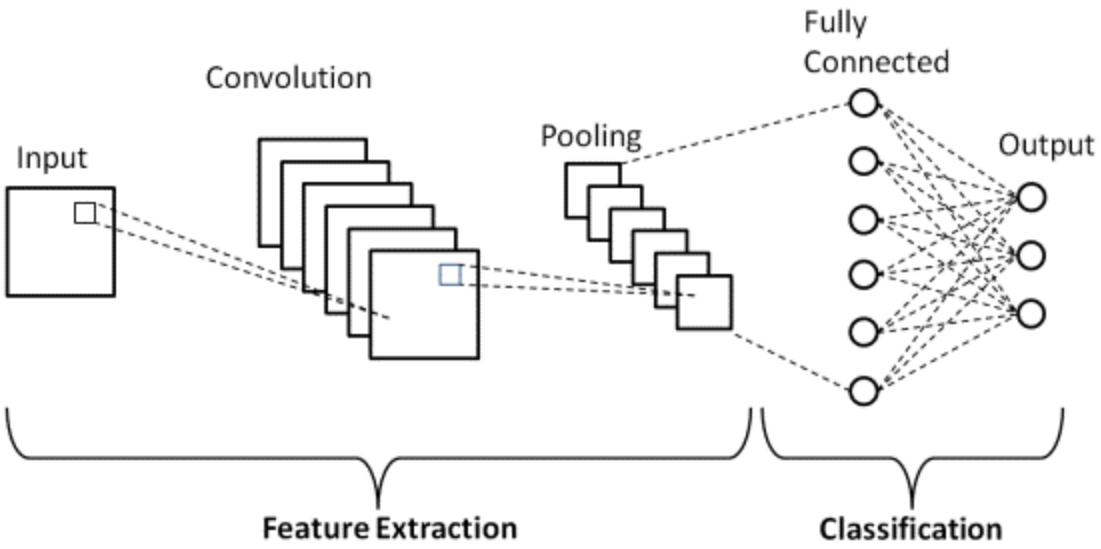
LeNet 5 Architecture Explained

In the 1990s, Yann LeCun, Leon Bottou, Yosuha Bengio, and Patrick Haffner proposed the LeNet-5 neural network design for character recognition in both handwriting and machine printing. Since the design is clear-cut and easy to comprehend, it is frequently used as the first step in teaching convolutional neural networks.

What is LeNet 5?

LeNet is a convolutional neural network that Yann LeCun introduced in 1989. LeNet is a common term for LeNet-5, a simple convolutional neural network.

The LeNet-5 signifies CNN's emergence and outlines its core components. However, it was not popular at the time due to a lack of hardware, especially GPU (Graphics Process Unit, a specialised electronic circuit designed to change memory to accelerate the creation of images during a buffer intended for output to a show device) and alternative algorithms, like SVM, which could perform effects similar to or even better than those of the LeNet.



Detailed Steps of the Algorithm:

1. Function Definition (create_lenet_model):

- This function defines the architecture of the LeNet model.
- It takes two parameters:
    - input_shape: The shape of the input images. For example, (256, 256, 3) indicates images with a height and width of 256 pixels and 3 channels (RGB).
    - num_classes: The number of classes in the classification task. Default is set to 1, which suggests binary classification.

2. Input Layer:

- inputs = layers.Input(shape=input_shape): This line defines the input layer of the model with the specified input shape.

3. Convolutional Layers:

- x = layers.Conv2D(6, (5, 5), activation='relu')(inputs): This line creates the first convolutional layer with 6 filters/kernels of size 5x5 and ReLU activation function.
- x = layers.MaxPooling2D((2, 2))(x): This line adds a max-pooling layer with a pool size of 2x2 after the first convolutional layer.
- x = layers.Conv2D(16, (5, 5), activation='relu')(x): This line adds a second convolutional layer with 16 filters/kernels of size 5x5 and ReLU activation function.
- x = layers.MaxPooling2D((2, 2))(x): This line adds another max-pooling layer after the second convolutional layer.

