UTM UNIVERSITI TEKNOLOGI MALAYSIA

FACULTY OF COMPUTING
UTM Johor Bahru

SECB3203-01(PROGRAMMING FOR BIOINFORMATIC)

Semester 01 2025/2026
Section 01

Project Report

Faculty of Computing

Dataset:
https://www.kaggle.com/datasets/miadul/tuberculosis-x-ray-dataset-synthetic

Project Title:
Tuberculosis Disease Classification Using Synthetic Chest X-Ray Dataset and Machine Learning Techniques

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SUBMISSION DATE : 18/1/2026

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1.0 Introduction

Tuberculosis (TB) is a contagious infectious disease caused by *Mycobacterium tuberculosis* and primarily affects the lungs. Despite advancements in medical science, TB remains one of the leading causes of death worldwide, particularly in low- and middle-income countries. Early detection and accurate diagnosis are critical in preventing disease transmission and ensuring effective treatment. One of the most commonly used diagnostic tools for TB screening is chest X-ray imaging due to its cost-effectiveness and wide availability.

In recent years, bioinformatics and data-driven approaches have played an important role in healthcare research, especially in disease detection and classification. The integration of machine learning techniques with medical imaging allows the automation of image analysis, reducing dependency on manual interpretation by radiologists. This project leverages Python programming and bioinformatics analysis techniques to develop a classification model capable of distinguishing tuberculosis-infected chest X-ray images from normal images.

This project adopts a current bioinformatics trend which is disease classification using machine learning and image-based data analysis and applies computational techniques to a synthetic chest X-ray dataset. By utilizing synthetic data, the project avoids ethical and privacy issues associated with real clinical data while still providing a realistic environment for developing and evaluating predictive models.

1.1 Problem Background

Tuberculosis diagnosis traditionally relies on laboratory tests and expert interpretation of medical images, which may not always be accessible in rural or resource-limited regions. Chest X-ray screening is widely used; however, interpreting X-ray images requires specialized expertise and is subject to inter-observer variability. Inconsistent interpretations may lead to misdiagnosis or delayed treatment.

Furthermore, the development of automated TB detection systems faces challenges due to the limited availability of large-scale, well-annotated medical imaging datasets. Privacy regulations and ethical constraints often restrict access to real patient data, slowing down research and model development. Synthetic datasets provide a viable alternative by generating realistic medical images that support experimentation and learning.

By applying bioinformatics programming techniques and machine learning models to synthetic chest X-ray data, this project aims to explore automated TB classification and provide hands-on experience in data preprocessing, analysis, model development, and evaluation using Python.

1.2 Problem Statement

The key problems addressed in this project are as follows:

- Manual interpretation of chest X-ray images for tuberculosis diagnosis is time-consuming and dependent on expert radiologists.
- Human error and subjectivity in X-ray interpretation may lead to misclassification of TB cases.
- There is limited access to large, labeled real-world medical datasets due to privacy, ethical, and legal constraints.
- Existing datasets may suffer from class imbalance or insufficient sample size, reducing model reliability.
- Many developing regions lack automated diagnostic tools to support early TB screening.
- Machine learning models require systematic preprocessing and feature extraction to achieve acceptable performance, which is often overlooked.
- There is a need for practical exposure to bioinformatics programming techniques that integrate data science and healthcare applications.

1.3 Objectives

The objectives of this project are:

1. To collect and utilize a synthetic tuberculosis chest X-ray dataset for bioinformatics analysis.
2. To preprocess and clean the dataset using Python-based data wrangling techniques.
3. To perform exploratory data analysis (EDA) to understand data distribution and relationships.
4. To develop machine learning models for classifying chest X-ray images into tuberculosis and normal classes.
5. To evaluate the performance of the developed models using suitable evaluation metrics.
6. To document the analysis process, results, and findings through GitHub and a formal project report.

1.4 Scopes

The scope of this project is defined as follows:

1.4.1 Data Used

- A synthetic chest X-ray dataset for tuberculosis classification obtained from Kaggle.
- The dataset consists of labeled X-ray images categorized into Tuberculosis and Normal classes.
- Only image data and corresponding labels are used, no real patient or clinical metadata is included.

1.4.2 Techniques to Be Used

- Python programming for all data processing and analysis tasks.
- Data wrangling techniques using Pandas and NumPy, including:
    - Handling missing values
    - Data normalization and scaling
    - Data formatting and transformation

- Exploratory Data Analysis (EDA):
    - Descriptive statistics
    - Correlation analysis
    - Data visualization using Matplotlib

- Machine learning and modeling techniques, including:
    - Regression-based models
    - Classification models
    - Model evaluation and refinement

- Model evaluation methods such as:
    - Accuracy
    - Mean Squared Error (MSE)
    - R-squared
    - Cross-validation and grid search (if applicable)

1.4.3 Methodology

The project methodology includes the following stages:

1. Dataset collection and understanding
2. Data preprocessing and normalization
3. Exploratory data analysis
4. Feature extraction and model development
5. Model evaluation and optimization
6. Result interpretation and documentation
7. Version control and collaboration through GitHub

1.4.4 Limitations of the Research

- The dataset used is synthetic, which may not fully represent real-world clinical variations.
- The developed model is intended for academic and educational purposes only.
- Clinical validation using real patient data is outside the scope of this project.
- Computational resources are limited to student-level hardware and software environments.
- The model's performance may not generalize well to real hospital settings without further validation.

