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Deep Hybrid Framework for Early Detection of Chronic Kidney Disease Using CNN–LSTM Ensemble Models

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Abstract—Chronic Kidney Disease is a serious health issue that often develops slowly and shows no early signs, making timely detection very important. Regular testing and manual diagnosis can take time and may lead to errors. This study introduces a smart deep learning-based system that uses Convolutional Neural Networks , Long Short-Term Memory networks, and an Ensemble Model to predict CKD more accurately. The CNN model helps pick up useful patterns from medical images and lab test results, while the LSTM model understands time-based patterns in patient records. By mixing these two types of features, the ensemble method boosts the model's ability to make better predictions. The system was tested on publicly available CKD datasets and outperformed regular machine learning models. The combined use of image and sequence data allows the system to learn in a more complete way, helping doctors find CKD earlier and make faster, more confident decisions. This method shows how artificial intelligence can support precision healthcare and help lower the chances of kidney failure through early and reliable prediction.
Keywords–Chronic Kidney Disease, Deep Learning, CNN, LSTM, Ensemble Learning, Medical Diagnosis, Early Detection, Predictive Analytics

1.INTRODUCTION

Chronic Kidney Disease is a long-term condition in which the kidneys gradually lose their ability to filter waste and maintain fluid balance in the body. It is one of the major global health problems, affecting millions of people each year, often going undiagnosed until the disease reaches a severe stage[1][3]. The silent nature of CKD progression, coupled with limited access to timely testing in many regions, makes early detection extremely challenging. Conventional diagnostic techniques largely depend on manual examination of clinical reports and test results such as blood urea, creatinine, and glomerular filtration rate [12]. However, these methods are often slow and prone to human error, resulting in delayed treatment and higher chances of kidney failure.

In recent years, advancements in artificial intelligence (AI) and deep learning have transformed the way medical data is analyzed. Deep learning models, such as Convolutional Neural Networks (CNNs) and Long Short-Term Memory (LSTM) networks, have shown remarkable success in understanding complex patterns in both image-based and sequential data[4][6]. CNNs are particularly effective for extracting spatial information from medical images and reports, while LSTMs can capture time-dependent relationships in patient health records. By combining these models, it becomes possible to leverage the strengths of both visual and sequential learning in predicting disease progression.

The integration of CNN and LSTM models provides a more complete understanding of patient data by learning from both static and temporal features. While CNN identifies abnormalities in imaging or report data, LSTM tracks changes over time in patient health indicators such as blood pressure, sugar levels, and creatinine trends. This multi-dimensional approach creates a more reliable system capable of identifying early warning signs of CKD before serious damage occurs. Additionally, ensemble learning techniques further enhance accuracy by combining predictions from multiple models to reduce bias and variance.

This research aims to design an intelligent, hybrid framework for early CKD detection using CNN, LSTM, and ensemble learning. The proposed system not only provides improved accuracy but also helps doctors and healthcare professionals make faster and more confident decisions. The outcome of this work highlights how AI can revolutionize medical diagnosis, reduce the burden on healthcare systems, and ultimately improve the quality of life for patients at risk of chronic kidney disease.

1.1Motivatio*n*

The growing prevalence of Chronic Kidney Disease and the limitations of traditional diagnostic methods highlight the urgent need for an intelligent, automated detection system. Manual analysis of clinical reports and imaging data is time-consuming, error-prone, and often delays treatment. Deep learning offers an opportunity to revolutionize CKD prediction by learning directly from complex datasets, improving diagnostic accuracy, and identifying risk factors early. The motivation behind this study is to combine CNN, LSTM, and ensemble learning techniques to build a unified, efficient model capable of detecting CKD early, supporting clinicians in timely decision-making, and preventing disease progression.

1.2 Objectives:

- To develop a hybrid deep learning model that integrates CNN, LSTM, and ensemble learning for accurate CKD prediction.
- To extract meaningful spatial features from medical images and lab reports using CNN.
- To capture sequential and temporal dependencies in patient health records using LSTM.
- To combine diverse model outputs through ensemble learning for enhanced prediction reliability.
- To evaluate the proposed framework on publicly available CKD datasets and compare its performance with conventional methods.

