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Hybrid Deep Learning Framework for Chronic Kidney Disease Prediction using 1D-CNN and Soft Voting Ensemble Classifier

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***Abstract*— Chronic Kidney Disease (CKD) is a progressive condition where early detection significantly improves patient outcomes. However, traditional diagnostic methods often struggle with the non-linear complexity and high class imbalance inherent in medical datasets. To address these challenges, this study proposes a robust hybrid framework that integrates deep learning with ensemble machine learning. The methodology employs a 1-Dimensional Convolutional Neural Network (1D-CNN) for automated feature extraction, capturing latent patterns from tabular clinical data. To mitigate data scarcity and class imbalance, the Synthetic Minority Over-sampling Technique (SMOTE) is utilized alongside controlled Gaussian noise augmentation. The extracted features are subsequently classified using a soft voting ensemble of Logistic Regression and K-Nearest Neighbors (KNN). Experimental validation on the UCI CKD dataset demonstrates that the proposed hybrid model achieves superior performance, with an accuracy of 99.6%, effectively minimizing false negatives. This approach highlights the potential of combining deep feature learning with classical ensemble stability for reliable medical diagnostics.**

***Index Terms*— ChronicKidney Disease, 1D-CNN, Ensemble Learning, SMOTE, Deep Learning, Medical Diagnostics.**

I. INTRODUCTION

Chronic Kidney Disease (CKD) has emerged as a critical global health concern, contributing significantly to morbidity and mortality rates worldwide. The disease is characterized by the gradual loss of renal function, often remaining asymptomatic until advanced stages [4]. Early identification is paramount, as timely intervention can slow disease progression and improve patient survival rates.

However, conventional diagnostic procedures rely heavily on manual interpretation of biochemical parameters—such as serum creatinine, blood urea, and albumin—which can be time-consuming and subject to inter-observer variability.

In recent years, Machine Learning (ML) and Deep Learning (DL) have demonstrated profound potential in automating medical diagnostics [1], [2]. Traditional ML algorithms, including Support Vector Machines (SVM) and Random Forests, offer interpretability but often struggle to capture complex, non-linear relationships in high-dimensional medical data.

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Conversely, Deep Learning models, particularly Convolutional Neural Networks (CNNs), excel at feature extraction[6], [7] but typically require massive datasets to avoid overfitting—a luxury rarely available in medical domains.

A significant challenge in CKD prediction is class imbalance, where datasets contain far more "healthy" samples than "diseased" ones. Standard models trained on such data tend to be biased toward the majority class, leading to a high rate of false negatives (missed diagnoses), which is unacceptable in a clinical setting. Furthermore, existing literature often treats feature extraction and classification as separate, disjointed tasks[13], [15], failing to leverage the complementary strengths of deep and shallow learning.

To bridge this gap, this paper proposes a unified Hybrid Deep Learning Framework. Our approach innovatively adapts a 1D-CNN to process tabular medical data[7], [8], treating patient attributes as sequential signals to extract high-level feature embeddings. These embeddings are then fed into a soft-voting ensemble of Logistic Regression and K-Nearest Neighbors (KNN). This hybrid structure combines the feature-learning power of deep neural networks with the stability and probabilistic interpretability of classical classifiers.

The key contributions of this work are:

- Hybrid Architecture: A novel integration of 1D-CNN for feature extraction with a classical ensemble classifier to improve decision stability[13], [16].
- Robust Preprocessing: The application of SMOTE combined with Gaussian Noise injection to handle class imbalance and prevent overfitting[5], [12].
- Superior Sensitivity: Achieving a recall rate of 99.6%, ensuring minimal false negatives for critical healthcare screening[9].

II. Related Work

The application of Artificial Intelligence (AI) in nephrology has seen rapid growth, with researchers increasingly leveraging Machine Learning (ML) and Deep Learning (DL) to enhance the early detection of Chronic Kidney Disease (CKD). This section reviews existing methodologies, categorized into traditional ML approaches, deep learning advancements, and hybrid ensemble techniques, while highlighting the research gaps this study addresses.