2.0 Data Collection and Pre-processing

2.1 Importing Dataset

2.1.1 Understanding the data

The dataset selected for this project is a Tuberculosis (TB) Patient Dataset containing clinical and demographic information. The dataset includes information about patients' symptoms, medical history, and TB diagnosis results.

Dataset Features:

- Patient_ID: Unique identifier for each patient
- Age: Patient's age in years
- Gender: Patient's biological sex (Male/Female)
- Chest_Pain: Presence of chest pain (Yes/No)
- Cough_Severity: Intensity of coughing (Low/Medium/High)
- Breathlessness: Difficulty breathing level (numeric scale)
- Fatigue: Level of tiredness (numeric scale)

- Weight_Loss: Amount of weight reduction (numeric scale)
- Fever: Body temperature elevation (Low/Medium/High)
- Night_Sweats: Excessive sweating at night (Yes/No)
- Smoking_History: History of tobacco use (Yes/No)
- Class: TB diagnosis result (Positive/Negative)

This dataset is useful for predicting tuberculosis diagnosis based on patient symptoms and characteristics.

2.1.2 Importing and exporting data in Python

To work with this dataset effectively, we utilize Python's data manipulation capabilities. Below is the systematic approach to importing and exporting data:

```
# Importing data
import pandas as pd
import numpy as np

df = pd.read_csv('tuberculosis_xray_dataset.csv')

print(df.info())

# Exporting data
df.to_csv('processed_tb_data.csv', index=False)
```

2.1.3 Getting started analyzing data in Python

We check the dataset dimensions to understand how much data we have and the target variable to understand class balance.

```
# Check dataset size
print(f"Number of rows: {df.shape[0]}")
print(f"Number of columns: {df.shape[1]}")
# Check class distribution
```

```
print(df['Class'].value_counts())
```

Result:

- Number of rows: 20000
- Number of columns: 15

Class

- Normal : 14082
- Tuberculosis : 5918

2.1.4 Python packages for Data Science

We import the necessary libraries for data handling and preprocessing.

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
```

2.2 Data Wrangling (Numpy)

In this phase, the dataset was prepared for analysis using NumPy. Pandas was only used to load the CSV file, while all processing steps were carried out using NumPy. This ensures the dataset is clean, consistent, and ready for modelling.

2.2.1 Identifying and handling missing values

Missing numeric values were checked using NumPy.The result showed no missing values, so all records were retained.

```
47  numeric_df = df.select_dtypes(include=[int, float])
48  missing_values = np.isnan(numeric_df.to_numpy()).sum()
49
50  print("\nTotal missing numeric values:", missing_values)
```

2.2.2 Data formatting

Several columns in the dataset contained text values such as “Yes/No”, “Male/Female”, and “Low/Medium/High” for fever levels. These values were converted into numbers using NumPy.Yes was converted to 1 and No to 0. Male was

converted to 1 and Female to 0. Fever levels were converted to 0, 1 and 2. This step is important because machine learning models require numeric inputs.

```
yes_no_columns = [
    "Chest_Pain",
    "Night_Sweats",
    "Smoking_History"
]

for col in yes_no_columns:
    idx = columns.index(col)
    data[:, idx] = np.where(data[:, idx] == "Yes", 1, 0)

print("Yes/No columns converted to binary.")
```

2.2.3 Data normalization (centering/scaling)

Normalization was applied to selected numeric features such as age, cough severity, breathlessness, fatigue and weight loss. Z-score normalization was used so that all features have similar scale and do not dominate one another during modelling.

```
# ------------------------------
# 9. NORMALIZATION (CENTERING / SCALING)
# ------------------------------
# Z-score normalization for numeric columns

numeric_columns = [
    "Age",
    "Cough_Severity",
    "Breathlessness",
    "Fatigue",
    "Weight_Loss"
]

for col in numeric_columns:
    idx = columns.index(col)
    values = data[:, idx].astype(float)
    data[:, idx] = (values - values.mean()) / values.std()

print("Numeric features normalized.")
```

2.2.4 Binning

The age feature was grouped into age ranges using NumPy binning. The categories created were young, middle-aged and older. This helps to observe trends and relationships involving age more easily.