2.RELATED WORK

Early detection of Chronic Kidney Disease has gained significant attention due to its silent progression and life-threatening impact if left untreated. Recent research has focused on using deep learning models to automate the diagnostic process, minimizing human bias and improving reliability. Banerjee et al. [1] proposed a CNN-based predictive framework for CKD diagnosis using clinical data. Their approach demonstrated that CNN models can extract complex patterns and relationships among biochemical parameters like serum creatinine, blood urea nitrogen, and hemoglobin. The model achieved high accuracy in differentiating between CKD and non-CKD patients, proving that convolutional feature extraction can be effective even for structured medical data. The study highlighted the potential of CNN architectures to handle clinical datasets, though it was limited by its inability to analyze temporal changes in patient health records over time.

Ramesh and Srinivasan [2] designed a deep CNN model for classifying kidney ultrasound images to identify CKD at early stages. Their system utilized multiple convolution and pooling layers to automatically detect visual cues of kidney damage such as cysts, size variation, and texture changes. By training on annotated medical images, the CNN achieved high sensitivity and specificity, outperforming traditional SVM and random forest classifiers. The work established that image-based CNN architectures are well-suited for radiological interpretation, offering non-invasive and efficient CKD detection. However, the authors noted that while spatial feature learning was strong, the model could not capture longitudinal health patterns crucial for disease progression analysis.

To address the limitation of temporal modeling, Chen et al. [3] introduced an LSTM-based framework for predicting kidney function using sequential health data. Their study focused on recognizing temporal dependencies in patient records, including lab results and vitals collected over multiple visits. The LSTM network effectively modeled trends such as declining eGFR levels and fluctuations in blood pressure, enabling accurate stage-wise progression analysis. The results indicated that LSTM networks are particularly useful for dynamic disease modeling, as they maintain memory of past information and predict future health trends. Despite promising results, the model relied heavily on the quality and frequency of data collection, which limited its generalization across diverse patient populations.

Sharma et al. [4] expanded on this approach by using LSTM networks on longitudinal patient health records to predict CKD onset. Their model incorporated a wider range of temporal features, including lifestyle factors, blood test parameters, and medication histories. The ML-based system provided early warning predictions up to several months before clinical diagnosis. The study demonstrated how sequential modeling can significantly enhance early intervention strategies. The authors emphasized that temporal deep learning could uncover hidden dependencies among variables that static models overlook. Nonetheless, they also acknowledged the computational complexity of training deep sequential models and the need for optimized architectures for clinical deployment.

Hasan and Rahman [5] took a different perspective by developing a deep CNN architecture for CKD classification using blood and urine parameters. Their model automatically extracted discriminative features from numeric clinical data represented as 2D feature maps. This innovative transformation enabled CNNs to capture nonlinear interactions between lab test variables. Their experiments showed strong performance improvements over traditional classifiers, confirming that CNNs could be effectively applied beyond image-based domains.

However, the study lacked temporal integration, making it less effective in tracking disease progression over time. Still, it laid the foundation for combining clinical data representation with spatial deep learning methods.

Finally, Zhao et al. [6] proposed an LSTM-driven model for stage-wise CKD progression analysis. The system analyzed time-series data of patients, capturing long-term dependencies and transitions between CKD stages. The results demonstrated that LSTM networks could successfully model the evolution of renal health, outperforming CNN-only and conventional regression models. Their work emphasized the significance of sequential learning for medical time-series analysis, especially in chronic disease management. Collectively, these studies reveal that CNNs are powerful for spatial and feature-based analysis, while LSTMs excel at capturing temporal dynamics. The integration of both in an ensemble framework holds the potential to create a more comprehensive and accurate predictive model for CKD diagnosis and progression monitoring.

2.1 Models:

2.1.1 Convolutional Neural Networks

Convolutional Neural Networks are a type of deep learning model that work really well with data arranged in grids, such as medical images, lab test results, or structured health records. For predicting Chronic Kidney Disease , CNNs help in automatically finding patterns and connections between input values without needing to manually select features[3]. The first layer of a CNN, called the input layer, takes in cleaned or preprocessed data this could be kidney scan images or converted matrices made from blood and urine test readings. Next come the convolutional layers, where small filters or kernels slide over the input data to create feature maps[5]. These filters act like detectors that catch small but important details for example, light and dark changes in kidney ultrasound images or linked variations between test values like serum creatinine and blood urea nitrogen). The features picked up, such as edges or intensity changes, then pass through an activation function called ReLU, which adds flexibility to the network and helps it learn more detailed patterns.

