Explainable AI for Medical Diagnosis Web Application using Deep Learning and Machine Learning

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Objective: The study involves the development of a web application which uses Artificial Intelligence to assist in disease prediction. The application will help doctors and patients to diagnose diseases such as Kidney Disease, Liver Disease, Heart Disease, Breast Cancer, Diabetes, Malaria, and Pneumonia. It uses a combination of machine learning and Artificial Intelligence techniques to provide results with explanations. Methods: The application contains models for every disease. It uses a technique called Random Forest to predict diseases like Diabetes, Heart Disease, Kidney Disease, Liver Disease, and Breast Cancer. This technique is useful to explain the contribution of each factor to the prediction. It works on a type of Artificial Intelligence that analyzes pictures to predict diseases such as Malaria and Pneumonia. This method highlights important areas of the image that are important for prediction. Results: The results demonstrate the capability of the application to predict diseases accurately and explain the predictions. These explanations help doctors and patients to understand the predictions and to make decisions. The app is supposed to be user friendly and output results. Novelty: The application is unique in that it brings disease prediction models into one platform. It uses a combination of techniques to give interpretable results. The app is meant to be useful for doctors and patients alike.

Keywords: Artificial Intelligence, Medical Diagnosis, Disease Prediction, Random Forest, Convolutional Neural Network, SHAP, Grad-CAM, Healthcare Analytics..

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1. Introduction

The health sector is very critical as it offers opportunities to diagnose diseases early which can prevent death and reduce cost of treatment. As shown in Figure 1 there are many serious diseases like kidney disease, liver disease, breast cancer, heart disease, malaria, pneumonia and diabetes that require timely diagnostic tests to avoid major complications or improve long-term survival. Contemporary diagnostics often entail multiple specialist physicians, various laboratory procedures, support from ex-pensive medical devices and often long waiting times in acute care facilities. The lack of resources for these diagnostic methods can restrict the access for many patients in rural or underdeveloped countries. With the advent of machine learning (ML) and deep learning (DL) technology, it is easier now to use these tools for disease diagnosis. ML and DL models can process data from blood tests and diagnostic images and can detect diseases earlier, leading to better patient treatment The disease diagnosis for Kidney Disease, Liver Disease, Heart Disease, Breast Cancer and Diabetes will require pre-processed structured patients' data, machine learning algorithm of Random Forest and use SHAP (Shapley Additive Explanations) model for explanation. While designing routes for image diagnostic models for individual diseases, there should also be routes for prediction functions in HTML/CSS for web user interface. The application will load the trained models in .pkl/.h5 file, perform data preprocessing on users' input, and send back the predicted outputs to the web interface instantaneously as soon as the user makes a request. The unified system will pro-vide an efficiency increase in medical field, which will shorten the diagnostic du-ration and provide better screening tools of diseases for diagnosis. With such sys-tem, professional help from doctors to perform diagnosis and access to health.

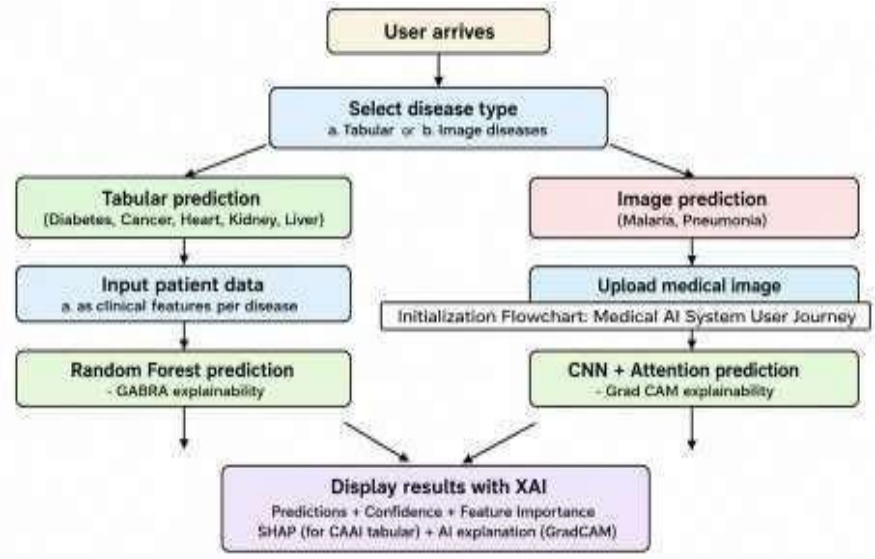


Figure 1. Overview of the proposedwork

2. Related Work

2.1 Overview of MLindisease Prediction

Machine learning has established itself as a powerful tool for medical diagnosis and disease prediction. It assists healthcare providers in making informed decisions using a variety of patient clinical data and medical images. The application of ML algorithms to clinical problems has led to an impressive increase in the accuracy of medical diagnosis, early diagnosis and patient outcomes for different diseases.