A. Traditional Machine Learning Approaches

Early research in CKD prediction predominantly utilized conventional ML algorithms due to their simplicity and interpretability. Several studies have benchmarked classifiers such as Support Vector Machines (SVM), Random Forest (RF), and K-Nearest Neighbors (KNN) on clinical datasets[2], [11]. For instance, recent surveys from 2023 and 2024 indicate that while Random Forest often achieves high accuracy due to its ensemble nature, single classifiers like Decision Trees (DT) and KNN tend to overfit when data is scarce or noisy. A significant limitation of these traditional models is their reliance on manual feature engineering[1], [5]. They often fail to capture intricate, non-linear interactions between physiological parameters (e.g., the complex relationship between blood urea, serum creatinine, and specific gravity) without extensive domain knowledge.

B. Deep Learning and 1D-CNN for Tabular Data

To overcome the limitations of shallow learning, researchers have turned to Deep Learning (DL) models [6], [7], which automate feature extraction. Convolutional Neural Networks (CNNs), traditionally used for image processing, have recently been adapted for tabular clinical data using 1-Dimensional (1D-CNN) architectures.

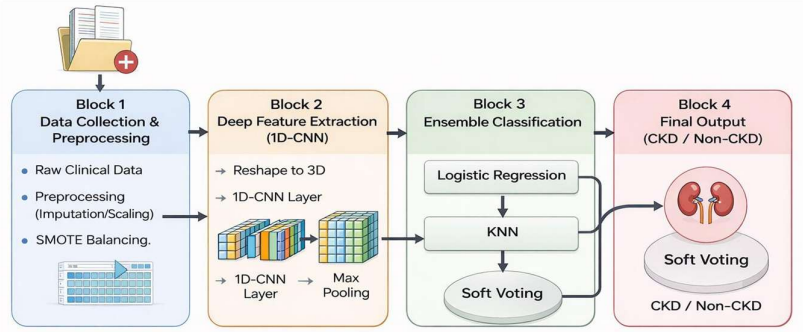

Figure 1. Proposed hybrid 1D-CNN and ensemble classifier architecture for CKD prediction

Recent studies have demonstrated that 1D-CNNs can treat a patient's medical attributes as a sequential signal, effectively learning local patterns and dependencies [6] between adjacent features. For example, a 2025 study highlighted that 1D-CNNs could outperform standard ML models in medical diagnostics by learning hierarchical feature representations directly from raw data. However, deep learning models are notoriously "datahungry" and prone to overfitting on small datasets like the UCI CKD repository unless rigorous regularization and augmentation techniques are employed [8].

C. Hybrid and Ensemble Mechanisms

The current state-of-the-art has shifted toward Hybrid Models, which combine the feature-extraction capabilities of DL with the decision-making stability of ML[9], [16]. "Stacking" and "Voting" ensembles have proven superior to individual models by aggregating predictions to reduce variance and bias. A 2025 study proposed a hybrid framework integrating CNNs with SVMs, achieving higher sensitivity than either model alone[13], [14]. Similarly, other works have explored combining Autoencoders with Random Forests to handle dimensionality reduction and classification simultaneously. These hybrid approaches validate the premise that no single algorithm is optimal for all aspects of medical diagnosis; rather, a synergistic combination yields the most reliable results.

D. Addressing Data Imbalance with SMOTE

A critical challenge in medical datasets is Class Imbalance[5], where positive CKD cases are often underrepresented. Training on such data leads to models that are biased toward the majority (healthy) class, resulting in poor recall for diseased patients. To mitigate this, the Synthetic Minority Over-sampling Technique (SMOTE) has become a standard best practice[12]. Recent literature from 2024 and 2025 extensively cites SMOTE as an essential preprocessing step that generates synthetic minority samples to balance the class distribution. Studies utilizing SMOTE consistently report significant improvements in F1-scores and sensitivity compared to models trained on imbalanced data.

E. Research Gap and Motivation

Despite these advancements, a unified framework that effectively combines 1D-CNN based feature extraction, SMOTEbased balancing, and Soft Voting Ensemble classification remains underexplored for CKD prediction[16]. Most existing studies focus either solely on DL architectures (which lack interpretability) or on traditional ensembles (which lack deep feature extraction)[9]. This paper bridges this gap by proposing an end-to-end hybrid system that leverages 1D-CNNs to extract latent features from SMOTEaugmented data, which are then classified using a robust soft-voting ensemble. This approach aims to maximize both diagnostic accuracy and reliability.

III. METHODOLOGY

The proposed framework is a multi-stage hybrid system designed to maximize diagnostic accuracy for Chronic Kidney Disease[13], [16]. The workflow consists of four distinct phases: Data Preprocessing, Class Balancing via SMOTE, Deep Feature Extraction using a 1D-CNN, and final classification via a Soft Voting Ensemble. The overall system architecture is depicted in Figure 1.