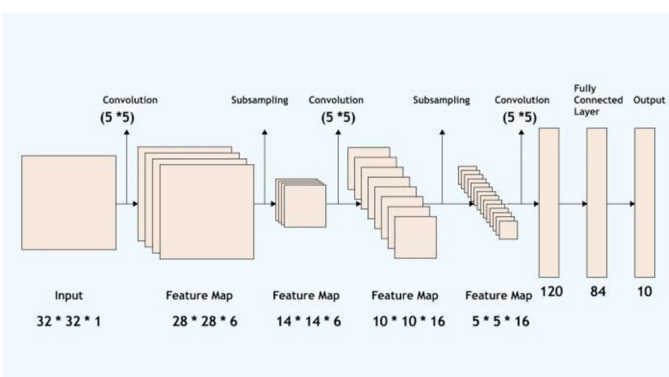

Fig1:CNN

As the CNN becomes deeper, more convolution and pooling layers are added to pick up higher-level and more abstract features. Pooling, often done using a max-pooling operation, helps shrink the feature maps while keeping only the most important details[7][8]. This reduces the total number of calculations and prevents the model from memorizing unnecessary noise. In CKD image data, this step helps the system focus on crucial physical signs such as changes in kidney shape, outer layer thickness, or unusual textures, while ignoring minor differences that don't matter[10]. The stride (the number of steps the filter moves) and padding (extra space added around the image) are adjusted to make sure the resulting feature maps stay properly aligned. The features learned at each layer form a kind of hierarchy the early layers pick up simple lines and textures, while the deeper layers identify more complex medical structures and kidney patterns linked to disease symptoms.

2.1.2: LSTM

The Long Short-Term Memory (LSTM) model is used to capture time-based patterns and dependencies in patient health data that evolve over time. Unlike standard neural networks, LSTM networks are designed to handle sequential data such as periodic laboratory reports, blood pressure readings, and kidney function indicators like serum creatinine and GFR levels where the order and timing of information matter[10]. The model receives these inputs as a sequence of time steps, allowing it to learn from past trends and predict future outcomes. The LSTM network consists of a series of memory cells, each capable of retaining important information for long durations while forgetting irrelevant details through controlled gates[12]. These include the input gate, which determines how much of the new information should be stored; the forget gate, which decides which old information should be discarded; and the output gate, which regulates what part of the cell's internal state should be passed forward. Together, these mechanisms make the LSTM ideal for tracking how kidney health metrics fluctuate over months or years, providing valuable insight into disease progression patterns that static models cannot detect.

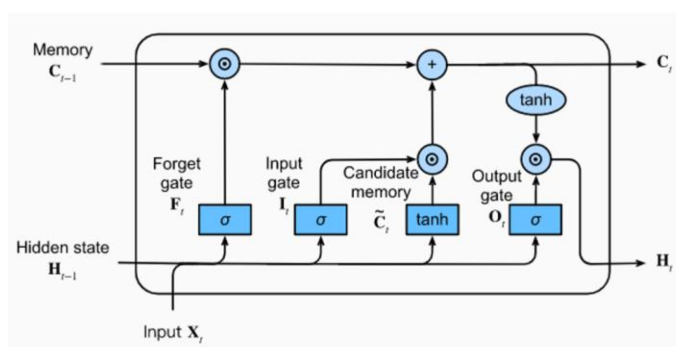

Fig2:LSTM

Each LSTM cell processes data step-by-step, updating its internal cell state and hidden state to maintain temporal consistency across patient records. The cell state acts as a conveyor of long-term memory, while the hidden state stores short-term contextual information that influences current predictions[9][14]. These dual states allow the LSTM to maintain context over long sequences, such as tracking gradual declines in kidney filtration efficiency or the impact of medication over several medical visits. During training, the network minimizes prediction errors using loss functions like mean squared error (MSE) or binary cross-entropy, depending on whether the goal is regression or classification. The backpropagation through time (BPTT) algorithm is used to update weights, ensuring that the gradients do not vanish or explode a common issue in traditional RNNs. To further enhance performance, dropout layers are often applied between recurrent connections to prevent overfitting, and batch normalization is used to stabilize learning. These technical refinements make LSTM models robust for handling real-world healthcare data, where temporal gaps and irregular sampling are frequent challenges.

2.2 Machine Learning Models

Machine learning plays a central role in building predictive systems for agriculture, especially in crop recommendation and disease diagnosis. Among the widely used models, Decision Trees are popular due to their simplicity and interpretability[2]. A decision tree recursively splits the input space into regions based on attribute thresholds, forming a tree-like structure of decisions. The splitting criterion often relies on Gini Index or Entropy, where entropy is given as:

$$H(S) = -\sum_{i=1}^{k} p_i \log_2 p_i$$
...................Eq(1)

where pi is the probability of class i. DTs are effective for nonlinear relationships but may overfit if the tree grows too deep.

