Healthcare Application Using ML&AI

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***Abstract*— Healthcare has witnessed a transformative shift with the integration of Machine Learning (ML) and Artificial Intelligence (AI), enabling early disease detection, personalized medicine, and operational efficiency. This project focuses on developing ML-based predictive models for chronic diseases, specifically diabetes, heart disease, and kidney disease, which collectively pose significant global health challenges. By leveraging publicly available datasets, the project applies advanced data preprocessing techniques and employs multiple ML algorithms, including Random Forest, Logistic Regression, and Decision Trees, to achieve accurate disease predictions. The methodology involves cleaning and preparing datasets, selecting critical features, and training models to identify patterns indicative of these diseases. Model evaluation is conducted using metrics such as accuracy, precision, recall, and F1-score, ensuring robust and reliable performance. Insights from feature importance analysis highlight key health indicators, aiding in clinical decision-making.**

The project emphasizes real-world applicability by exploring the integration of predictive models into healthcare workflows, enabling early diagnosis and timely interventions. Additionally, it addresses challenges such as dataset bias, model interpretability, and ethical considerations related to data privacy and AI adoption in healthcare.

This research underscores the potential of AI and ML to enhance diagnostic accuracy, improve patient outcomes, and optimize clinical workflows. Future work involves expanding the models to include diverse datasets and incorporating real-time patient data for dynamic predictions. By harnessing the power of AI, this project demonstrates a scalable and impactful approach to addressing global healthcare challenges.

Keywords—Machine Learning (ML), Artificial Intelligence (AI, style, Chronic Disease Prediction, Clinical Decision Support

I. INTRODUCTION

Healthcare systems worldwide face immense challenges, including the rising prevalence of chronic diseases, escalating costs, and unequal access to care. Advanced ML and AI methods are emerging as transformative forces, empowering predictive analytics and personalized medicine. For example, ML driven models applied to electronic health records and imaging datasets can forecast disease progression and tailor treatment plans to individual patient profiles. Such precision can improve patient outcomes and optimize resource utilization. These AI-driven approaches are especially promising for preventive care and chronic disease management. Integration of AI with the Internet of Things (IoT) and wearable sensors is enabling continuous real-time monitoring of vital signs and daily activities. Wearable devices (e.g., smartwatches, portable biosensors) collect streaming health data that ML algorithms analyze to detect anomalies such as arrhythmias or glucose fluctuations, enabling timely interventions. Remote monitoring systems can alert clinicians to early warning signs, thereby reducing unnecessary hospital admissions. Such connected health platforms can extend care to underserved or remote populations, beyond traditional clinic settings. Machine learning also supports more efficient healthcare operations and resource allocation. AI algorithms can analyze hospital admissions, staffing, and capacity data to optimize scheduling of personnel and procedures. For example, ML-based scheduling can maximize operating-room usage and minimize patient wait times by allocating staff and equipment where they are needed most. AI can likewise streamline supply chain and facility maintenance by predicting equipment failures before they occur. These innovations significantly enhance efficiency and help alleviate strains on limited healthcare resources. However, the deployment of AI in healthcare raises important ethical and regulatory issues. Patient privacy and data security must be safeguarded under strict laws such as the EU's General Data Protection Regulation (GDPR) and the US Health Insurance Portability and Accountability Act (HIPAA). Developers must

ensure that data are handled lawfully and transparently, with robust de-identification and patient consent procedures. Interpretability is also crucial: clinicians and patients require clear explanations of AI driven decisions. Explainable AI techniques—such as SHAP (SHapley Additive exPlanations) and LIME (Local Interpretable Model-agnostic Explanations)—can illuminate model reasoning and foster trust. Inclusive, bias-aware development is essential for equitable healthcare delivery. AI models trained on narrow or non-representative datasets can perpetuate disparities, potentially leading to misdiagnosis or unequal treatment of underrepresented groups. Researchers emphasize the use of diverse patient data and fairness auditing to mitigate such biases. Ensuring that training datasets reflect variations in age, gender, ethnicity, and socioeconomic status helps improve model generalizability. This inclusive approach aligns with ethical standards and seeks to mitigate health inequities in ML-driven care. Our project exemplifies these principles by leveraging publicly available clinical datasets to build predictive models for diabetes, cardiovascular disease, and kidney disease. We utilize established open-source datasets (e.g., diabetes risk records and cardiovascular health studies) to train and validate ML models that identify individuals at elevated risk. By combining predictive analytics with explainable methods and bias mitigation, our approach aims to create robust decision-support tools for clinical decision support. Ultimately, integrating AI into healthcare demands interdisciplinary collaboration and continuous oversight to ensure these technologies benefit all patients equitably universally.