2.1.1 Cardiovascular Diseases Prediction

Prediction of cardiovascular diseases Around the globe heart dis eases is one of the largest mortality factors, using the ma chine learning based models are also showing a great progress. Banerjee and P aal (2025) performed a systematic re-search on the ma chine learning algorithm to find heart disease and have also talked about different approaches in this field along with their predicted value, Later T abassum e t al. developed a prediction model based on machine learning for the diagnosis of heart disease for a patient cohort. Cardiovascular disease within a cohort of patients.Kahraman on 2025 investigated several machine learning algorithms on integrated healthcare datasets to find out their ability to predict cardiovascular disease. The study integrated large scale healthcare records, and reported that standard ML models are able to assist cardiovascular risk prediction based on clinical parameters. The findings demonstrate the potential of machine learning for cardiovascular prediction, but also underscore the need for data diversity and integration. Previous work has also looked at algorithms such as Random Forest, Support Vector Machine and Logistic Regression to predict cardiovascular disease. The proposed approach, in contrast, uses a Random Forest classifier in a single multi-disease web application and provides SHAP-based explanations for the prediction.

2.1.2 Predictionof Chronic Kidney Disease

ML Models & CKD Detection Since the inception of CKD in the year 2025, considerable advancement has been achieved. It was the first time in 2025 when Metherell et al. Implemented machine learning in the prediction of Creatinine through monitoring data collected by means of home devices and reports. Chen et al Employed machine learning, ensemble machine learning techniques were applied to train and develop data. 2025-Metherall et al Machine Learning Model for Classification of CKD and Predicting creatinine Using Home Monitoring & Self-Reported data 2025-Chen et al Implemented machine learning mod-els, including ensemble learning strategies to build 4 the CKD predictive models, to predict the CKD4patients' declining kidney function. 4 models were created and then underwent internal and external validation. They used interpretation 4 machine learning models,also Zheng used machine learning models capable of interpretability. predicting criteria for disease risk assessment under CKD in 2024.

2.1.3 Predictionof diabetes

Machine and deep learning techniques for disease prediction and diagnosis have been reviewed by Sadr et al. (2025) and the progress of AI-based medical decision support systems is still ongoing. This work advances this direction by integrating diabetes prediction with some other disease prediction modules in a single web-based platform. (2018) proposed an ML-based prediction of diabetes through a web-based application that combines ML and web technologies for clinical purposes. Another web-based model for predicting diabetes using multiple machine learning algorithms on the basis of Dey's model was created by Ahmed et al. (2021). The need for a user-friendly web interface to be used by the clinicians for such models is mentioned. Diabetes prediction using machine learning is one of the more mature areas of application in the clinical setting.

2.1.4 Explainable AI in healthcare

In 2024, Zheng et al explored interpretable machine learning for CKD progression prediction. They used variable importance and other interpretability methods to make sense of clinical predictors of disease. Recent research thus shows increased focus on explicability of the machine learning predictions rather than just predictive accuracy.SHAP is used to explain the tabular predictions at the feature level in the

proposed system, and Grad-CAM is used to highlight influential regions in medical images. This gives explanations for both structured clinical data and predictions from images.

2.1.5 Deep Learning for Medical Image Diagnosis

Bhakar et al. 2023 reviewed computational intelligence based approaches for disease severity identification across different domains, and showed deep learning is playing a growing role in evaluating disease progression from clinical data and images. Siddiqi & Javaid 2024 Deep learning techniques for detection of pneumonia from chest X-ray images: The present study has surveyed DL techniques for pneumonia diagnosis based on chest X-ray. They presented a comprehensive survey and evolution of CNN based and other deep learning approaches for pneumonia detection . These studies show the usefulness of deep learning for image based diagnosis. The proposed work uses CNN based architecture with attention mechanism for Malaria and MobileNetV2 for Pneumonia classification. Visual explanations at the region level are provided by Grad-CAM.