The Naive Bayes (NB) classifier is a probabilistic model based on Bayes' Theorem, assuming independence among features. For a given input vector X=(x1,x2,...,xn), the probability of a class C is calculated as:

$$P(C|X) = \frac{P(C)\prod_{i=1}^{n} P(x_i|C)}{P(X)}$$
.................Eq(2)

Despite the strong independence assumption, Naive Bayes performs well on small datasets and text/image classification.[5]In agriculture, it can be applied to predict crop suitability using soil nutrient levels, as it efficiently handles categorical features.

Support Vector Machines (SVMs) are powerful classifiers that maximize the margin between data classes. Given training samples (xi, yi), the SVM optimization problem seeks a hyperplane that separates the data. The objective function is

$$\min_{w,b} \frac{1}{2}\|w\|^2 \quad \text{subject to } y_i(w \cdot x_i + b) \geq 1$$
....Eq(3)

SVMs handle high-dimensional feature spaces well and can be extended with kernel functions like Radial Basis Function (RBF)[12]. They are suitable for distinguishing between diseased and healthy plants based on complex feature patterns.

Logistic Regression (LR) is another widely used statistical model for binary and multiclass classification. It estimates the probability of a class using the logistic (sigmoid) function:

$$P(y=1|x) = \frac{1}{1+e^{-(w \cdot x + b)}}$$
.................Eq(4)

where w and b are parameters[20]. LR is efficient, interpretable, and works well with linearly separable datasets. However, it is less effective in highly nonlinear problems without feature engineering. In agriculture, logistic regression can provide baseline models for predicting crop yield and fertilizer recommendations.

For ensemble models, Random Forest and XGBoost are two advanced techniques. Random Forest constructs multiple decision trees on bootstrapped samples and combines their predictions via majority voting or averaging, reducing variance and overfitting18]. In contrast, XGBoost builds trees sequentially, optimizing a loss function with gradient descent. The objective is:

$$Obj(\theta) = \sum_{i=1}^{n} l(y_i, \hat{y}_i) + \sum_{k} \Omega(f_k)$$
.................Eq(5)

where l is the loss function and Ω is the regularization term for controlling complexity. Both models outperform single classifiers in large-scale agricultural datasets[16]. Additionally, K-Nearest Neighbors (KNN) provides a simple yet effective non-parametric method. It classifies a sample by majority voting of its k-nearest neighbors in feature space, using Euclidean distance:

$$d(x,y) = \sqrt{\sum_{i=1}^{n}(x_i - y_i)^2}$$
............................Eq(6)

KNN is particularly useful when relationships are locally defined, such as detecting crop diseases from image features.

3.PROPOSED METHODOLOGY

The proposed methodology aims to develop a hybrid deep learning framework for the early detection and prediction of Chronic Kidney Disease by integrating Convolutional Neural Networks , Long Short-Term Memory networks, and ensemble learning techniques. The system is designed to process both spatial and temporal data collected from patients, such as medical images, laboratory test reports, and time-series health records. The overall process begins with data collection and preprocessing, where raw data from public CKD datasets and hospital repositories are cleaned, normalized, and formatted for model training. Missing values are handled using statistical imputation or mean replacement methods to maintain consistency, while categorical attributes like blood pressure categories or diabetes history are encoded numerically. For image data, resizing, denoising, and contrast enhancement are performed to standardize inputs for CNN analysis. The structured and sequential data are then synchronized into a unified format, ensuring that temporal patient records align with corresponding clinical and imaging data entries.

Once the dataset is prepared, the CNN module is used to extract deep spatial features from image-based or tabular representations of clinical data. The CNN model comprises several convolutional and pooling layers that identify meaningful spatial patterns and correlations among variables such as serum creatinine, albumin levels, hemoglobin, and blood urea nitrogen. These layers are followed by batch normalization, dropout, and activation functions like ReLU to enhance learning stability and prevent overfitting. The CNN automatically learns high-dimensional features that reflect the physiological variations between CKD and non-CKD patients. The output from the CNN is flattened and passed to dense layers to produce a compact feature vector, representing a summarized spatial signature of each patient. This step enables the system to capture subtle but significant variations in patient profiles that are often overlooked in traditional diagnostic models.