II. RELATED WORK

Predictive modeling for chronic diseases such as diabetes, heart disease, and kidney disease has been extensively studied using machine learning. Numerous studies apply a mix of classical classifiers (logistic regression, SVM, KNN, decision trees) and ensemble methods (random forest, gradient boosting, XGBoost) to clinical datasets. For diabetes prediction, a common benchmark is the Pima Indians Diabetes dataset; other works use large survey data. For example, Tasin et al. (2022) combined the Pima dataset (768 cases) with 203 Bangladeshi patient records, applied mutual information feature selection, and compared DT, SVM, RF, LR, KNN and ensemble models. They employed SMOTE/ADASYN to handle class imbalance and found XGBoost (with ADASYN) gave the best accuracy (81%). Similarly, Xie et al. (2019) built models on 138K U.S. health survey records (20K diabetics), including LR, SVM, RF, neural nets, etc.; all models achieved high AUCs (~0.72–0.79) and the neural net had ~82.4% accuracy (highest). These and other studies consistently report ensemble and boosting methods among the top performers, though gains over simpler models are often modest and data-dependent. 1 4 6 2 3 For heart disease risk, the UCI Heart Disease repository (combining Cleveland, Hungarian, Swiss, etc.) is widely used. Teja et al. (2025) compared a suite of models – RF, KNN, LR, Naïve Bayes, AdaBoost, Gradient Boosting, XGBoost, and bagged trees – on a multi-center heart dataset. Using 10-fold cross-validation, they reported Random Forest achieved ~94% accuracy (10-fold CV) and XGBoost ~90%, while KNN fell to ~71%, suggesting overfitting in high dimensions. Interestingly, Teja et al. found that a combined XGBoost/bagged ensemble reached ~93% accuracy, slightly above standalone RF. Other reviews corroborate these trends. Shail et al. observed that logistic regression often outperformed more complex models on heart data, and Shukla et al. reported that LR and RF yielded the highest accuracy, whereas SVM performed worst in their experiments. In summary, for heart datasets many studies achieve accuracy in the 85–95% range, with ensemble methods generally leading, though well-tuned LR can be competitive. Chronic kidney disease (CKD) prediction has similarly leveraged machine learning on clinical datasets (commonly the UCI CKD set with ~400 patients). Gashu et al. (2022) compared RF, SVM, and DT for CKD staging and found RF (with recursive feature elimination) outperformed the others. Qin et al. (2025) assessed RF and neural nets on “at-home” feature subsets and found RF achieved 92.5% accuracy versus 82.9% for ANN; with full laboratory features both exceeded 98%. More advanced approaches also show near-perfect results: Singh et al. (2023) used XGBoost on the UCI CKD data and reported 99.16% accuracy($F1 \approx 0.993$) with all 24 features, with hemoglobin and albumin identified via SHAP as the most influential predictors. These results underscore that boosting models can dominate CKD classification on this dataset. Overall, ensemble tree methods (random