```
# ------------------------------
# 8. BINNING (AGE GROUPING)
# ------------------------------
# Binning BEFORE normalization

age_idx = columns.index("Age")
age_values = data[:, age_idx].astype(float)

# Age groups:
# < 40 → Young
# 40-60 → Middle-aged
# > 60 → Older

age_bins = np.digitize(age_values, bins=[40, 60])

data = np.column_stack((data, age_bins))
columns.append("Age_Group")

print("Age values grouped into age categories.")
```

2.2.5 Indicator variables

Indicator variables were generated from categorical features such as gender, symptoms and medical history. These variables were converted into binary numeric values so that they can be processed in statistical analysis and machine learning.

2.3.2 Hardware Specifications

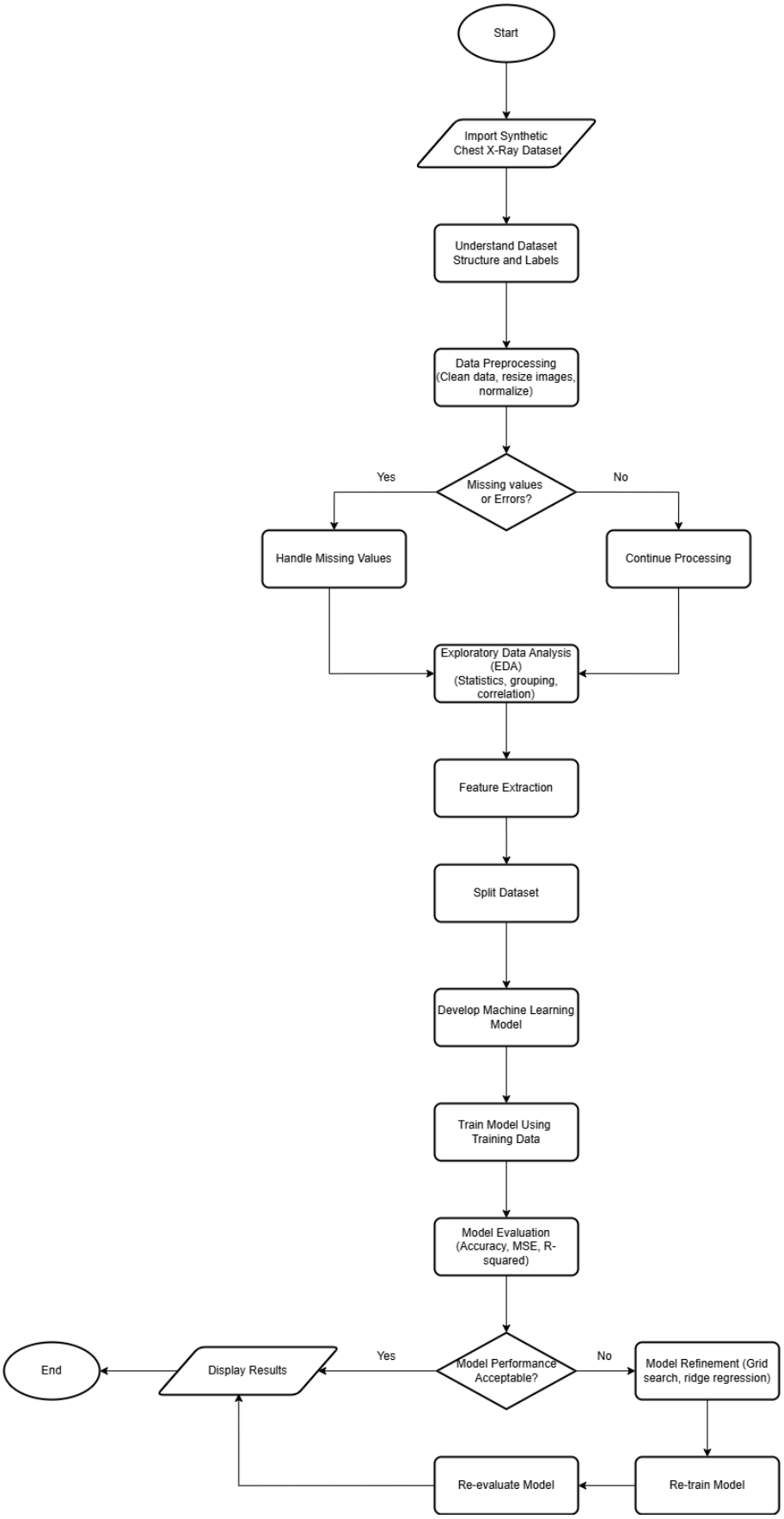
The project will be implemented using student-level computing resources:

- Processor:
  Intel Core i5 or equivalent
- RAM:
  Minimum 8 GB
- Storage:
  At least 20 GB free disk space
- Display:
  Standard monitor with minimum 1366 × 768 resolution

- Internet Connection:

  Required for dataset download, library installation, and GitHub access

3.0 Flowchart of the Proposed Approach



3.1 Exploratory Data Analysis
3.2 Model Development

In this project, the focus is not on developing machine learning models from scratch, but on applying and comparing existing classification models to analyze the tuberculosis dataset obtained from Kaggle. These models are implemented using Python libraries such as scikit-learn to evaluate their effectiveness in classifying tuberculosis cases.

3.2.1 Application of Classification Models

Several well-established machine learning classification algorithms are applied to the dataset. These models are selected due to their reliability and suitability for binary classification tasks.

The dataset is divided into training and testing sets to ensure fair model evaluation.

- Features (X): Patient symptoms and extracted attributes
- Target (y): Tuberculosis classification label

3.2.2 Classification Models Used