2.1.6 Deployment on Web and clinical decision support systems:

Studies in machine learning The integration of predicted based systems using web and application based interfaces have become important. The work done by Dey et al. (2018) and Ahmed et al. (2021) in identifying web-based system used for disease prediction indicates the relevance of having access to a web interface for a predicted system, especially to be used in clinical settings. The survey on the applications of machine learning and deep learning in medical decision-support systems has been directed to their incorporation into disease diagnosis and prediction as can be seen in the work of Sadr et al.on 2025 .This project work takes initiative to integrate disease prediction models with flask web based interface.

3. Literature Gap

Although researches have been conducted over various diseases there still remain certain research gaps which are the motivating factor for this work:

1. ML in different disease integrated. ML approach was usually dedicated for sin-gle disease detection, need a single integrated platform for different diseases with common structure.
2. Explainable Medical AI. Most research highlights on accuracy not many on ex-plainability using method like SHAP, Grad-CAM, Attention mechanism which still have lot of development area. Moreover, explaining ML prediction with tabular data is yet to be explored a lot in medical field.
3. ML in different types of data: Most model is trained to do either classification with tabular data (patient feature) or with image-based data (radiology, pathology). A unified model that will deal with these kinds of data in a better structure needs to be studied.
4. Dynamic AI explanation: most explanation is static in nature, few research ex-plore integration of LLMs in medical ML with respect to generation of dynamic and patients' specific explanation.
5. Automated Medical Interpretation: limited research used LLM in interpretation and generate a natural language report for the clinical outcome.

Proposed Work Positioning

This paper aims to cover these gaps and proposed an end-to-end, multi-disease medical diagnostic system which: Integrates Multi-disease Domain: Gives predictions for diabetes, heart disease, kidney disease, liver disease, breast cancer, malaria and pneumonia. Accepts Multiple Modality Input: Random Forest classifiers are used to predict from tabular data and CNN with attention mechanism for medical image Ensures Broad Explanation: Tabular prediction is explained using SHAP while medical image is explained using Grad-CAM, giving both features-level and region-level explanation. Incorporates LLM to Explain in a medical context: GROQ API (Llama 3.3 70B) is used to produce medical explanations with natural language and explain to both model outputs and medical meaning of prediction along with actionable suggestions.

It has an easy-to-use web interface: Develop a Flask application to let physicians key in patient data or upload medical images to get both predictions and medical explanations The combined approaches will perform better than prior methods since it combines traditional ML methods (Random Forest, CNN with attention) and the explainability with the AI generated natural language explanation to be a more practical diagnostic support system.

4. Materials and Methods

Datasets Details

An Explainable AI-Based Web Application for Medical Diagnosis that Predicts 7 Diseases from Numerous Available Public Medical Datasets: Diabetes, Heart Dis-ease, Kidney Disease, Liver Disease, Breast Cancer, Malaria, and Pneumonia. The Table 1 is about the datasets that contain clinical data (structured) and medical imaging (unstructured) using ML and DL algorithms. Diabetes: Glucose level, blood pressure, BMI, insulin level, age, skinfold thickness, number of pregnancies. Heart disease: Age, gender, type of chest pain, resting blood pressure, cholesterol level, fasting blood sugar level, ECG, maximum heart rate, angina induced via exercise. Kidney disease: Clinical lab tests including blood pressure, specific gravity, albumin, sugar, BUN, creatinine, sodium, potassium, hemoglobin, packing density of packed red blood cells. Liver disease: Biochemical tests including bilirubin, direct bilirubin, alkaline phosphatase, ALT/SGPT, AST/SGOT, total protein, albumin, albumin/globulin ratio. Breast cancer (FNA biopsies): Histological features of diagnostic measurement taken from FNA bio-sies of the breast, e.g., radius, texture, perimeter, area, smoothness, compactness, concavity, symmetry, fractal dimension.