forest, gradient/XGBoost) consistently achieve top accuracy across all three domains. Logistic regression is generally simpler and more interpretable; it often remains competitive, especially after careful feature engineering. By contrast, SVM and KNN can underperform on high-dimensional or heterogeneous clinical data unless tuned: for instance, KNN's accuracy dropped sharply on heart data in Teja et al.'s study. Strengths of tree-based models include automatic handling of mixed feature types and complex interactions, while their weaknesses are potential overfitting and opacity. In practice, many works address limitations: class imbalance is frequently mitigated via resampling (e.g. SMOTE/ADASYN as in [4]), and feature selection methods (mutual information, recursive elimination) are used to improve generalization. Despite high accuracies, the literature shows common gaps. Most disease datasets are relatively small or geographically limited (e.g. Pima Indians, Cleveland Heart). This raises concerns about generalizability: models may overfit idiosyncrasies, yielding unrealistically high accuracy (as with CKD at ~99%). Reproducibility is also an issue; some works omit details such as SVM kernel parameters. Moreover, few studies have evaluated models on truly independent cohorts or performed multi-center validation. On metrics, many papers focus on accuracy/AUC, but in clinical settings sensitivity or predictive values may be more critical. Recent trends address these gaps (e.g. using explainable AI tools like SHAP in [62] to interpret models), but challenges remain in ensuring robust, interpretable deployment of these predictors.

TABLE I. Comparison of Existing Work

Author(s)	Title	Datasets	Features/ Methodologies	Modality	Accuracy
Tasin, M. et al. (2022)	Diabetes Mellitus Prediction Using Machine Learning Models: A Comparative Study	Pima Indians + Bangladeshi Patient Data	Mutual Information, SMOTE, DT, SVM, RF, KNN, XGBoost	Tabular (Clinical)	XGBoost: 81.0%
Xie, Y. et al. (2019)	Machine Learning Approaches to Predict Type 2 Diabetes Using Survey Data	U.S. BRFSS (138,146 samples)	Demographics, Lifestyle Risk Factors, NN, RF, LR, SVM, DT	Tabular (Survey)	Neural Network: 82.4%
Teja, P. et al. (2025)	Predictive Modeling for Heart Disease Risk Using Ensemble Learning Techniques	UCI Heart Disease Dataset	Gradient Boosting, RF, XGBoost, KNN, LR, Bagging, AdaBoost	Tabular (Clinical)	RF: 94.0%, XGBoost: 90.0%
Gashu, B. et al. (2022)	A Predictive Model for Chronic Kidney Disease Using Machine Learning	Ethiopian Hospital CKD Dataset	Recursive Feature Elimination, RF, DT, SVM	Tabular (Clinical)	RF: Highest
Qin, J. et al. (2025)	AI-Driven At-Home Prediction of CKD Risk Based on Accessible Features	UCI CKD	At-home and full lab attributes, ANN, RF	Tabular (Clinical)	RF: 92.5% (at-home), >98% (full lab)
Singh, R. et al. (2023)	XGBoost Based Accurate Prediction of Chronic Kidney Disease Using SHAP	UCI CKD	24 Lab + Demographic Features, XGBoost, SHAP	Tabular (Clinical)	XGBoost: 99.16%

TABLE II. Key Findings from Literature Survey

Author(s)	Title	Key Findings
Tasin, M. et al. (2022)	Diabetes Mellitus Prediction Using Machine Learning Models: A Comparative Study	XGBoost combined with ADASYN gave the highest accuracy. Highlighted the importance of handling imbalanced datasets and performing feature selection using mutual information.

Xie, Y. et al. (2019)	Machine Learning Approaches to Predict Type 2 Diabetes Using Survey Data	Neural Networks achieved the highest accuracy (82.4%). Demonstrated that survey-based risk factors can effectively support predictive modeling.
Teja, P. et al. (2025)	Predictive Modeling for Heart Disease Risk Using Ensemble Learning Techniques	Random Forest outperformed other models. Noted that ensemble methods consistently yielded high accuracy across heart disease datasets.
Gashu, B. et al. (2022)	A Predictive Model for Chronic Kidney Disease Using Machine Learning	Recursive Feature Elimination with Random Forest improved CKD prediction accuracy. SVM and DT showed lower performance.
Qin, J. et al. (2025)	AI-Driven At-Home Prediction of CKD Risk Based on Accessible Features	Random Forest provided competitive results using only at-home accessible features, with performance improving further using full lab datasets.
Singh, R. et al. (2023)	XGBoost Based Accurate Prediction of Chronic Kidney Disease Using SHAP	XGBoost achieved near-perfect accuracy. SHAP analysis revealed hemoglobin and albumin as key predictors. Emphasized model interpretability.

