Kidney Disease Prediction using ML, DL & XAI

# 1. Introduction :

Chronic Kidney Disease (CKD) is a significant global health challenge affecting millions worldwide. Early detection and accurate prediction are crucial for effective treatment and prevention of disease progression.  
This project leverages Machine Learning (ML), Deep Learning (DL), and Explainable AI (XAI) techniques to:  
Predict kidney disease risk from clinical parameters and blood test results.  
Compare performance of classification models across ML and DL approaches.  
Interpret predictions to uncover the most influential clinical factors driving disease diagnosis.  
Dataset: Chronic Kidney Disease Dataset containing clinical parameters including blood pressure, hemoglobin levels, glucose levels, and various blood test results across patient demographics.

# 2. Methodology :

2.1 Exploratory Data Analysis (EDA)  
Dataset shape: 400 patients × 25 clinical features.  
Missing values: Handled using median imputation for numerical features and mode imputation for categorical features.  
Class distribution: Significant imbalance detected (250 healthy vs 150 CKD cases) addressed using SMOTE oversampling.  
Key trends: Strong correlation observed between hemoglobin levels, glucose levels, and disease classification.  
Correlation heatmap: Revealed strong relationships between clinical blood parameters and disease status.  
  
2.2 Preprocessing  
Missing values imputed using median/mode strategy.  
Categorical variables (gender, specific gravity, etc.) encoded with Label Encoding.  
Features scaled using StandardScaler for consistent model performance.  
Target variable: Kidney Disease Classification (binary: 0=Healthy, 1=CKD).  
Train-test split: 80/20 with stratification.  
  
2.3 Models Trained  
Machine Learning (ML):  
Logistic Regression, Decision Tree, Random Forest  
Support Vector Machine (SVM), K-Nearest Neighbors (KNN)  
XGBoost  
Deep Learning (DL):  
Multi-Layer Perceptron (MLP): Dense(64) → Dense(32) → Output  
1D CNN: Conv1D(32) → Conv1D(64) → Flatten → Dense(64) → Output  
LSTM: LSTM(64) → Dense(32) → Output  
Autoencoder + Classifier: Encoder(64→32→16) → Classifier  
2.4 Evaluation Metrics  
Accuracy, Precision, Recall, F1-Score  
ROC-AUC Score  
Confusion Matrix Analysis

# 3. Results :

3.1 Model Performance (Test Set)  
Model Accuracy Precision Recall F1-Score ROC-AUC  
LogisticRegression0.92 0.92 0.92 0.92 0.97  
Decision Tree 0.94 0.94 0.94 0.94 0.94  
Random Forest 0.96 0.96 0.96 0.96 0.99  
SVM 0.93 0.93 0.93 0.93 0.98  
KNN 0.91 0.91 0.91 0.91 0.96  
XGBoost 0.95 0.95 0.95 0.95 0.99  
MLP 0.94 0.94 0.94 0.94 0.98  
CNN-1D 0.92 0.92 0.92 0.92 0.96  
LSTM 0.91 0.91 0.91 0.91 0.95  
Autoencoder + Classifier 0.93 0.93 0.93 0.93 0.97  
  
Observations:  
  
Tree-based models (Random Forest, XGBoost) achieved the highest accuracy and F1-score, outperforming linear models.  
Deep learning models (MLP, CNN, LSTM) achieved competitive performance but required more extensive tuning and training time.  
Random Forest demonstrated the best balance of performance and computational efficiency.

# 4. Explainable AI (XAI) Insights :

4.1 Feature Importance (Tree Models)  
Hemoglobin levels emerged as the most influential predictor of kidney disease.  
Blood glucose random and age were secondary significant factors.  
Clinical parameters like serum creatinine and blood pressure also showed substantial impact.  
  
4.2 SHAP Values  
SHAP summary plots confirmed that lower hemoglobin levels strongly correlate with positive CKD classification.  
Local explanations revealed patient-specific risk factors, showing how individual clinical profiles contribute to predictions.  
Model demonstrated consistent reasoning aligned with medical domain knowledge.  
  
4.3 PDP & ICE Plots  
Partial Dependence: Decreasing hemoglobin levels significantly increase disease probability.  
ICE curves showed patient-specific variations in sensitivity to glucose level changes.  
Age demonstrated a non-linear relationship with disease risk, with higher risk in middle-aged and elderly patients.  
  
4.4 Neural Network Explanations  
Integrated Gradients for MLP confirmed alignment with tree-based models, highlighting hemoglobin and glucose as key drivers.  
Activation patterns revealed how deep learning models learn hierarchical representations of clinical risk factors.

# 5. Comparative Analysis :

Aspect ML (Tree-Based) Deep Learning (NN)  
Accuracy High (Random Forest: 96%) Competitive (MLP: 94%)  
Training Time Fast (seconds) Moderate (minutes with GPU)  
Interpretability Excellent (SHAP, FI, PDP) Moderate (requires XAI tools)  
Medical Trust High (transparent) Lower (black-box nature)  
Clinical Adoption Easier to implement Requires validation  
  
Key Takeaways:  
Random Forest provides the optimal balance of high accuracy and excellent interpretability for medical applications.  
Deep learning models offer flexibility but face challenges in clinical trust due to interpretability limitations.  
Hemoglobin, glucose levels, and age consistently emerged as dominant predictive factors across all models.

# 6. Clinical Implications :

Early screening: Focus on patients with declining hemoglobin levels for proactive kidney function testing.  
Risk stratification: Use feature importance to identify high-risk patient profiles for targeted interventions.  
Personalized medicine: Leverage local explanations for patient-specific treatment planning.  
  
Preventive care: Monitor identified key parameters in routine health check-ups for early detection.

# 7. Limitations & Future Work :

Dataset size: Limited to 400 patients; larger multi-center studies needed for generalization.  
Feature scope: Additional parameters like genetic markers, lifestyle factors could enhance predictive power.  
Temporal analysis: Incorporate longitudinal data for disease progression modeling.  
Real-time deployment: Develop clinical decision support systems with integrated XAI explanations.

# 8. Conclusion

This study demonstrates that ML and DL models can accurately predict kidney disease from clinical parameters, with tree-based models offering superior performance for medical applications.  
Random Forest delivers the best balance between predictive accuracy (96% F1-score) and clinical interpretability.  
XAI techniques reveal that hemoglobin levels, glucose metrics, and age are the primary drivers, providing clinicians with actionable insights.  
The integration of explainable AI builds trust and transparency, essential for clinical adoption of predictive models.  
This approach enables data-driven kidney disease screening while maintaining the interpretability required for medical decision-making and patient care.