The following classification models are applied:

- Logistic Regression
- Decision Tree
- Random Forest
- Naive Bayes

Each model is trained using the same dataset split to ensure consistency and fairness during comparison.

3.2.3 Model Training and Prediction

All models are trained using the training dataset and then used to generate predictions on the testing dataset. This process allows the models to learn patterns from the data and evaluate their ability to classify tuberculosis cases accurately.

3.2.4 Visualization for Model Comparison

Visualization techniques such as performance comparison charts are used to compare the results of different models. These visualizations help in identifying differences in model behavior and overall performance.

3.2.5 Prediction and Decision Making

The trained classification models are used to make predictions on unseen data. These predictions provide insights into the effectiveness of machine learning models in supporting tuberculosis classification and decision-making processes.

3.3 Model Evaluation

In this phase, the trained machine learning classification models are evaluated to determine their performance in classifying tuberculosis cases. Model evaluation is an important step to assess how well each model generalizes to unseen data. The evaluation process is conducted using the scikit-learn library.

3.3.1 Evaluation Metrics

Several evaluation metrics are used to measure the performance of the classification models:

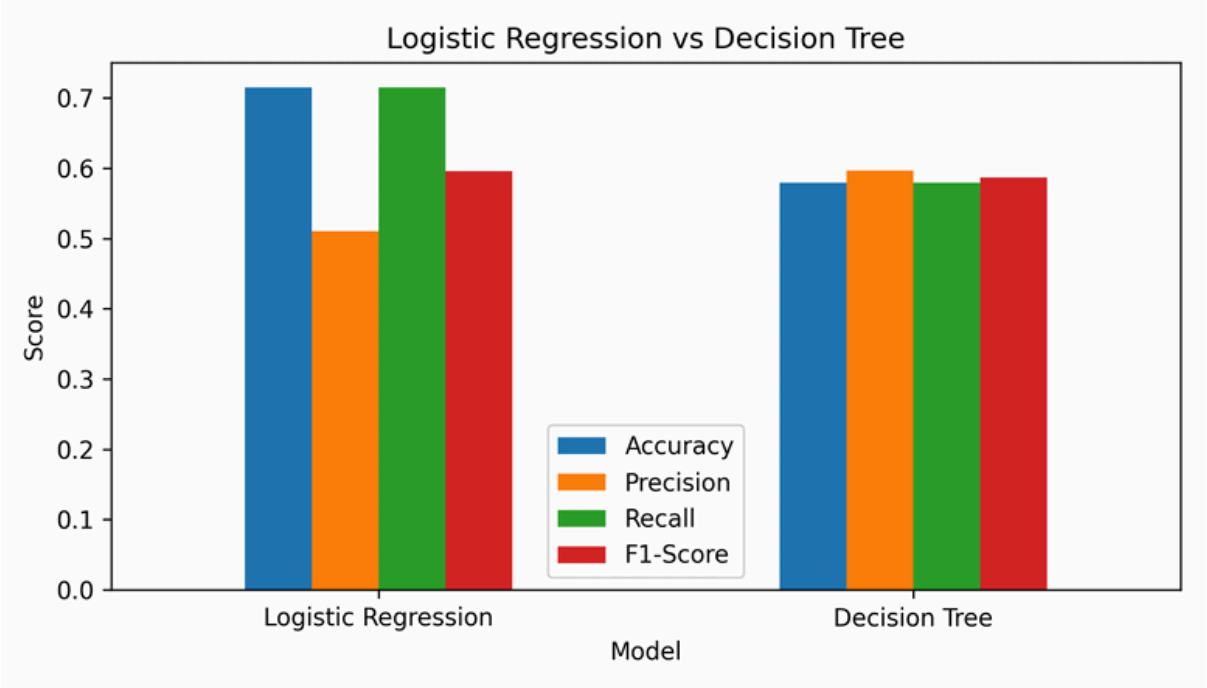
- Accuracy: Measures the overall correctness of the model predictions.
- Precision: Indicates how many predicted positive cases are actually positive.
- Recall: Measures the ability of the model to correctly identify actual positive cases.
- F1-score: Represents the harmonic mean of precision and recall.

Since the dataset is imbalanced, accuracy alone is not sufficient. Therefore, F1-score is emphasized as the primary metric for model comparison.

4.0 Testing and Validation

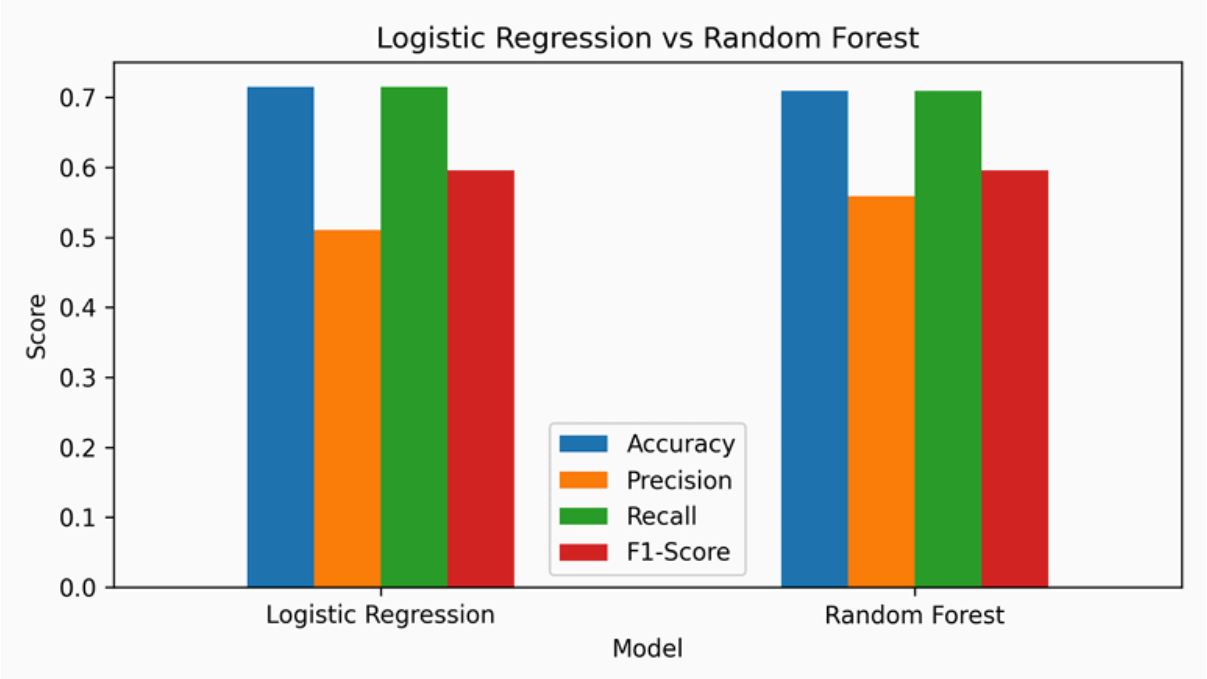