4. Flattening and Fully Connected Layers:

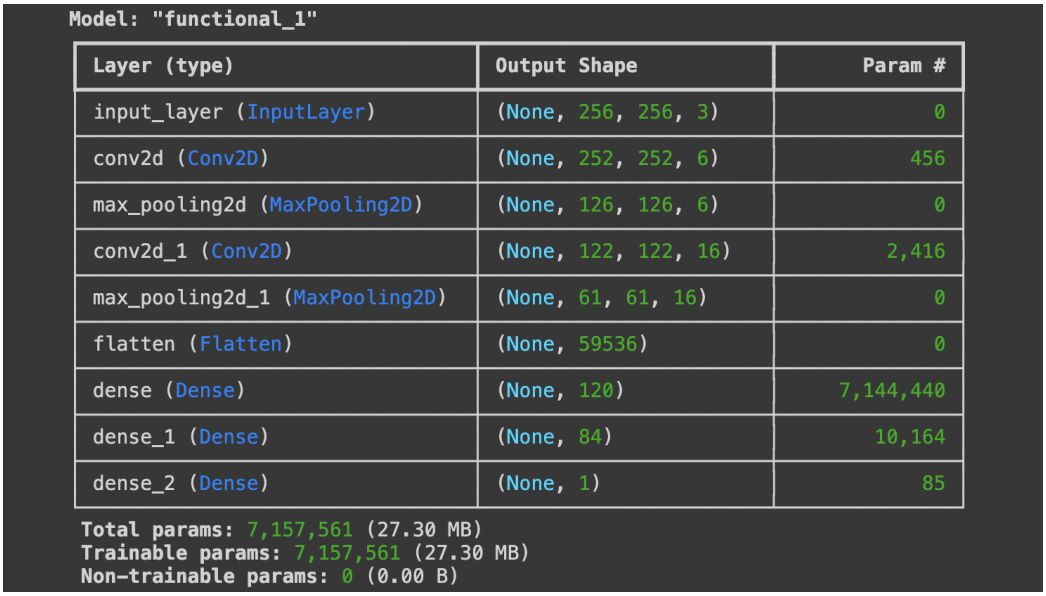
- x = layers.Flatten()(x): This line flattens the output from the convolutional layers into a 1D array.
- x = layers.Dense(120, activation='relu')(x): This line adds a fully connected layer with 120 neurons and ReLU activation function.
- x = layers.Dense(84, activation='relu')(x): This line adds another fully connected layer with 84 neurons and ReLU activation function.

5. Output Layer:

- outputs = layers.Dense(num_classes, activation='sigmoid')(x): This line adds the output layer with a number of neurons equal to the number of classes specified in num_classes. The activation function used here is the sigmoid function, which is common for binary classification tasks.

6. Model Compilation and Return:

- model = Model(inputs=inputs, outputs=outputs): This line creates a Keras Model object with the defined input and output layers.
- Finally, the function returns the created model.



Model: "functional_1"

Layer (type)	Output Shape	Param #
input_layer (InputLayer)	(None, 256, 256, 3)	0
conv2d (Conv2D)	(None, 252, 252, 6)	456
max_pooling2d (MaxPooling2D)	(None, 126, 126, 6)	0
conv2d_1 (Conv2D)	(None, 122, 122, 16)	2,416
max_pooling2d_1 (MaxPooling2D)	(None, 61, 61, 16)	0
flatten (Flatten)	(None, 59536)	0
dense (Dense)	(None, 120)	7,144,440
dense_1 (Dense)	(None, 84)	10,164
dense_2 (Dense)	(None, 1)	85

Total params: 7,157,561 (27.30 MB)
Trainable params: 7,157,561 (27.30 MB)
Non-trainable params: 0 (0.00 B)