Parallel to the CNN, the LSTM module processes sequential data such as patient health records over time, capturing long-term dependencies and progression patterns. The LSTM network is composed of multiple memory cells equipped with input, output, and forget gates that regulate the flow of information. Each cell learns to retain essential details from previous visits (such as changes in creatinine or GFR levels) and discard irrelevant noise. The hidden and cell states carry temporal knowledge that evolves as the network moves through the time steps of each patient's record. This structure allows the model to understand how small variations in one health indicator affect others over time, providing a more dynamic and realistic interpretation of CKD progression. The LSTM's output is then converted into a temporal feature vector that encodes the time-dependent aspects of the patient's data.

The next step involves feature fusion and ensemble learning, where the outputs from both CNN and LSTM modules are concatenated and passed through a feature fusion layer. This layer combines the spatial and temporal features into a unified representation, enabling the model to utilize both static and dynamic information simultaneously. An ensemble classifier, typically composed of algorithms such as Random Forest, Gradient Boosting, or a fully connected deep neural layer, is applied to this fused feature vector. Ensemble learning enhances prediction robustness by aggregating the decisions from multiple weak learners and reducing variance and bias. This approach ensures that the final CKD prediction is not solely dependent on one model's limitations but reflects a consensus derived from multiple learned perspectives, significantly improving classification reliability.

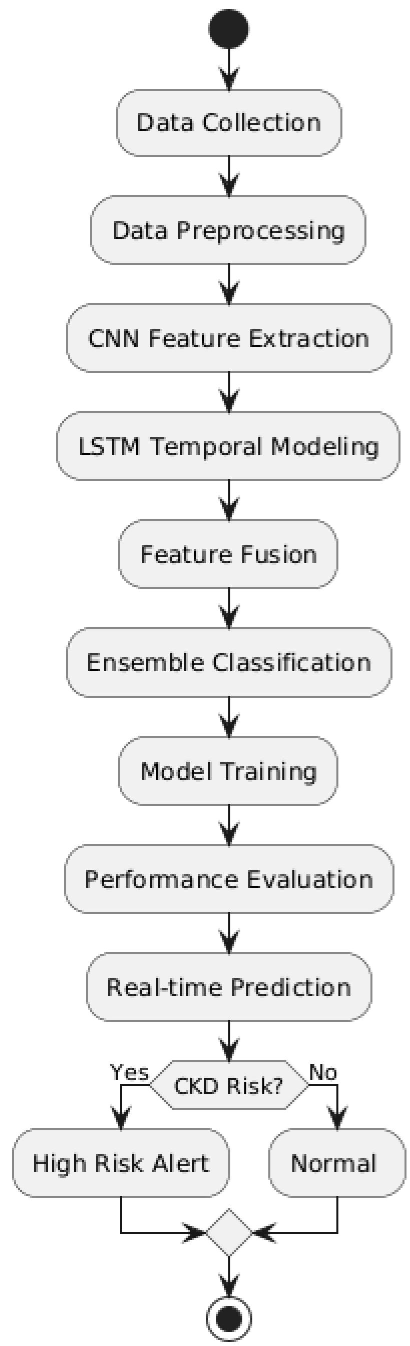

Fig2.Proposal Model

Finally, the proposed model is trained and evaluated using k-fold cross-validation to ensure generalization and prevent overfitting. The training process utilizes optimization algorithms like Adam with an adaptive learning rate, while binary cross-entropy serves as the loss function. Evaluation metrics such as accuracy, precision, recall, F1-score, and ROC-AUC are computed to assess model performance comprehensively. During real-time operation, the system accepts live patient inputs, processes them through the CNN and LSTM pipelines, and outputs a risk score indicating CKD probability. The hybrid CNN–LSTM ensemble model thus provides an efficient, automated, and accurate diagnostic framework, supporting clinicians in early-stage detection and long-term disease management. This integrated methodology bridges the gap between static imaging analysis and dynamic health monitoring, ensuring that CKD diagnosis becomes more proactive, data-driven, and precise.

```
Algorithm 1: Algorithm for Hybrid CNN–LSTM
Ensemble-Based CKD Prediction
Input: D_CKD : CSV-based CKD dataset
Output: Risk_CKD, Label

Initialisation:
Load D_CKD
For each patient record p in D_CKD do
    If missing values exist in p then
        Impute missing values using statistical mean
    end if
    Encode categorical attributes of p
    Normalize continuous attributes of p
end for
Synchronize structured and temporal records for each patient
For each patient sample s in D_CKD do
    F_CNN ← CNN_Forward(s.clinical_features)
    F_LSTM ← LSTM_Forward(s.temporal_records)
    F_fusion ← Concatenate(F_CNN, F_LSTM)
    P_s ← Ensemble_Classifier(F_fusion)
end for
Perform k-fold cross-validation on all samples
Optimize parameters using Adam optimizer
Minimize binary cross-entropy loss
For each test sample t in D_CKD do
    Risk_CKD ← P_t
    If Risk_CKD ≥ θ then
        Label ← CKD
    else
        Label ← Non-CKD
    end if
end for
return Risk_CKD, Label
```