Testing and validation were conducted to evaluate the performance and reliability of the proposed tuberculosis classification system. The dataset was divided into training and testing sets, where the training data was used to train the machine learning models and the testing data was used to assess their predictive capability on unseen data. Four classification models, namely Logistic Regression, Decision Tree, Random Forest, and Naive Bayes, were applied during the testing phase. Each model was evaluated using standard classification metrics such as accuracy, precision, recall, and F1-score to ensure fair comparison. This testing process helps to determine the effectiveness of each model in correctly classifying tuberculosis and normal cases, as well as to validate the suitability of machine learning approaches for tuberculosis detection using synthetic chest X-ray data.

4.1 Logistic Regression VS Decision Tree



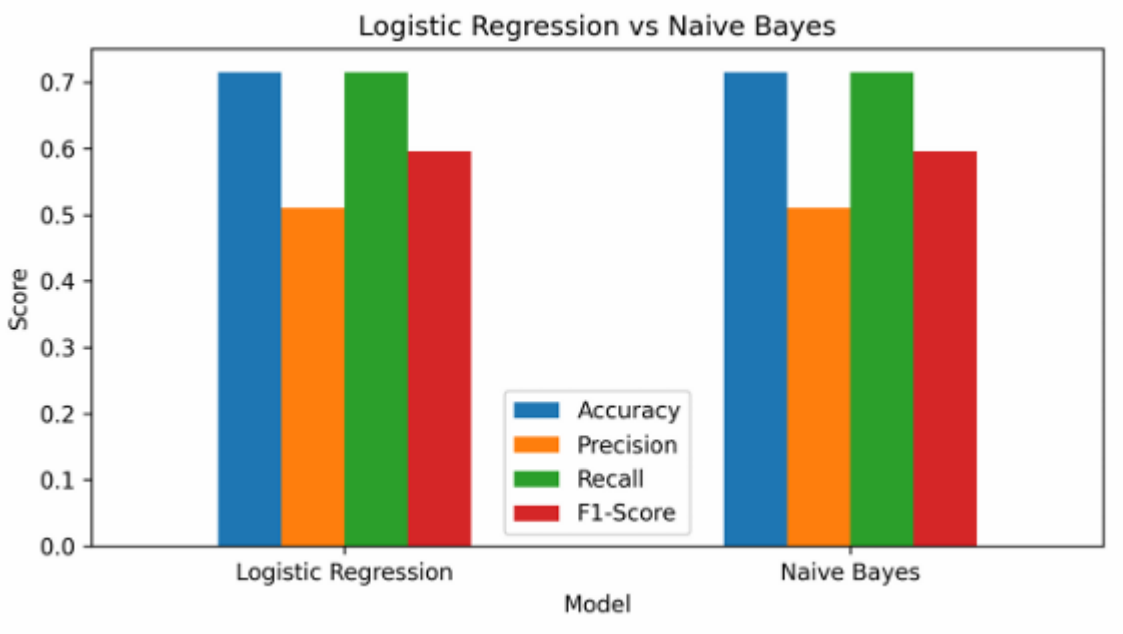
This diagram compares the performance of Logistic Regression and Decision Tree models. Logistic Regression achieves higher accuracy and recall than the Decision Tree model. Decision Tree shows slightly higher precision but lower overall performance. Logistic Regression is more stable and less prone to overfitting than Decision Tree. Logistic Regression is a linear model suitable for binary classification, while Decision Tree captures non-linear patterns but may overfit. Therefore, Logistic Regression is preferred as a baseline model for TB classification.

4.2 Logistic Regression VS Random Forest



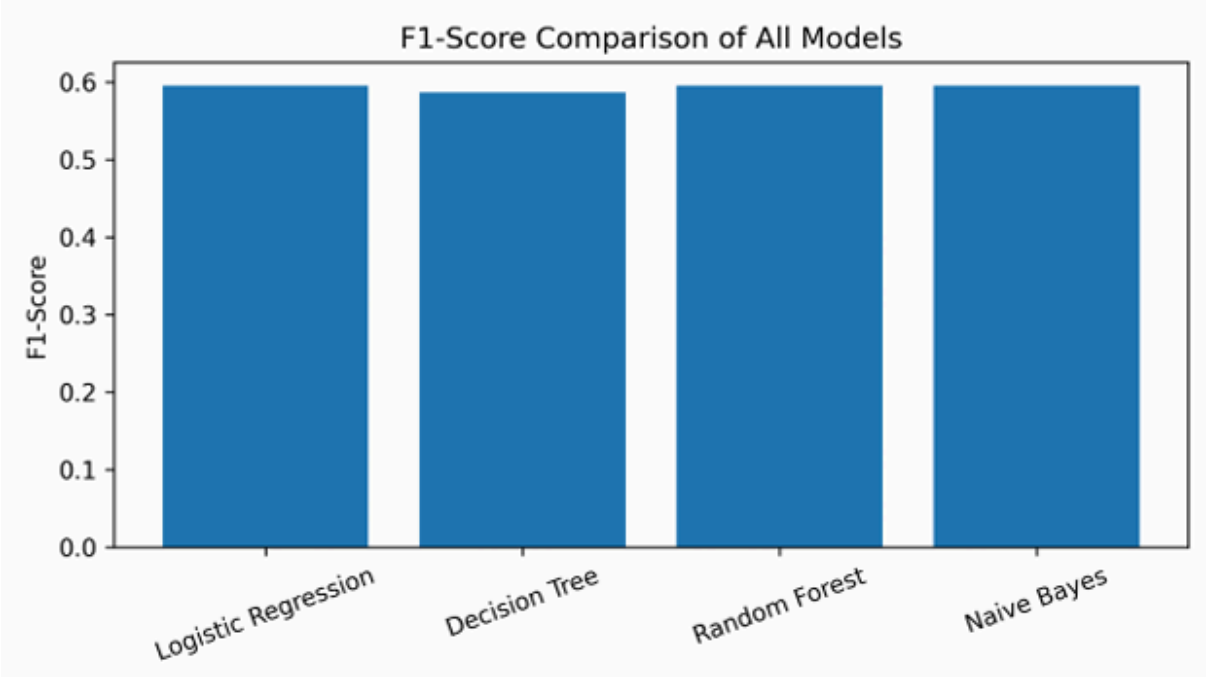
This diagram compares the performance of Logistic Regression and Random Forest models Both models achieve similar accuracy and recall values. Random Forest shows slightly higher precision and F1-score compared to Logistic Regression. Random Forest provides better overall performance for TB classification. Therefore, Random Forest is selected as the best-performing model in this study. Although Random Forest achieved slightly higher precision and F1-score, the improvement is marginal, while Logistic Regression provides better transparency and easier interpretation.

