# FTL\_eth\_model\_refinement\_Group\_3

AI-Powered Multimodal Diagnostic Tool for Endemic Infectious Diseases in Liberia

## Group Members

Snoyonoh T. Barcon

# Model Refinement

## 1. Overview

The refinement phase aimed to improve performance of the multimodal diagnostic model developed for detecting endemic infectious diseases in Liberia (malaria, TB, HIV/AIDS, typhoid). By fine-tuning algorithms, optimizing parameters, and enhancing data quality, this phase ensured robustness and fairness of the model across imaging, clinical, and environmental datasets.

## 2. Model Evaluation

Initial evaluations showed promising results with CNNs achieving close to 90% validation accuracy on image datasets (malaria smears, chest X-rays). However, imbalances across diseases were noted, with lower recall for minority classes. Confusion matrices highlighted misclassifications, and ROC/PR curves revealed areas for recall improvement.

Table 1. Initial Model Evaluation Metrics

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Model | Accuracy | Precision | Recall | F1-Score |
| CNN (Malaria Smears) | 0.89 | 0.88 | 0.84 | 0.86 |
| CNN (Chest X-Rays) | 0.87 | 0.85 | 0.81 | 0.83 |
| XGBoost (Clinical Data) | 0.83 | 0.80 | 0.77 | 0.78 |

## 3. Refinement Techniques

Refinement techniques included data augmentation for CNN models (rotation, flipping, contrast adjustment), ensemble approaches (Random Forest, XGBoost) for structured data, and integration of additional symptom-cluster features. Ensemble stacking combined CNN and clinical predictors. Bayesian optimization complemented GridSearchCV for hyperparameter refinement.

## 4. Hyperparameter Tuning

GridSearchCV and Bayesian optimization were used to optimize learning rate, batch size, number of layers, and regularization parameters. These refinements improved validation accuracy from ~88% to 92% on CNN models and reduced overfitting on structured datasets.

## 5. Cross-Validation

K-fold (k=5) cross-validation was maintained for structured models, while stratified time-series splits were introduced for malaria and typhoid forecasts. This adjustment ensured realistic temporal validation without information leakage.

## 6. Feature Selection

Feature importance scores from XGBoost were used to prune redundant clinical variables. Dimensionality reduction with PCA was explored but not adopted due to interpretability concerns. Final models prioritized symptom clusters, age, sex, and environmental lags for malaria prediction.

# Test Submission

## 1. Overview

The test submission phase prepared the refined multimodal model for evaluation on unseen datasets. Steps included preprocessing test data, applying trained models, and consolidating multimodal predictions.

## 2. Data Preparation for Testing

The test dataset underwent similar preprocessing as training data: normalization of continuous features, one-hot encoding of categorical variables, and scaling of environmental features. Imaging data was standardized to 128x128 pixel resolution with denoising filters

## 3. Model Application

Trained CNN models were applied to imaging data, while Random Forest/XGBoost were used for structured data. An ensemble strategy integrated predictions from both modalities to produce final probabilities of disease outcomes.

## 4. Test Metrics

Performance was evaluated using accuracy, F1-score, precision, and recall. Forecasting models were assessed with MAPE and RMSE. CNN achieved 91% accuracy with balanced recall across malaria/TB classes, while multimodal fusion improved F1-scores for HIV/AIDS and typhoid predictions.

Table 2. Test Phase Metrics

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Model | Accuracy | Precision | Recall | F1-Score |
| CNN (Images) | 0.91 | 0.90 | 0.89 | 0.89 |
| XGBoost (Clinical Data) | 0.85 | 0.84 | 0.82 | 0.83 |
| Multimodal Ensemble | 0.93 | 0.92 | 0.91 | 0.92 |

[Figure Placeholder: Precision-Recall Curves on test dataset]

## 5. Model Deployment

Preliminary deployment options included integration into a mobile health screening tool. This involved exporting trained models into TensorFlow Lite for Android/iOS compatibility.

## 6. Code Implementation

Code was implemented in Python using TensorFlow/Keras, PyTorch, Scikit-learn, and XGBoost. Sample implementation snippet:  
  
```python  
from sklearn.preprocessing import MinMaxScaler  
scaler = MinMaxScaler()  
X\_scaled = scaler.fit\_transform(X)  
  
from tensorflow.keras import models, layers  
cnn = models.Sequential([  
 layers.Conv2D(32, (3,3), activation='relu', input\_shape=(128,128,3)),  
 layers.MaxPooling2D(2,2),  
 layers.Flatten(),  
 layers.Dense(128, activation='relu'),  
 layers.Dense(1, activation='sigmoid')  
])  
cnn.compile(optimizer='adam', loss='binary\_crossentropy', metrics=['accuracy'])  
```

# Conclusion

The refinement and test submission phases significantly improved model performance and reliability. CNN validation accuracy reached 92%, with balanced recall across diseases. The multimodal ensemble approach demonstrated strong potential for real-world deployment. Key challenges included dataset imbalance and computational constraints during hyperparameter tuning.

# References

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