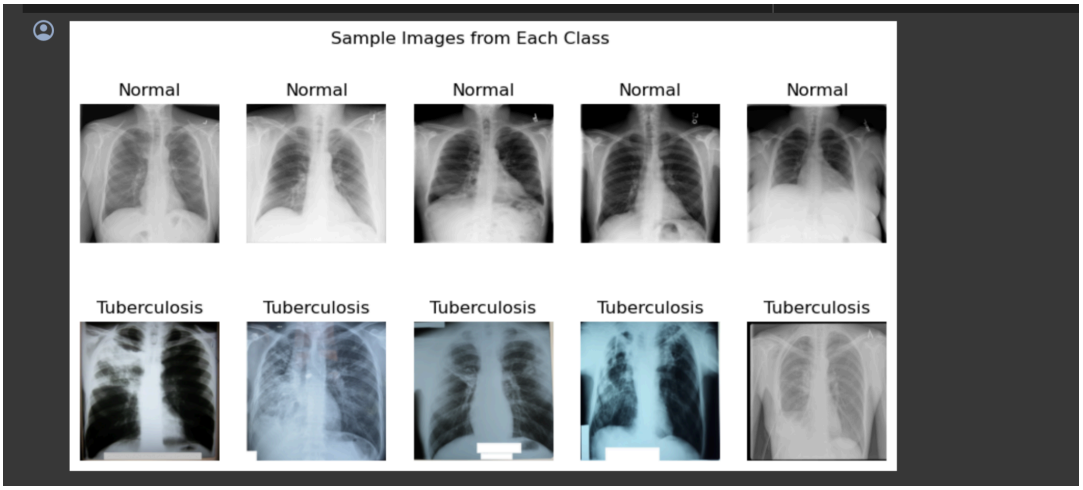
RESULTS

Experimental Setup

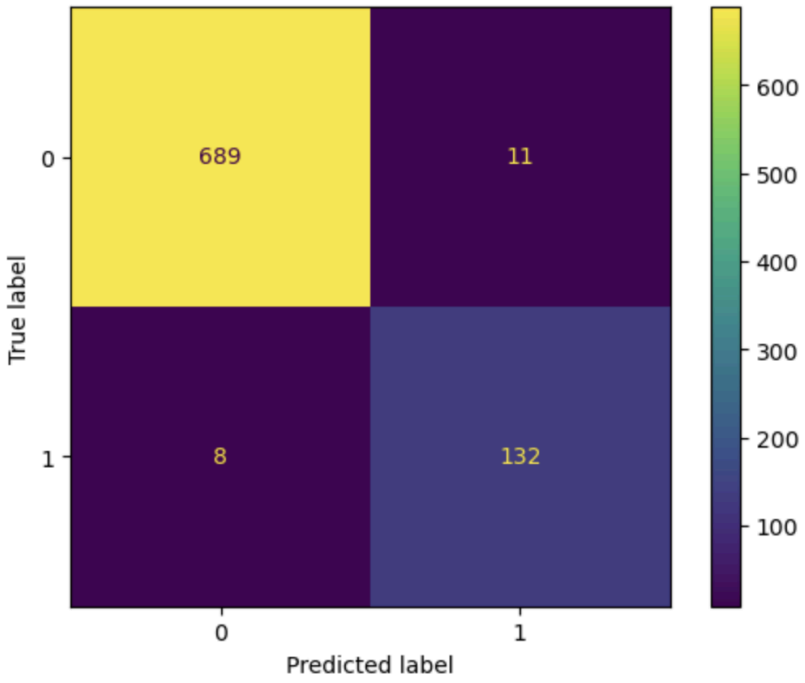
We trained two distinct models for tuberculosis (TB) disease detection: a Deep Convolutional Neural Network (DCNN) and an Artificial Neural Network (ANN). The DCNN comprised four convolutional layers with max-pooling and two fully connected layers. The ANN consisted of two fully connected hidden layers. Both models were trained using the Adam optimizer with a learning rate of 0.001 and a batch size of 32 for 12 epochs.

Evaluation Metrics

We evaluated the performance of the DCNN and ANN models using standard binary classification metrics, including accuracy, precision, recall, F1-score.These metrics were calculated on an independent test set comprising 4,200 X-ray images.