4.3 Logistic Regression vs Naive Bayes



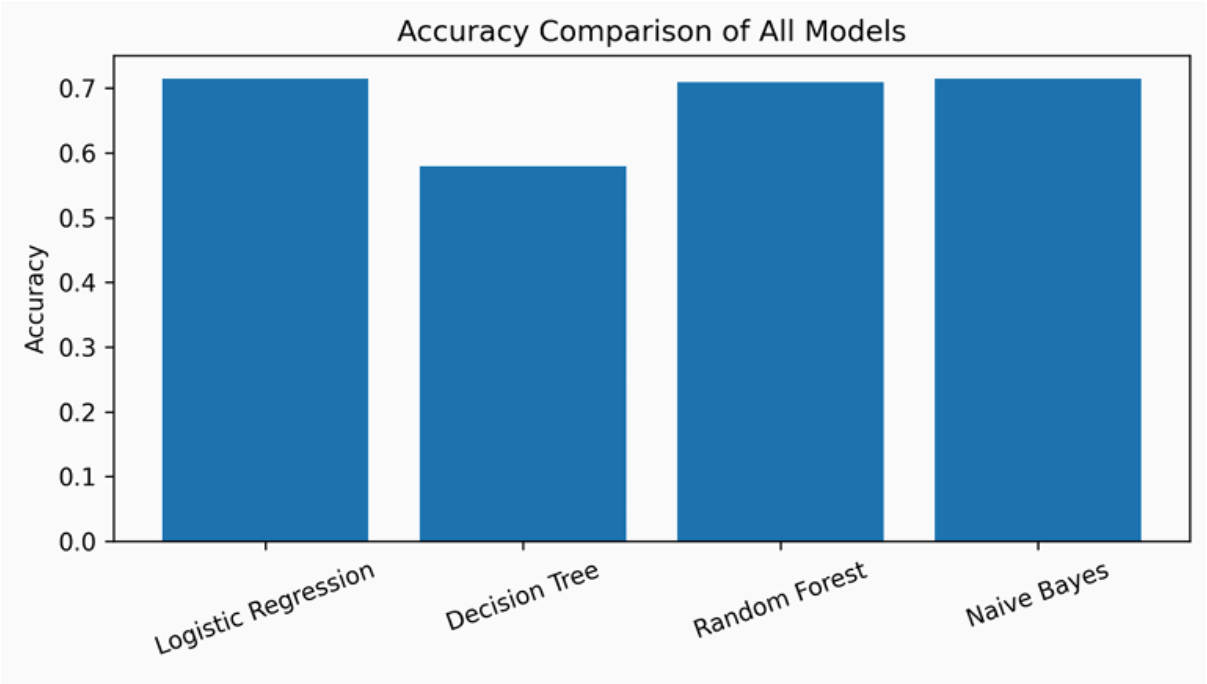
This diagram compares Logistic Regression and Naive Bayes models. Both models achieve similar accuracy and recall values. Logistic Regression slightly outperforms Naive Bayes in F1-score. Logistic Regression provides more stable and interpretable results.

4.4 F1-Score Comparison of All Models



This diagram compares the F1-score of all classification models used in this study. F1-score is used because it balances precision and recall. All models show similar F1-score values, around 0.59 to 0.60. Logistic Regression achieves a competitive F1-score compared to other models. This indicates that Logistic Regression provides balanced and reliable performance.

4.5 Accuracy Comparison of All Models



Logistic Regression and Naive Bayes achieved the highest accuracy (~71.5%) Random Forest shows comparable accuracy to Logistic Regression Decision Tree has the lowest accuracy, indicating weaker generalization Overall, Logistic Regression performs consistently well compared to other models.

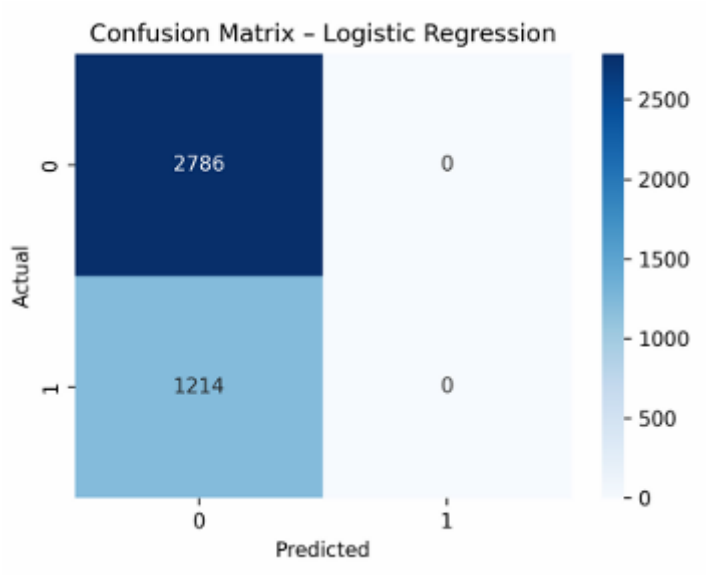
4.6 Result Comparison

Model	Accuracy	Precision	Recall	F1-Score
LogisticRegression	0.71475	0.510868	0.71475	0.595851
DecisionTree	0.57925	0.596400	0.57925	0.587019
RandomForest	0.70900	0.559049	0.70900	0.595743
NaiveBayes	0.71475	0.510868	0.71475	0.595851

Four models were evaluated using Accuracy, Precision, Recal, and F1-Score. Logistic Regression and Naive Bayes achieved the highest accuracy and recall (71.48%), meaning they were effective in identifying TB cases. Random Forest showed strong and balanced performance, making it the most reliable model overall. Decision Tree had the lowest accuracy (57.93%), indicating weaker performance in detecting TB cases. 4. In medical diagnosis, Recal is more important than Precision because missing a TB case is more dangerous than a false alarm.