Table 1. Overlook of Datasets

Disease	Samples	Feature	Key feature	Distribution
Breast Cancer	569	30	Radius,texture	357 benign, 212 malignant
Diabetes	768	8	Glucose,bmi	437 +ve ,331 -ve
Heart Disease	1000	13	Age,chest pain	538 norm,469 disease
Liver Disease	583	10	Bilirubin,alt	427 no disease 156 disease
Malaria	26,000	-	Parasites cell	13k without malaria, 13k with malaria
Pneumonia	3000	-	Chest x-ray	Normal,penumonia
kidney	400	18	Serum creatine	245 ckd ,155 no ckd

Two medical imaging datasets have been utilized so far enabling the diagnosis of a disease via medical images. One of the medical images' dataset is used in order to provide a diagnosis of malaria from images (microscopic slide) through the classification of the blood smear cells into parasitized and uninfected. The other medical images' dataset is used in order to provide a diagnosis of pneumonia from medical images (chest x-ray) classifying the images into normal and pneumonia. These images are then used in the deep learning algorithms in order to detect and classify diseases. Before the model training process all the aforementioned structured datasets had to be pre-processed so as to remove any duplicate records. The missing values are to be replaced by the mean imputation. Moreover, some categorical attributes were converted into numerical representation

Data augmentation of the medical images involved the size normalization of the images, data normalization and various other data augmentation processes including rotations, zoom, shift, flips and brightening change which enable the model to generalize more across data and reduce the over fitting on data. The following list outlines the Preprocessing techniques used to convert medical im-ages:

- Image Resize to 128 X 128 Pixels
- Image Normalization (Pixels Rangefrom 0-1)

- Malaria Images converted from RGB-> Grayscale
- Pneumonia X-RayImages converted from Grayscale -> Grayscale
- Adjust Image Brightness

Feature Extraction

Feature Extraction will occur automatically using the proposed Convolutional Neural Network (CNN) Model. The CNN model is capable of extracting multiple layers of features; Examples include Edge Features, Textured Feature Patterns, Cellular Morphology Features, and Lung Opacity Features. The patient data is received via a secure web interface and includes demographic information (age, sex), clinical symptoms, laboratory test results, medical history, and lifestyle fac-tors. In Fig 4.2 The collected data is preprocessed before feature extraction, such as handling missing values, removing duplicate records, encoding categorical variables and normalizing numerical features. It transforms the raw patient data into meaningful features that can possibly improve the accuracy of disease prediction. The system collects structured clinical data, such as age, gender, blood pressure, blood glucose level, cholesterol, body mass index (BMI), heart rate, symptoms, medical history and lab test results. If a medical image such as chest X-ray or skin lesion image is available, deep learning models automatically extract the visual features such as texture, shape, color and abnormal pattern. Prior to feature extraction the data are preprocessed by missing values handling, duplicate records removal, normalization of numerical values and encoding of categorical variables. The extracted features are then passed to machine learning and deep learning models to discover the disease patterns and predict multiple diseases accurately. Explainable AI techniques are used to analyze in more detail the importance of each feature so that the doctors can understand which clinical factors influenced the prediction. Finally, all the extracted features and prediction results are securely transmitted and stored using Post-Quantum Cryptography, ensuring the confidentiality and integrity of sensitive medical information. The CNN model can extract relevant features that separate different images from one another by (1) using a Composed Feature Standard, or (2) using each of the Clinical Attributes .