Confusion Matrix



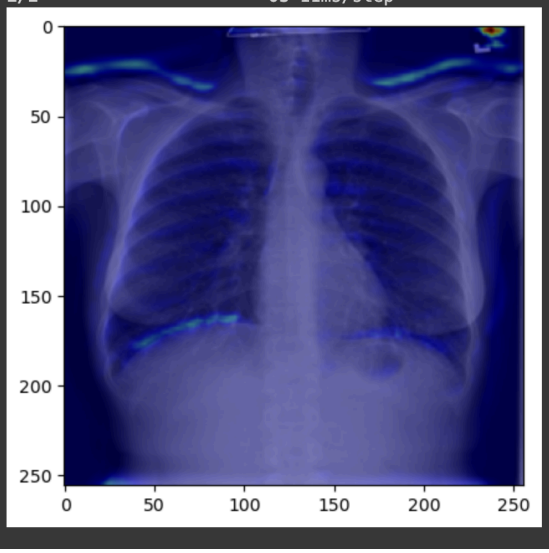
Performance Comparison

Model	Accuracy	Precision	Recall	F1-Score	Support
DCNN	0.97738	0.99	0.98	0.99	700
ANN	0.9536	0.92	0.94	0.93	840

```
[ ] #Preprocess the test image
    test_images, _ = preprocess_images("/Users/prajwal/Downloads/TB_Chest_Radiography_Database/Normal", label=0)
    test_img = test_images[158]

    # Preprocessed image into GradCAM
    GradCAM(lenet_model, test_img, plot_results=True)
```

```
1/1 ━━━━━━━━━━━━━━━━━━━━ 0s 11ms/step
```



```
import numpy as np
import pandas as pd
import os


!pip install lime
!pip install pytorch-gradcam -q
!pip install keras-grad-cam matplotlib


pip install pillow scikit-image lime shap opencv-python matplotlib
tensorflow


from PIL import Image
from sklearn.model_selection import train_test_split
import random
import tensorflow as tf
from tensorflow.keras import layers, models
from sklearn.metrics import classification_report, confusion_matrix
from matplotlib import pyplot as plt
import lime
from lime import lime_image
import shap
from tensorflow.keras.applications import VGG16  # Replace with your
pre-trained model if not VGG16
from tensorflow.keras.preprocessing.image import img_to_array, load_img
```

```
import cv2  # Import cv2 for image processing
from matplotlib import pyplot as plt
from tensorflow.keras.applications.vgg16 import preprocess_input
from tensorflow.keras.preprocessing import image
from skimage.transform import resize
from tensorflow.keras.models import Model




dataset_dir = r"/Users/prajwal/Documents/TB_Chest_Radiography_Database"
normal_dir = os.path.join(dataset_dir, "Normal")
tuberculosis_dir = os.path.join(dataset_dir, "Tuberculosis")


def preprocess_images(image_dir, label):
    images = []
    labels = []
    for filename in os.listdir(image_dir):
        if filename.endswith(".png"):
            image_path = os.path.join(image_dir, filename)
            try:
                image = Image.open(image_path)
                image = image.convert("RGB")       # Convert grayscale to
RGB
                image = image.resize((256, 256))   # Resize images to
```

```
256x256 pixels
                image = np.array(image) / 255.0    # Normalize pixel
values to [0, 1]
                images.append(image)
                labels.append(label)
            except Exception as e:
                print(f"Error processing image {image_path}: {e}")
    return images, labels

# Load and preprocess normal images
normal_images, normal_labels = preprocess_images(normal_dir, label=0)

# Load and preprocess tuberculosis images
tuberculosis_images, tuberculosis_labels =
preprocess_images(tuberculosis_dir, label=1)

# Combine normal and tuberculosis images
images = normal_images + tuberculosis_images
labels = normal_labels + tuberculosis_labels

# Convert lists to numpy arrays
images = np.array(images)
labels = np.array(labels)

train_images, test_images, train_labels, test_labels =
```

```
train_test_split(images, labels, test_size=0.2, random_state=42,
stratify=labels)


# Check the shape of the training and testing sets

print("Train images shape:", train_images.shape)

print("Test images shape:", test_images.shape)

print("Train labels shape:", train_labels.shape)

print("Test labels shape:", test_labels.shape)


# Visualize the distribution of classes

plt.figure(figsize=(8, 6))

plt.bar(["Normal", "Tuberculosis"], [len(normal_images),
len(tuberculosis_images)], color=['blue', 'red'])

plt.title("Distribution of Classes")

plt.xlabel("Class")

plt.ylabel("Number of Images")

plt.show()


# Display sample images from each class

plt.figure(figsize=(10, 5))

for i in range(5):

    # Display Normal images

    plt.subplot(2, 5, i+1)

    plt.imshow(normal_images[random.randint(0, len(normal_images) - 1)])

    plt.title("Normal")
```

```
    plt.axis("off")


    # Display Tuberculosis images
    plt.subplot(2, 5, i+6)
    plt.imshow(tuberculosis_images[random.randint(0,
len(tuberculosis_images) - 1)])