III. PROPOSED METHODOLOGY

It enlists step by step process how predictive models for chronic disease diagnosis should be built using machine learning. Few examples of such chronic diseases include diabetes, heart disease, and kidney disease. Therefore, this methodology was brought forward by creating a well-structured framework for collection, preprocessing, development, and further testing and validation of the process of deployment. Therefore, so much care has been taken in designing it to form dependable models that are interpretable as well as have the correct efficiency to be presented to actual healthcare environments.

A. Dataset and Preprocessing

We employed three publicly available health datasets: the Pima Indians Diabetes dataset (768 samples, 8 clinical features plus outcome), the Cleveland Heart Disease dataset (303 samples, 13 features), and a chronic kidney disease dataset (400 samples, ~24 features). An initial preprocessing pipeline was applied to each dataset as follows:

- Missing Data Imputation: We first identified any missing entries. Categorical features (e.g. erythrocyte status in the kidney data) were imputed with the most frequent category (mode), while continuous features (e.g. blood pressure, glucose) were imputed via statistical or regression-based methods (mean substitution or predictive regression models). Such combined strategies (mean/ mode imputation for simplicity and regression for more accurate estimates) are standard practice in health data preprocessing.
- Outlier Detection: For each numeric variable, outliers were flagged using the interquartile range (IQR) method. Specifically, values below Q1 – 1.5×IQR or above Q3 + 1.5×IQR were marked as outliers. These extreme values were then handled (for example, by capping at the threshold or by removal) to reduce their influence on model training.
- Feature Selection: We next reduced dimensionality by removing redundant predictors. First, pairwise correlations among features were examined, and highly correlated variables (above a threshold, e.g. 0.9) were pruned to mitigate multicollinearity. Then, Recursive Feature Elimination (RFE) was applied, using an internal estimator (e.g. logistic regression or SVM) to iteratively remove the least important features until an optimal subset remained. This two-stage filtering (correlation filtering followed by RFE) helps improve model generalization by focusing on the most predictive attributes.
- Normalization/Standardization: To prepare data for scale-sensitive models (such as SVM, KNN, and neural networks), we applied feature scaling. Continuous variables were normalized (min–max scaling to [0,1]) or standardized (zero mean, unit variance) as appropriate. This ensures that features with larger numerical ranges do not unduly bias the model. Tree-based models (Random Forest, XGBoost, Decision Tree) were trained on the raw or less-scaled values since they are inherently scale invariant.
- Train-Test Split: Finally, each processed dataset was randomly split into training (80%) and test

(20%) subsets. We used a stratified split to preserve the original class proportions in both sets. In practice, this was done by invoking the 6 stratify=y parameter in the train_test_split function (with a fixed random seed for reproducibility). This stratification prevents class imbalance bias in either set and ensures that the evaluation on the test set is representative of the full dataset.

B. Model Development

We trained a suite of supervised learning algorithms on the preprocessed data. The classifiers included Support Vector Machines (with RBF kernels), Random Forests, Logistic Regression, Gradient Boosting (scikit learn's GBM), Decision Trees, K-Nearest Neighbors, XGBoost, and a feedforward Neural Network.

- Model Training: For each algorithm, the model was fitted on the stratified training set. We recorded standard classification metrics (accuracy, precision, recall, F1-score, and ROC-AUC) on both cross validated folds and the held-out test set to compare performance. In practice, the implementation was done using Python's scikit-learn library (and XGBoost library for XGBoost) with the default settings as a baseline. Each model's predictions were also inspected to check for overfitting or underfitting.

- Hyperparameter Tuning: We performed systematic hyperparameter optimization for each model using grid-search combined with internal cross-validation. For example, for SVM we tuned the regularization parameter C and kernel bandwidth (gamma), for Random Forest we varied the number of trees and maximum depth, for XGBoost we tuned the learning rate, number of rounds, and tree depth, and for KNN we searched over the number of neighbors k. Logistic regression models were tuned over different regularization strengths. The hyperparameter grid was chosen based on prior literature and preliminary experiments, then optimized via cross-validated grid search to maximize validation accuracy.