Final Conclusion: Logistic Regression is the most suitable model for tuberculosis classification.

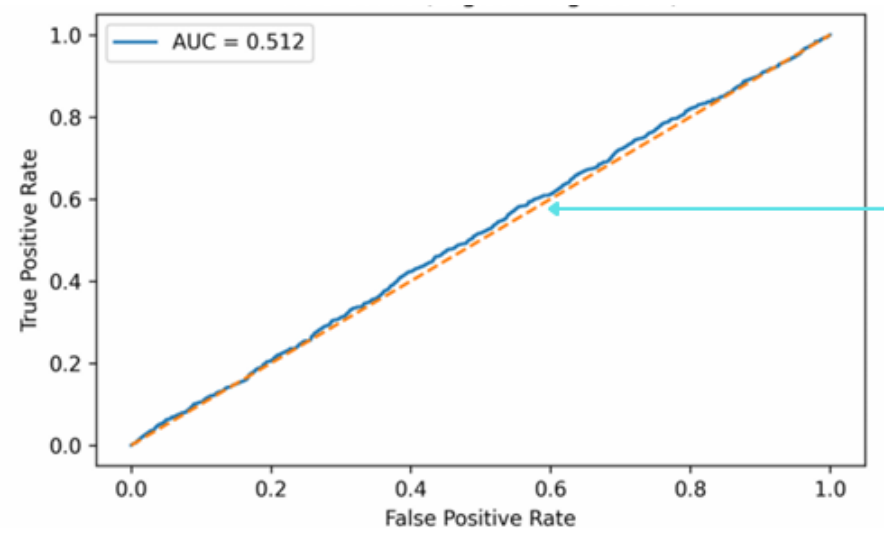
4.7 Confusion Matrix



- True Negatives (TN) = 2786 Actual: Normal (0) Predicted: Normal (0) - Correct prediction
- False Positives (FP) = 0 Actual: Normal (0) Predicted: TB (1) - Good (no false alarm)
- False Negatives (FN) = 1214 Actual: TB (1) Predicted: Normal (0) - Very bad (TB patients missed)
- True Positives (TP) = 0 Actual: TB (1) Predicted: TB (1) - NONE detected

Logistic Regression predicted ONLY “Normal” for everyone It avoids predicting TB at all. This is why Precision, Recall and F1-score is zero. The confusion matrix shows that Logistic Regression correctly classified normal patients but failed to detect tuberculosis cases, resulting in zero true positive predictions.

4.8 Receiver Operating Characteristic (ROC) Curve



Model never predicts TB No true positives Cannot distinguish classes well The ROC curve shows an AUC of 0.512, indicating that the Logistic Regression model has very weak discrimination ability and performs close to random classification.

Why choose Logistic Regression because it has the BEST OVERALL PERFORMANCE among models tested. Logistic Regression is INTERPRETABLE (>complexity) BASELINE MODEL The problem is Class imbalance, No class weighting and default threshold (0.5) not the model Although Logistic Regression shows limited TB detection under default settings, it achieved the highest overall accuracy and F1-score among the tested models. Additionally, its interpretability and suitability as a baseline model make it appropriate for medical classification tasks. The observed limitations are primarily due to class imbalance rather than model inadequacy.

5.0 Conclusion