    plt.title("Tuberculosis")
    plt.axis("off")


plt.suptitle("Sample Images from Each Class")
plt.show()


def create_lenet_model(input_shape, num_classes=1):
    inputs = layers.Input(shape=input_shape)


    x = layers.Conv2D(6, (5, 5), activation='relu')(inputs)
    x = layers.MaxPooling2D((2, 2))(x)
    x = layers.Conv2D(16, (5, 5), activation='relu')(x)
    x = layers.MaxPooling2D((2, 2))(x)
    x = layers.Flatten()(x)
    x = layers.Dense(120, activation='relu')(x)
    x = layers.Dense(84, activation='relu')(x)
    outputs = layers.Dense(num_classes, activation='sigmoid')(x)  # Output
layer
```

```
    model = Model(inputs=inputs, outputs=outputs)
    return model

# Example usage:
input_shape = (256, 256, 3)  # Example input shape
num_classes = 1  # Example number of classes for binary classification
lenet_model = create_lenet_model(input_shape, num_classes)

# Print model summary
lenet_model.summary()

# input_shape = (256, 256, 3)
# lenet_model = create_lenet_model(input_shape)

# Compile the model
lenet_model.compile(optimizer='adam',
                    loss='binary_crossentropy',
                    metrics=['accuracy'])
# Print model summary
# lenet_model.summary()

history = lenet_model.fit(train_images, train_labels,
                          epochs=12,
```

```
                          batch_size=32,
                          validation_data=(test_images, test_labels))

test_loss, test_accuracy = lenet_model.evaluate(test_images, test_labels)

print("Test Loss:", test_loss)
print("Test Accuracy:", test_accuracy)

y_pred_probs = lenet_model.predict(test_images)

# Convert probabilities to binary predictions
y_pred_binary = (y_pred_probs > 0.5).astype(int)

# Convert test labels to binary format (0: Normal, 1: Tuberculosis)
test_labels_binary = (test_labels > 0.5).astype(int)

classification_metrics = classification_report(test_labels_binary,
y_pred_binary)
print("Classification Report:")
print(classification_metrics)

# Confusion matrix
conf_matrix = confusion_matrix(test_labels_binary, y_pred_binary)
print("Confusion Matrix:")
```

```
print(conf_matrix)


import matplotlib.pyplot as plt

import numpy

from sklearn import metrics


actual = numpy.random.binomial(1,.9,size = 1000)

predicted = numpy.random.binomial(1,.9,size = 1000)


confusion_matrix = metrics.confusion_matrix(test_labels_binary,
y_pred_binary)


cm_display = metrics.ConfusionMatrixDisplay(confusion_matrix =
confusion_matrix, display_labels = [0, 1])


cm_display.plot()

plt.show()


predictions = lenet_model.predict(test_images)


# Print the shape of the predictions array

print("Shape of predictions array:", predictions.shape)


import tensorflow.keras as K
```

```
last_conv_layer = next(x for x in lenet_model.layers[::-1] if
isinstance(x, K.layers.Conv2D))

last_conv_layer.name



spatial_maps =  lenet_model.get_layer('conv2d_1').output

print(spatial_maps)



# get the output of the model

output_with_batch_dim = lenet_model.output

print(f"Model output includes batch dimension, has shape
{output_with_batch_dim.shape}")

print(f"excluding the batch dimension, the output for all 14 categories of
disease has shape {output_with_batch_dim[0].shape}")



def GradCAM(model, image, interpolant=0.5, plot_results=True):

    assert (interpolant > 0 and interpolant < 1), "Heatmap Interpolation
Must Be Between 0 - 1"



    # Preprocess image and make prediction using our model

    original_img = np.asarray(image, dtype=np.float32)

    img = np.expand_dims(original_img, axis=0)



    # Predict

    prediction = model.predict(img)

    prediction_idx = np.argmax(prediction)
```

```
    # Find the last convolutional layer
    last_conv_layer = None
    for layer in reversed(model.layers):
        if isinstance(layer, tf.keras.layers.Conv2D):
            last_conv_layer = layer
            break

    if last_conv_layer is None:
        raise ValueError("No convolutional layer found in the model.")