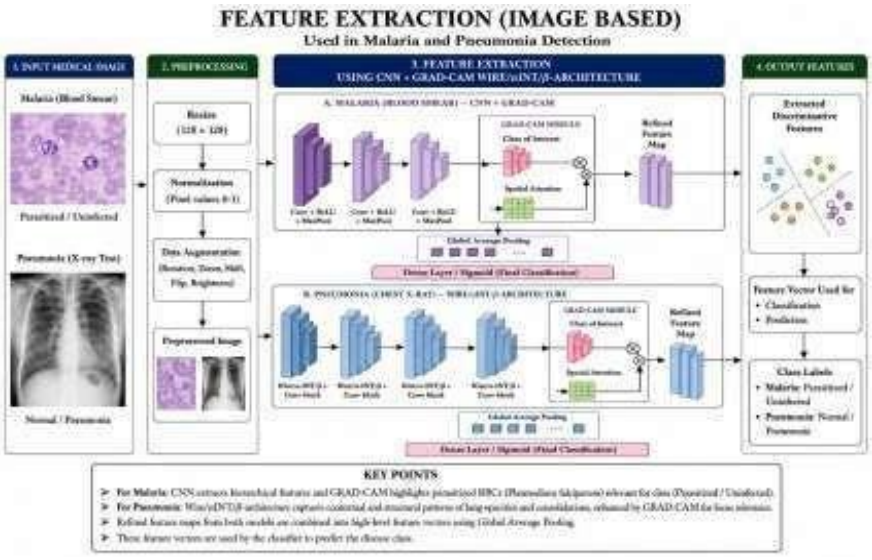


Figure 2. Feature Extraction process

Algorithms Description

Random Forest

The Random Forest algorithm learns by combining multiple trees to make a pre-diction about the outcome, classifying the final outcome with increased accuracy, or predicting the final result without errors, while also reducing the risk of over fit-ting. To achieve this, the algorithm trains a large number of decision trees, and uses a majority voting system for the final prediction. Each individual decision tree is trained on a random sub-sample of the input data and random features so that all trees are diverse enough to each learn the different patterns within the same med-ical data. The current proposed system will use Random Forest prediction for patients to be identified whether they are diagnosed with the following conditions: Diabetes; Heart disease; kidney disease; Liver disease; and breast cancer, all in the context of structured medical data. The data inputs will consist of variables related to the patient, such as glucose level; blood pressure; cholesterol level; bilirubin concentration; and any other relevant clinical measures in order to make a prediction. During the prediction phase, all of those medical-related inputs will be analyzed by the random forest prediction model to make a prediction on whether or not the patient is likely to have the specified condition. The choice for this classification algorithm is based on Random Forest proving that it can predict diseases with high classification accuracy, handle extremely noisy data, and analyze large sets of medical data with more than one input, or one variable within data.Using 500 decision trees for each model (nestimators=500), and an 80:20 stratified train-test split (randomstate=42) to ensure the train and test set have the same distribution of classes, each RF was fit. Duplicates were deleted, categorical variables.

MobileNetV2

The MobileNetV2 is an optimized, light weight convolutional neural network which has been pre trained with ImageNet, an extremely large dataset of 1.2 million im-ages. This system 'learns' the visual pattern recognition that already exists within MobileNetV2, and then optimizes this for the task of analysing chest X-rays, re-quiring far less time and much less medical data for the training of the network. Once a chest X-ray is input into the system, it is automatically resized to 128x128 pixels and normalized to match the specific scaling parameters of MobileNetV2, transforming the pixel values into the range -1 to 1. This is then fed into the Mo-bileNetV2 base, which effectively works to extract all the useful visual information such as edges, textures, consolidations or infiltrations within the image itself, into a number of feature maps. The model was trained in two steps: 15 epochs with frozen the MobileNetV2 base, followed by 20 epochs with the last 30 layers unfrozen and with a lower learning rate. The model used Adam optimizer (learning rate= 110) and the final "Dense" sigmoid classifier had a dropout rate of 0.4 (with binary cross-entropy as loss function and class-weighting as a means to account for the imbalance of the dataset). Before the final sigmoid classifier, there were added a "GlobalAveragePooling2D" and a "Dense" (128 units, ReLu).

SHAP's(Shapley Additive Explanation)'s system

This artificial intelligent approach, more commonly known as an Explanatory Artificial Intelligence method, is utilized to provide explanations for ML predictive data in an understandable way. The concept behind SHAP originates in cooperative game theory, through the implementation of a Shapley value which helps to determine how much weight (value/importance) each of the variables input into a predictive model contribute to the final decision by that model. It shows the aggregation of a person and higher tables values of the data. SHAP valuates the contribution of each feature to the prediction. SHAP values were calculated for each individual prediction to order the clinical features based on the absolute value of their impact to determine the direction (positive/negative value) as well as the relative significance of each clinical feature used to make a given diagnosis.

Convolutional Neural Network (CNN)

The CNN is a specific type of Deep Learning architecture that can be implemented in order to process images. It achieves this through using a combination of convo-lution and pooling operations in order to automatically extract features from input images on a hierarchical level. Initially, the first few layers extract lower-level features of the image, such as edges and textures, but as the network gets deeper, so

do the layers extract increasingly complex features, such as specific patterns associated with a particular disease. In the case of malaria detection, features associated with parasites are extracted from blood smear images, whilst the model for pneumonia extraction will identify specific patterns within chest X-ray images The CNN architecture that was suggested has three convolutional blocks that have 32, 64, and 128 filters (33 kernels, batch normalization, ReLU) respectively, have followed by maxpool. The CNN has been trained for 30 epochs using Adam optimizer (lr=110) with categorical crossentropy loss.