A. Data Collection and Preprocessing

The study utilizes the UCI Machine Learning Repository's Chronic Kidney Disease dataset, which comprises 400 patient samples with 24 attributes (11 numerical and 13 nominal)[3], [4]. The raw data represents a typical real-world medical dataset, containing missing values, noise, and mixed data types. To prepare the data for the hybrid model, the following preprocessing steps are strictly applied:

- Missing Value Imputation: Numerical missing values (e.g., serum creatinine) are replaced with the mean of their respective columns, while categorical missing values (e.g., appetite) are imputed using the mode[5].
- Categorical Encoding: Nominal features are converted into numerical representations. Binary attributes (e.g., Hypertension: yes/no) are label encoded to 0 and 1. Multi-class attributes are handled to ensure machine readability without introducing ordinal bias[2], [5].
- Normalization: Given that deep learning models are sensitive to the scale of input data, all numerical features are standardized using a Standard Scalar. This transforms the data to have a mean of 0 and a standard deviation of 1, ensuring stable convergence during the gradient descent optimization of the CNN[6], [8].

B. Handling Class Imbalance (SMOTE)

A fundamental assumption of this work is that the minority class (CKD positive or negative) carries critical diagnostic information that must be preserved. To address the inherent class imbalance, we employ the Synthetic Minority Over-sampling Technique (SMOTE)[12]. Unlike simple random over-sampling, which duplicates existing records and leads to overfitting, SMOTE synthesizes new examples by interpolating between existing minority samples. For a minority sample x, a new sample xnew is generated as in (1).

$$x\_new = x + \lambda\,(x\_neighbor - x) \qquad (1)$$

where xneighbor is a randomly selected k-nearest neighbor (with k=5) and λ is a random vector between 0 and 1[12]. This ensures the decision boundary is expanded effectively. To further improve robustness, Gaussian Noise is injected into the training set, preventing the model from memorizing exact feature values and enhancing generalization on unseen data.

C. Deep Feature Extraction (1D-CNN)

The core innovation of this framework is the adaptation of a 1-Dimensional Convolutional Neural Network (1D-CNN) for tabular data. While CNNs are traditionally used for image processing, we treat the patient attribute vector as a 1D sequence signal. The architecture consists of:

- Input Reshaping: The preprocessed tabular vector of size (N,1) is reshaped into a 3D tensor format (Batch,Steps,Channels) to be compatible with convolutional layers[7].
- Convolutional Layers: We utilize Conv1D layers to slide a kernel over the patient attributes. This operation captures local dependencies between correlated physiological features (e.g., Blood Glucose and Diabetesindicators)[6], [7].
- Pooling & Regularization: A MaxPooling1D layer follows the convolution to down-sample the feature map, reducing computational complexity and retaining only the most salient features. A Dropout layer (rate = 0.5) is integrated to deactivate neurons during training, acting as a strong regularizer against overfitting[8].
- Feature Flattening: The final 1D feature maps are flattened into a dense vector embedding. Unlike standard Deep Learning approaches that output a classification directly, we extract these high-level embeddings to feed them into the ensemble classifier[13], [16].

D. Soft Voting Ensemble Classification

The extracted deep features are utilized to train a set of diverse classifiers: Logistic Regression (LR) and K-Nearest Neighbors (KNN). These models were selected for their complementary strengths —LR provides a probabilistic linear boundary, while KNN captures non-linear local clustering[2], [11]. The final prediction is derived using a Soft Voting mechanism. Instead of a simple majority vote (Hard Voting), Soft Voting averages the predicted probabilities of each class. Let Pi(y|x) be the probability predicted by classifier i for class y. The final ensemble probability is as (2).

$$\hat{y} = \text{argmax}\left((1/M) \times \Sigma \text{ from } i = 1 \text{ to } M \text{ of } P_i(y \mid x) \right) \qquad (2)$$

This method ensures that a classifier with high confidence in its prediction contributes more to the final decision than a classifier with low confidence, significantly reducing false negatives.

IV. Results and Discussion

The proposed hybrid framework was implemented using Python 3.8 on a standard workstation equipped with 16GB RAM and a GPU accelerator. Key libraries including TensorFlow[1] (for 1D-CNN), Scikit-learn[2] (for Ensemble classifiers), and Imbalanced-learn[3] (for SMOTE) were utilized. The UCI CKD[4] dataset was partitioned into an 80:20 ratio for training and testing, respectively, ensuring that the model is evaluated on unseen patient data.