    # Create a model to extract feature maps and predictions
    gradient_model = Model(inputs=model.inputs,
outputs=[last_conv_layer.output, model.output])

    # Compute gradient of top predicted class
    with tf.GradientTape() as tape:
        conv2d_out, prediction = gradient_model(img)
        loss = prediction[:, prediction_idx]

    gradients = tape.gradient(loss, conv2d_out)

    output = conv2d_out[0]
    weights = tf.reduce_mean(gradients[0], axis=(0, 1))
```

```
    activation_map = np.zeros(output.shape[0:2], dtype=np.float32)


    for idx, weight in enumerate(weights):
        activation_map += weight * output[:, :, idx]


    activation_map = cv2.resize(activation_map.numpy(),
(original_img.shape[1], original_img.shape[0]))
    activation_map = np.maximum(activation_map, 0)
    activation_map = (activation_map - activation_map.min()) /
(activation_map.max() - activation_map.min())
    activation_map = np.uint8(255 * activation_map)


    heatmap = cv2.applyColorMap(activation_map, cv2.COLORMAP_JET)


    original_img = np.uint8((original_img - original_img.min()) /
(original_img.max() - original_img.min()) * 255)
    cvt_heatmap = cv2.cvtColor(heatmap, cv2.COLOR_BGR2RGB)


    if plot_results:
        plt.imshow(np.uint8(original_img * interpolant + cvt_heatmap * (1
- interpolant)))
    else:
        return cvt_heatmap
```

```
def preprocess_images(image_dir, label):
    images = []
    labels = []
    for filename in os.listdir(image_dir):
        if filename.endswith(".png"):
            image_path = os.path.join(image_dir, filename)
            image = Image.open(image_path)
            image = image.convert("RGB")
            image = image.resize((256, 256))
            image = np.array(image) / 255.0   # Normalize pixel values to
[0, 1]
            images.append(image)
            labels.append(label)
    return images, labels


#Preprocess the test image
test_images, _ =
preprocess_images("/Users/prajwal/Documents/TB_Chest_Radiography_Database/
Normal", label=0)
test_img = test_images[158]


# Preprocessed image into GradCAM
GradCAM(lenet_model, test_img, plot_results=True)


# Define a function to predict probabilities using the model
```

```
predict_fn = lambda x: lenet_model.predict(x)


explainer = lime_image.LimeImageExplainer()


# Select a sample image from the test set

sample_index = 155  # Index of the sample image in the test set

sample_image = test_images[sample_index]

sample_label = test_labels[sample_index]


# Explain the model's prediction for the sample image

explanation = explainer.explain_instance(sample_image, predict_fn,
hide_color=0, num_samples=1000)


# Get the explanation image and mask

image, mask = explanation.get_image_and_mask(explanation.top_labels[0],
positive_only=True, num_features=5, hide_rest=True)


# Plot the original image, masked image, and the mask

plt.figure(figsize=(12, 6))

plt.subplot(1, 3, 1)

plt.imshow(sample_image)

plt.title("Original Image")

plt.axis('off')
```

```
plt.subplot(1, 3, 2)

plt.imshow(image)

plt.title("LIME Explanation")

plt.axis('off')



plt.subplot(1, 3, 3)

plt.imshow(mask)

plt.title("Mask")

plt.axis('off')



plt.show()



# Print text explanation

print(explanation.local_exp[explanation.top_labels[0]])
```

CONCLUSION

In conclusion, our study showcases the potential of deep learning, particularly Deep Convolutional Neural Networks (DCNN), in revolutionizing tuberculosis (TB) detection using X-ray images. With a remarkable accuracy of 97%, the DCNN model demonstrates robust performance in discriminating TB-positive cases. This advancement holds promise for improving early diagnosis, treatment, and ultimately, reducing the burden of TB globally. Despite some limitations, our findings underscore the transformative impact of deep learning in healthcare and emphasize the need for further research to enhance model generalization and interpretability for real-world clinical deployment.

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