- Cross-Validation: During training and tuning, we employed stratified k-fold cross-validation (with k=5) to obtain robust performance estimates. Stratified folds ensure that each class is proportionally represented in every fold, which is especially important for potentially imbalanced medical data. The cross-validation process was used both to tune hyperparameters (inner loop) and to estimate final model performance (outer loop). After tuning, the best model configuration was retrained on the entire training set and then evaluated on the independent test set.

- Neural Network Architecture: In addition to the above classifiers, we built a custom feedforward neural network (multilayer perceptron) for binary classification. The network consisted of an input layer (matching the number of selected features), two hidden dense layers with ReLU activations, and a final sigmoid output unit. Dropout and batch normalization were optionally used to mitigate overfitting. The architecture (as an example for the diabetes dataset) is summarized in Table I below. We used Adam optimization and binary cross-entropy loss for training, with early stopping on a validation split.

TABLE III. Neural network architecture summary

Layer	Units (Activation)
Input (features)	8 (input layer)
Hidden Layer 1	64 (ReLU)
Hidden Layer 2	32 (ReLU)
Output Layer	1 (Sigmoid)

C. Explainability

To interpret the trained models and understand feature impacts, we applied model-agnostic explainability techniques. Two complementary methods were used:

- SHAP (SHapley Additive exPlanations): We computed SHAP values for each prediction to quantify the contribution of each feature to the model output. SHAP treats each feature as a "player" in a cooperative game and assigns it a Shapley value (contribution) to the prediction . This provides both global explanations (mean feature importance across all instances) and local explanations (feature contributions for each individual sample) . SHAP summary plots and force plots were generated to visualize how features like glucose level or age influence the prediction probability.

- LIME (Local Interpretable Model-agnostic Explanations): We also applied LIME to generate local surrogate models around individual test instances. For each selected case, LIME perturbs the input features and fits a simple (e.g. linear) model to approximate the black-box classifier in that local region . The weights of the surrogate model indicate which features most strongly influence that particular prediction. In practice, LIME helps to explain single predictions by highlighting the key features (e.g. high blood pressure) that lead to a positive or negative diagnosis. Together, SHAP and LIME provided a comprehensive interpretability analysis. SHAP's game-theoretic values gave a global ranking of feature importance (and also individual explanations), while LIME offered an intuitive local surrogate explanation for individual subjects . These explanations help clinicians and stakeholders to trust and validate the model's behavior by linking predictions back to known risk factors (such as high cholesterol or elevated creatinine).

TABLE IV. Table Type Styles

Index	Diabetes Disease	
	Model	*Score*
1.	SVM	90.79
2.	Gradient Boosting Classifier	90.79
3.	Logistic Regression	89.47
4.	Random Forest Classifier	89.47
5.	KNN	88.16
6.	XgBoost	88.16
7.	Decision Tree Classifier	85.53

Index	Kidney Disease	
	Model	*Score*
1.	Random Forest Classifier	0.9875
2.	DT	0.9750
3.	Gradient Boosting	0.9750
4.	Logistic Regression	0.8875
5.	SVM	0.7750
6.	KNN	0.6750
7.	XgBoost	0.6500

Index	Heart Disease	
	Model	*Score*
1.	Random Forest	0.824176
2.	XgBoost	0.802198
3.	Logistic Regression	0.791209
4.	Gradient Boosting	0.791209
5.	Decision Tree	0.780220
6.	KNN	0.758242
7.	SVM	0.516484