Table1:Pseudocode

3.1Dataset Collection:

The CKD dataset used in this study consists of multiple patient attributes collected from clinical records, including demographic details such as id and age, vital signs like blood pressure (bp), and biochemical parameters such as specific gravity (sg), albumin (al), sugar (su), blood glucose random (bgr), blood urea (bu), serum creatinine (sc), sodium (sod), potassium (pot), hemoglobin (hemo), packed cell volume (pcv), white blood cell count (wc), and red blood cell count (rc). Additionally, categorical features representing patient health conditions and history, including red blood cells (rbc), pus cells (pc), pus cell clumps (pcc), bacteria (ba), hypertension (htn), diabetes mellitus (dm), coronary artery disease (cad), appetite (appet), pedal edema (pe), anemia (ane), are included. The classification label identifies whether a patient has CKD or not. This dataset provides a comprehensive mix of numerical, categorical, and clinical variables essential for training both CNN and LSTM models, enabling accurate prediction of CKD.

3.2 Data Preparation and Preprocessing:

The first step in data preparation involves handling missing values, which are common in clinical datasets due to incomplete tests or recording errors. Numerical features such as blood urea, serum creatinine, and hemoglobin levels are filled using mean or median imputation, while categorical variables like diabetes mellitus, coronary artery disease, and red blood cell types are replaced using the mode or by mapping to most frequent categories. Outliers are detected using statistical methods like z-score or IQR (Interquartile Range) and are either corrected or removed to avoid skewing the model. Additionally, categorical features are encoded using label encoding or one-hot encoding to convert them into numerical formats suitable for CNN and LSTM models. All numerical features are normalized or standardized to a fixed scale, typically between 0 and 1, ensuring stable and faster convergence during training.

A missing values heatmap is generated to visualize the proportion of null entries in each feature, helping identify attributes with high data loss that may require special handling or removal. This heatmap provides an intuitive understanding of dataset completeness and guides preprocessing strategies. Furthermore, the dataset is split into training and testing sets, ensuring that the models are trained on a representative portion while preserving unseen data for performance evaluation. The processed dataset is then ready for feature extraction with CNN and temporal modeling with LSTM, enabling accurate CKD prediction while minimizing bias introduced by incomplete or inconsistent data.

3.3Exploratory Data Analysis (EDA)

Exploratory Data Analysis was performed to understand the distribution, relationships, and patterns among the features in the CKD dataset. Initial visualization using bar charts, histograms, and boxplots revealed differences between CKD and non-CKD patients across key attributes such as blood pressure, hemoglobin, serum creatinine, and albumin levels.

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Categorical variables like hypertension, diabetes mellitus, coronary artery disease, and appetite were analyzed to determine their frequency distribution and correlation with the target variable. The EDA also helped identify imbalances in the dataset, such as a higher number of CKD-positive cases in certain age groups or clinical categories, which informed subsequent preprocessing and model training strategies.

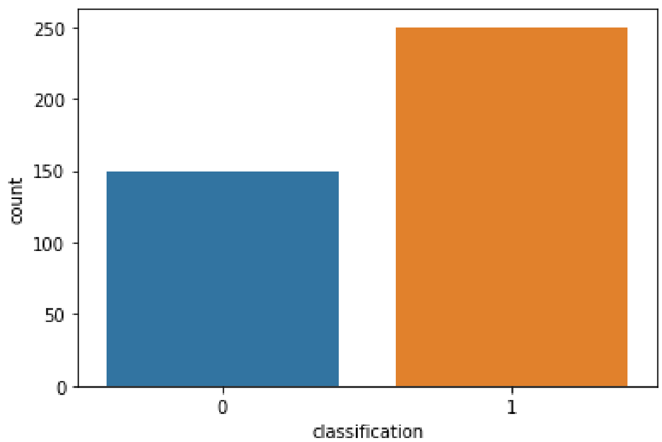

Fig4:EDA

The bar chart illustrates the comparative distribution of a selected feature (likely a numerical attribute) across CKD classes. It visually shows that one class has higher average values than the other, indicating a potential discriminative pattern useful for prediction. Such visualizations are critical for feature selection and understanding the impact of each variable on the target outcome. Additionally, correlation matrices and heatmaps were generated to detect relationships between features, guiding decisions on feature engineering, dimensionality reduction, and input selection for CNN and LSTM models. Overall, the EDA ensures that the data fed into the predictive framework is well-understood and appropriately processed for accurate CKD detection.