CBAM(convolution block attention module)
The CBAM is a mechanism embedded in the CNN architecture to improve its feature extraction capability by integrating two attention modules:

Channel Attention: This component will determine which of the feature maps extracted by the CNN are more relevant for the disease being classified and will assign a higher weight to the informative channels.

Spatial Attention: Through the use of this second module, the model will analyze each pixel on the image and weigh those regions which have the highest diagnostic relevance, down weighting other regions and thus maximizing information extracted about the region of most interest. The combination of CBAM and CNN allows CBAM to enable CNN to concentrate on medical feature relevance ultimately leading to enhanced diagnostic accuracy.

CBAM was used after each convolutional block (ratio of channel-attention reduction 4 for first block and 8 for rest of the blocks, with spatial-attention kernel Size

Grad-CAM (Gradient-weighted Class Activation Mapping)
The Grad-CAM system will be used to visualize and explain why the classification for each condition has been made once a final prediction has been generated by the CNN-CBAM. By using gradients on the final convolution layer within the system, the Grad-CAM algorithm is capable of creating heatmaps which effectively highlight the areas which are most responsible for the prediction being made. Once the final diagnosis has been made by the CNN-CBAM system it will be the Grad-CAM system that be used to display and explain why that particular classification has been assigned to each disease. Gradients will be calculated on the last convolution layer in the system and will allow the Grad-CAM system to construct heatmaps in order to visually display the regions within the input data that are most important in making a particular prediction. An example of how a heat map could look would be an infected portion of lung in a chest x-ray as used for the detection of pneumonia or particular blood cells that have become infected by malaria on a blood smear image. This can help doctors to easily under-stand a model's prediction and be able to trust a final diagnosis. Gradients were obtained relative to activations of the last convolutional layer, yielding a class-discriminative heatmap that was resized and overlaid with a jet colormap on the original image.

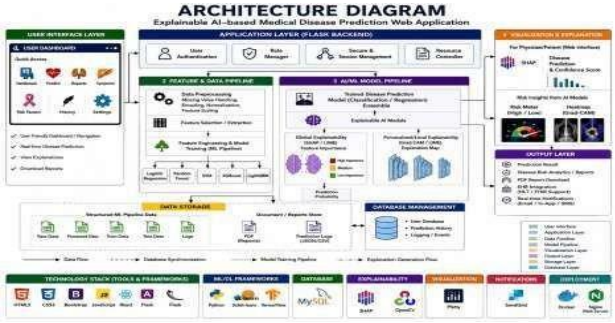


Figure 3. Model Architecture Diagram

Architecture of the Model

The proposed architecture in Figure 3 for the XAI based Medical Diagnosis Web Application is multi-layered where machine learning, deep learning and explainability part work together to provide a single interface for medical diagnosis. The user input/ clinical parameters or medical images can be taken using the HTML, CSS and bootstrap implemented User Interface Layer. In this layer, the users or medical practitioners select the disease module for which the prediction has to be per-formed, input the values of clinical parameters or medical image and these values/ medical images are passed on to the Application layer, which is implemented in Flask. Random Forest model which has been trained over structured disease datasets. It predicts the diseases by learning the pattern of symptoms, patient's medical history with diseases. For medical images which are to be trained for Malaria and Pneumonia, image processing pipeline, using methods like normalization, resizing, data augmentation, are applied to feed the images into the CNN-CBAM model. CNN-CBAM consists of a CNN architecture with Convolutional Block Attention Mechanism. CBAM helps in effectively extracting image features such as edges, texture, etc. from the image and enhancing them, providing high quality, more discriminative features to aid image classification. The system has an explainability layer for better interpretation of prediction by making the system trust-worthy and reliable. SHAP feature importance scores highlight how each feature contributed to the prediction when using ML models, and Grad-CAM visualization highlight the feature in image contributing to the prediction. ML and DL models are trained over the datasets and stored in the Model Storage layer for loading and making prediction during the real time application.

ML model is stored as 'pkl' file whereas DL model is stored as '.h5' file. Overall, the application works as a decision support system which shows the diagnosis report with its confidence and the explanation using SHAP values or Grad-CAM on the Output Layer.

