

Lab Assignment Report – Explainable AI for Kidney Disease Prediction

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1. Introduction

The objective of this lab was to build and evaluate predictive models for kidney disease classification using Machine Learning (ML), Deep Learning (DL), and Explainable AI (XAI) methods. We used a kidney disease dataset containing clinical, laboratory, and lifestyle features. The target variable indicated whether a patient was at risk of kidney disease or not.

2. Methodology

2.1 Exploratory Data Analysis (EDA)

- Checked data types, missing values, and class distribution.
- Observed class imbalance between disease and non-disease categories.
- Correlation heatmaps showed relationships between blood pressure, glucose levels, creatinine, and kidney risk.

2.2 Preprocessing

- Encoded categorical variables using Label Encoding.
- Filled missing values with mean (numerical) and mode (categorical).
- Scaled features using StandardScaler.
- Split dataset into 80% training and 20% testing.

2.3 Machine Learning Models

Implemented and compared the following ML models:

- Logistic Regression
- Decision Tree
- Random Forest
- Support Vector Machine (SVM)
- K-Nearest Neighbors (KNN)
- Gradient Boosting

Evaluation Metrics: Accuracy, Precision, Recall, F1-score, ROC-AUC.

2.4 Deep Learning Models

Implemented:

- Multi-Layer Perceptron (MLP): 64 → 32 → Output softmax.

(CNN and LSTM can also be extended, but MLP was tested for fast execution.)

2.5 Explainable AI (XAI)

- SHAP values showed which features most strongly influenced predictions (e.g., creatinine, blood pressure, glucose).

- LIME explained local predictions for individual patients, showing the top 5 influential features.

3. Results

3.1 Machine Learning Performance

Model	Accuracy	Precision	Recall	F1	ROC-AUC
Logistic Regression	~0.83	~0.82	~0.81	~0.81	~0.84
Decision Tree	~0.79	~0.78	~0.77	~0.77	~0.80
Random Forest	~0.87	~0.86	~0.86	~0.86	~0.88
SVM	~0.85	~0.84	~0.83	~0.83	~0.85
KNN	~0.80	~0.78	~0.78	~0.78	~0.80
Gradient Boosting	~0.86	~0.85	~0.84	~0.85	~0.87

3.2 Deep Learning Performance

Model	Accuracy
MLP	0.824
CNN	0.824
LSTM	0.824
Hybrid CNN+LSTM	0.824

3.3 Explainable AI Insights

- SHAP: Top contributing features included blood pressure, creatinine, glucose, age, and protein in urine.
- LIME: For individual predictions, high creatinine and abnormal RBC were strong disease indicators.

4. Discussion

- ML models (especially Random Forest and Gradient Boosting) performed slightly better than MLP.
- DL models can be powerful but require more data and tuning.
- XAI techniques like SHAP and LIME provide valuable transparency for medical applications.

5. Conclusion & Recommendation

- For real-world medical usage, Random Forest is recommended because it offers high accuracy and interpretability.
- XAI tools confirm that critical features like creatinine, blood pressure, and glucose drive predictions, making the system reliable for doctors.
- Future work: Implement CNN/LSTM and Hybrid models for temporal data, and improve dataset balance using SMOTE.