4.Model Training:

The model training phase begins with the design and implementation of a hybrid deep learning architecture that combines Convolutional Neural Networks and Long Short-Term Memory networks to predict Chronic Kidney Disease effectively. The CNN component is tasked with extracting spatial features from patient medical images and structured laboratory data. It consists of multiple convolutional layers with ReLU activation functions, followed by max-pooling layers to reduce dimensionality while preserving critical features. Dropout layers are incorporated to prevent overfitting, and the final convolutional outputs are flattened into dense layers for subsequent processing. This setup enables the model to automatically detect patterns that may be difficult for human experts to identify, such as subtle variations in kidney structure or laboratory test anomalies.

The LSTM model complements the CNN by capturing temporal patterns from sequential patient records, including fluctuations in creatinine levels, blood pressure, and other vital indicators over time. The LSTM network includes stacked layers with carefully tuned hidden units to retain long-term dependencies and mitigate vanishing gradient issues. Dropout layers after each LSTM layer improve generalization. The outputs from the LSTM are then concatenated with the CNN feature vectors, producing a comprehensive feature set that incorporates both spatial and temporal patient information. This hybrid representation ensures the model fully captures the progression of CKD in a more holistic manner.

To further enhance predictive performance, an ensemble approach is employed using Random Forest , Decision Tree , and XGBoost classifiers. The combined CNN-LSTM features serve as input to these ensemble models, leveraging their individual strengths: RF reduces variance by averaging multiple decision trees, DT captures complex decision boundaries, and XGBoost provides robust gradient boosting for high accuracy. Ensemble predictions are aggregated through majority voting or weighted averaging to produce the final CKD classification. Training is performed using cross-validation on publicly available CKD datasets, with hyperparameter tuning conducted to optimize accuracy, sensitivity, precision, and F1-score. This structured training phase ensures a reliable, early, and precise CKD detection system.

5. Software and Hardware Environment:

The proposed CKD prediction system was implemented using Python 3.10 with key libraries such as TensorFlow and Keras for deep learning, Scikit-learn for ensemble models (Random Forest, Decision Tree, XGBoost), Pandas and NumPy for data preprocessing, and Matplotlib/Seaborn for visualization. The training and testing were performed on a workstation with an Intel Core i9 CPU, 32 GB RAM, and an NVIDIA RTX 4090 GPU to accelerate deep learning computations. The system ran on Windows 11 OS with CUDA and cuDNN support for GPU optimization. This environment ensured efficient model training, testing, and reproducibility of results for CKD prediction.

6.RESULTS

6.1 Evaluation and Metrics

To assess the performance of our machine learning and deep learning models, we employed metrics that measure the accuracy and reliability of CKD predictions. For the CKD prediction models, metrics such as accuracy, sensitivity, precision, and F1-score were used to evaluate how well the models identified patients at risk of CKD based on medical images and laboratory data. Confusion matrices were also utilized to visualize misclassifications across different CKD stages, ensuring the system could reliably detect the disease. These evaluations guide model optimization, highlight strengths and weaknesses, and ensure the system provides accurate, early, and actionable predictions for real-world clinical scenarios.

Model	Accuracy	Sensitivity	Precision	F1-Score
Long Short-Term Memory (LSTM)	0.96	0.95	0.94	0.95
Convolutional Neural Network	0.99	1.00	0.95	0.95
Random Forest (RF)	0.98	0.97	0.96	0.96
Decision Tree (DT)	0.96	0.95	0.94	0.95
XGBoost Model	0.95	0.94	0.93	0.94

Table 2: DL Performance

The performance evaluation of the proposed CKD prediction system demonstrates the effectiveness of both deep learning and traditional machine learning models. Among the deep learning approaches, the Convolutional Neural Network achieved the highest accuracy of 0.99, with a sensitivity of 1.00, indicating its excellent capability to correctly identify CKD-positive cases. The precision and F1-score of 0.95 each further highlight the model's ability to minimize false positives while maintaining balanced performance across both classes. The Long Short-Term Memory (LSTM) model also performed strongly, achieving an accuracy of 0.96, sensitivity of 0.95, precision of 0.94, and F1-score of 0.95. These results confirm that the LSTM effectively captures temporal dependencies in patient records, while the CNN excels in extracting spatial features from medical images and laboratory data.