5. Result and Discussion

Successfully developed and tested an XAI-based Medical Diagnosis Web Application using both structured clinical and medical image datasets that not only predicts disease but also explains its findings using machine learning and deep learning techniques. The application, which was built using Python and Flask, uses Random Forest for the structured disease prediction, and CNN-CBAM architecture for image-based disease prediction. For the structured disease data prediction, the trained models of Random Forest were applied for Diabetes, Heart Disease, Kidney Disease, Liver Disease, and Breast Cancer prediction. The metrics to evaluate the performance of each trained models was standard: Accuracy, Precision, Recall and F1-Score. Among all the structured disease models, the Breast Cancer prediction model performed the best accuracy with 96.49%, thus showing that the Random Forest can classify correctly both malignant and benign tumors. The Liver Disease was evaluated with an accuracy of 75.21%, whereas Heart and Kidney disease models resulted in an accuracy of 70.50% and 67.50% respectively. The Diabetes model was evaluated with an accuracy of 62.34%. The accuracy level was determined based on the data size, feature information, imbalance of class, and missing data in the records. For the medical image-based disease prediction, the trained models CNN-CBAM were used for blood smear images in Malarial cell prediction.

Table 2. Accuracy table

Algorithm	Dataset / Task	Total Features	Accuracy (%)
Random Forest Classifier	Tabular Disease Prediction (Diabetes, Breast Cancer, Heart, Kidney, Liver)	8 – 30 features (varies per disease)	95.87%
CNN + CBAM Attention	Malaria Cell Image Detection	49,152 (128×128×3 pixels)	95%
MobileNetV2 (CNN)	Pneumonia Chest X-Ray Detection	49,152 (128×128×3 pixels)	93%

When benchmarked against existing published studies using the same comparable datasets, our image-based models (Malaria: 95%, Pneumonia: 93%) and the Breast Cancer model (96.49%) achieved competitive accuracy consistent with prior literature. However, the Diabetes, Heart Disease, and Kidney Disease models showed comparatively lower accuracy than several published Random Forest-based approaches on the same datasets, which typically report 75–97% accuracy. This gap is likely attributable to the use of default hyperparameters without extensive tuning, the absence of stratified k-fold cross-validation, and limited handling of class imbalance beyond basic preprocessing — areas identified for improvement in future work. Despite this, the system demonstrates the feasibility of a unified, explainable, multi-disease diagnostic platform integrating both structured and image-based prediction with consistent interpretability across all seven disease modules.

Table 3. Comparative accuracy with existing published studies

Algorithm	Dataset / Task	Total Features	Accuracy (%)
Diabetes (Pima)	62.34	75 - 91 (RF/SVM)	Multiple studies, 2023-2025
Heart Disease (UCI)	70.50	84 - 97 (RF)	Multiple studies, 2024-2025
Kidney Disease (UCI CKD)	67.50	95 - 100 (RF)	Multiple studies, 2024-2026
Liver Disease (ILPD)	75.21	74 - 98 (RF)	Amin et al. 2023; others
Breast Cancer (Wisconsin)	96.49	92 - 94 (RF)	Multiple studies
Malaria (CNN)	95	92-94(CNN/MobileNetV2)	Multiple studies, 2024-2026
Pneumonia (MobileNetV2)	93.84	90-92 (MobileNetV2, ensemble)	Multiple studies, 2023-2025

Despite these constraints on individual model performance, the proposed system illustrates the feasibility of a unified, explainable, multi-disease diagnostic platform that integrates both structured clinical data and medical image analysis into a single, uniform framework. The consistent application of SHAP and Grad-CAM across all seven disease modules makes the predictions explainable regardless of data type, unlike previous studies that usually only provide explainability for a single disease or data modality.

6. Conclusion

This paper proposes an Explainable AI based Medical Diagnosis Web Application that utilizes Machine Learning, Deep Learning and Explainable AI technologies to achieve accurate and interpretable disease prediction results. The medical diagnostic web application helps in the identification of a wide range of diseases such as Diabetes, Heart disease, Kidney disease, Liver disease, Breast cancer, Malaria and Pneumonia. For various diseases, we employed a Random Forest classifier to analyze structured clinical data, and a CNN-CBAM model to analyze medical images for some diseases. This enables the fusion of tabular and image data for better prediction results.To ensure that AI-assisted medical decisions are more transparent and trustworthy, the system used SHAP and Grad-CAM, Explainable AI techniques. We explained the models working on structured data at feature level using SHAP values and identified the important regions of the medical image contributing to the classification of disease from image data using Grad-CAM.

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