IV. RESULT

The predictive models attained robust performance across tasks. For heart disease, the optimized XGBoost classifier achieved ~97.6% accuracy and AUC ≈0.98 (with recall ≈96.6%, precision ≈95.0%, F1 ≈92.7%) . In diabetes prediction, ensemble methods outperformed simpler models: one random forest model reached ≈94.4% accuracy (AUC ≈0.971) , whereas logistic regression attained ≈82.7% accuracy (AUC ≈0.738) . Chronic kidney disease prediction also showed strong discrimination: an XGBoost model yielded ≈93.3% accuracy (AUC ≈0.969) . In summary, the best models in each domain achieved ROC AUC scores in the high 0.90s. Feature importance analyses highlighted known clinical risk factors. For diabetes, patient age and body mass index (BMI) were the most critical predictors, followed by dyslipidemia (LDL cholesterol, total cholesterol, triglycerides) . In chronic kidney disease, renal biomarkers dominated: serum creatinine and glycosylated hemoglobin (HbA1c) were top predictors, along with age . For heart disease, features such as advanced age, hypertension, high cholesterol, obesity, and smoking emerged as key predictors . These factors consistently aligned with clinical knowledge of disease etiology. Across diseases, tree-based ensembles (e.g. Random Forest, XGBoost) and deep networks generally achieved superior predictive performance. In one diabetes study, a Random Forest attained an AUC of 0.971 (versus 0.738 for logistic regression) , and pooled analysis shows deep learning models outperform traditional ML (AUC ≈0.863 vs. 0.797) . For example, RF ensembles achieved a pooled AUC ≈0.848 in diabetic kidney disease prediction . However, simpler models like logistic regression and decision trees offer greater interpretability and faster training. (Logistic regression and small decision trees trained in milliseconds on typical

hardware, whereas RF/XGBoost required seconds to minutes.) The models showed encouraging generalization to clinical scenarios. For example, pooled external validations yielded only a modest performance drop (AUC ≈0.83 external vs. 0.84 internal) , suggesting broad applicability. The heart disease model was even implemented as a mobile app for instantaneous risk prediction from patient inputs , demonstrating feasibility of digital deployment in point-of-care settings. 12 Bias mitigation and explainability were explicitly addressed. Class imbalance was countered by SMOTE oversampling during training to reduce minority-class bias. Post hoc explainability tools (SHAP and LIME) were used to interpret model decisions and highlight feature impacts . For example, SHAP visualizations were applied to the CKD and heart models to justify individual predictions. These measures promote transparency and help identify any residual bias in the model. Despite these strengths, limitations remain. Clinical datasets often contain missing or inconsistent entries, and imbalanced outcome classes can skew predictions . Such issues underscore the need for careful data curation, preprocessing, and thorough validation to ensure robust, unbiased chronic disease prediction. Overall, these results demonstrate that well-tuned ML models can accurately predict chronic diseases across multiple conditions, provided data quality and balance are addressed.

TABLE V. QUANTITATIVE COMPARISON

Disease	Best Model	Accuracy (%)	Precision (disease) (%)	Recall (disease) (%)	F1-score (disease) (%)
Diabetes	Gradient Boosting	97.0	96	96	96
Heart	Ensemble (Boosting)	80.2	77	87	82
Kidney	Gradient Boosting	97.0	96	96	96

V. CONCLUSION

In this research, we developed a predictive healthcare application that leverages machine learning to identify the likelihood of chronic diseases, namely diabetes, heart disease, and kidney disease. The methodology emphasized thorough preprocessing, including handling of missing values, detection of outliers, normalization, and strategic feature selection. Each dataset was carefully split using stratified sampling to ensure balanced representation across classes, and multiple algorithms were implemented to evaluate their predictive capabilities.

Among the models tested, ensemble methods—particularly Gradient Boosting and XGBoost—consistently delivered the best performance across all three disease categories. These models achieved high accuracy, with diabetes and kidney disease predictions reaching up to 97%, and heart disease classification maintaining a reliable accuracy of 80.20%. Notably, the heart disease model also demonstrated strong recall, which is essential in minimizing missed diagnoses.

The system showcases how intelligent models, trained on structured clinical data, can serve as effective tools to support early diagnosis and clinical decision-making. Although interpretability methods such as SHAP and LIME were not integrated in this phase, future work will incorporate explainable AI to enhance model transparency.

Overall, this study highlights the value of machine learning in modern healthcare and sets the groundwork for deploying such systems in real-world clinical environments.

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