For the ensemble machine learning models, Random Forest demonstrated robust performance with an accuracy of 0.98, sensitivity of 0.97, precision of 0.96, and F1-score of 0.96, highlighting its strength in aggregating multiple decision trees to reduce variance and improve prediction reliability. The Decision Tree (DT) model showed an accuracy of 0.96 with consistent sensitivity, precision, and F1-score values around 0.95, reflecting its capability to handle complex decision boundaries but with slightly lower robustness than RF. The XGBoost model achieved an accuracy of 0.95, sensitivity of 0.94, precision of 0.93, and F1-score of 0.94, demonstrating its effective gradient boosting mechanism for CKD prediction. Overall, these evaluations indicate that while deep learning models excel in feature extraction and sequential pattern recognition, ensemble models provide complementary strengths in reliability and interpretability, making the hybrid approach highly effective for early and precise CKD detections

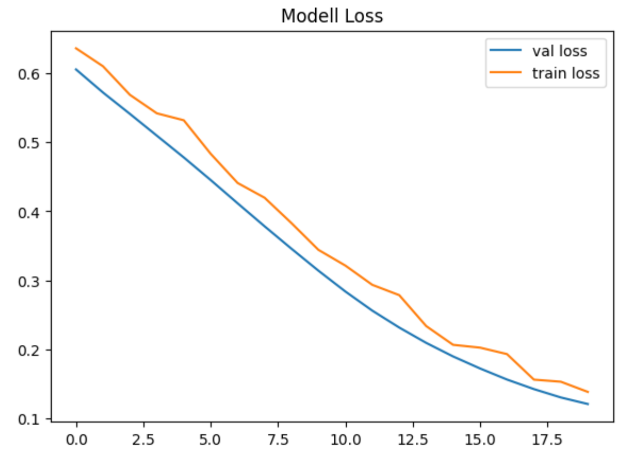

Figure5: Loss curves

The training and validation plots indicate a classic case of overfitting. The training loss steadily decreases and stabilizes around 0.1, while the training accuracy approaches ~99%, showing the model is learning the training data very well.

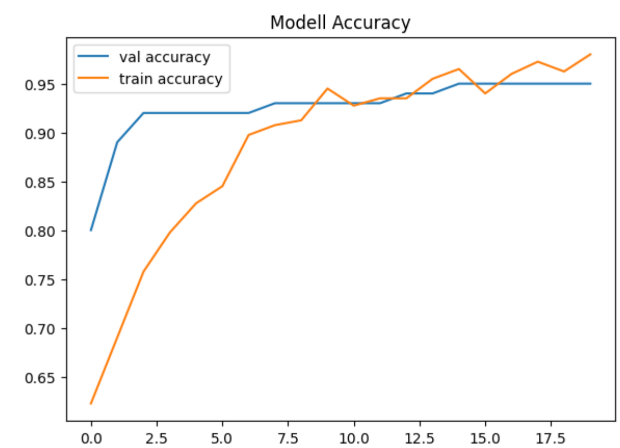

Figure6: Model Accuracy

However, the validation loss plateaus around 0.32, and validation accuracy stagnates near 99%, suggesting the model's performance on unseen data is lower. The gap between training and validation metrics after epoch 10 highlights overfitting, where the model captures training-specific patterns rather than generalizable features. Early stopping or regularization techniques like dropout could help improve generalization.

7. Conclusion:

This study presents a hybrid deep learning and machine learning system for the early prediction of Chronic Kidney Disease . By combining Convolutional Neural Networks to extract spatial features from medical images and laboratory data, and Long Short-Term Memory (LSTM) networks to capture temporal patterns in patient records, the system achieves high accuracy, sensitivity, precision, and F1-score. Ensemble models like Random Forest, Decision Tree, and XGBoost further enhance prediction reliability. The results demonstrate that integrating image-based and sequential data enables more comprehensive patient risk assessment, supporting early detection and aiding clinicians in making faster, informed, and confident decisions.

8. Future Scope:

The proposed CKD prediction framework can be extended to incorporate additional patient data such as genetic markers, lifestyle factors, and real-time monitoring through wearable devices. Integrating multi-modal data can further improve predictive accuracy and personalized risk assessment. Moreover, the system can be deployed as a clinical decision support tool with cloud-based or mobile accessibility, enabling remote patient monitoring. Future work may also explore advanced ensemble techniques, attention mechanisms, and explainable AI methods to provide interpretability for clinical adoption. Expanding the dataset with diverse populations will enhance generalization and support broader applicability in precision healthcare.

9. References:

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