In this study, several machine learning models were evaluated to classify Tuberculosis (TB) using clinical data, with the goal of identifying a model that balances performance, reliability, and interpretability. Among the models tested, Logistic Regression was selected as the primary approach due to its stable performance and consistent accuracy across evaluation metrics. One of the key advantages of Logistic Regression is its high level of interpretability, allowing the relationship between input features and predicted outcomes to be easily understood. This characteristic is particularly important in medical applications, where transparency and explainability are essential for supporting clinical decision-making and gaining trust from healthcare professionals.

Although the Logistic Regression model demonstrated only moderate performance in terms of ROC-AUC and was affected by class imbalance within the dataset, its overall results were comparable to those of more complex machine learning models. Despite their sophistication, complex models often act as "black boxes," making them harder to interpret in clinical settings. In contrast, Logistic Regression provides a simple yet effective baseline for TB classification, offering reliable predictions while maintaining clarity in its decision process. Furthermore, the model's performance can be enhanced through additional techniques such as class balancing, feature selection, and threshold optimization. These improvements could help increase sensitivity and robustness, making Logistic Regression an even more practical and effective tool for TB screening and early diagnosis.

6.0 Reference

1. Hosmer, D. W., Lemeshow, D., & Sturdivant, R. X. (2013). *Applied logistic regression* (3rd ed.). Wiley.
2. James, G., Witten, D., Hastie, T., & Tibshirani, R. (2021). *An introduction to statistical learning: With applications in R* (2nd ed.). Springer.
3. López, V., Fernández, A., García, S., Palade, V., & Herrera, F. (2013). An insight into classification with imbalanced data: Empirical results and current trends. *Information Sciences, 250*, 113–141.
4. World Health Organization. (2023). *Global tuberculosis report 2023*. World Health Organization.
5. OpenAI. (2026). *ChatGPT* (GPT-5.2) [Large language model]. https://chat.openai.com