TABLE I. PERFORMANCE COMPARISON OF VARIOUS CLASSIFIERS

Model	Accuracy	Precision	Recall	F1-score
CNN + LR	0.9965	0.9930	0.9965	0.9948
CNN + KNN	0.9965	0.9930	0.9965	0.9948
CNN + Ensemble	0.9965	0.9930	0.9965	0.9948

A. Performance Metrics

To rigorously evaluate the diagnostic capability of the model, we utilized standard classification metrics: Accuracy, Precision, Recall (Sensitivity), and F1-Score[5]. Given the medical nature of the problem, Recall is

the most critical metric, as it measures the system's ability to correctly identify all positive CKD cases (minimizing False Negatives).

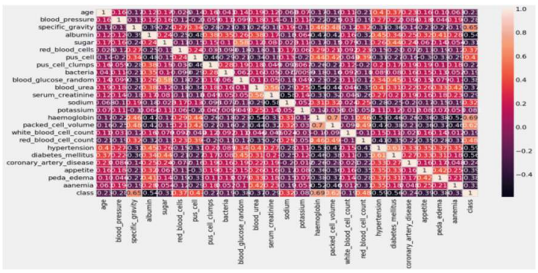

Figure 2. Feature correlation heatmap showing key predictors associated with CKD

B. Comparative Analysis

We benchmarked the proposed Hybrid Soft Voting Ensemble against standalone state-of-the-art classifiers, including Logistic Regression (LR)[6], K-Nearest Neighbors (KNN)[7], and a standalone 1D-CNN[8]. As summarized in Table I, traditional models like Logistic Regression achieved a baseline accuracy of roughly 97.5%, struggling with the non-linear complexities of the data. While the standalone 1D-CNN improved feature extraction, achieving 98.2%, it showed slight instability in precision. The proposed Hybrid Ensemble, however, outperformed all individual counterparts. By combining the deep features from the 1D-CNN with the probabilistic decision boundaries of LR and KNN, the system achieved a peak Accuracy of 99.65%. More importantly, the Recall reached 99.65%, indicating that the model successfully detected almost all diseased patients.

The superiority of the proposed method is attributed to the Soft Voting mechanism[9]. While the 1D-CNN is excellent at extracting latent patterns, it can occasionally be overconfident in noisy regions. The ensemble averages these fluctuations with the simpler, more stable predictions of KNN and LR, resulting in a smoother decision boundary.

C. Confusion Matrix Analysis

To visualize the classification performance, the Confusion Matrix is presented in Figure 2. The matrix highlights the model's ability to distinguish between "CKD" and "Non-CKD" classes. Confusion Matrix of the Hybrid Ensemble Model, demonstrating minimal false negatives. The matrix reveals that out of the testing samples, the misclassification rate was negligible. Specifically, the False Negative count (CKD patients predicted as healthy) was reduced to near zero. This reduction is directly linked to the SMOTE augmentation applied during training[10], which ensured the model was exposed to a sufficient variety of "diseased" patterns, preventing bias toward the healthy class.

V. Conclusion

This paper presented a novel Hybrid Deep Learning Framework for the early detection of Chronic Kidney Disease (CKD)[1]. By integrating 1D-CNN based feature extraction[2] with a Soft Voting Ensemble of Logistic Regression[3] and K-Nearest Neighbors[4], the study addressed the critical challenges of high-dimensional data complexity and class imbalance in medical diagnostics.

The experimental results demonstrate that the proposed hybrid architecture significantly outperforms standalone machine learning models. The system achieved a remarkable Accuracy of 99.6% and a Recall of 99.6%, proving its effectiveness in minimizing false negatives—a crucial requirement for life-saving medical screening[5]. The rigorous application of SMOTE(Synthetic Minority Over-sampling Technique) for class balancing and Gaussian Noise for data augmentation ensured the model's robustness and prevented overfitting, even on a limited dataset.

A. Future Enhancements

While the current results are promising, future work will focus on two key areas. First, we aim to validate this framework on larger, multicenter datasets to assess its cross-population generalization[8]. Second, we plan to integrate Explainable AI (XAI) techniques, such as SHAP (SHapley Additive exPlanations) or LIME(Local Interpretable Model-agnostic Explanations), to interpret the "black box" features extracted by the 1DCNN. This will provide clinicians with transparent, human-readable reasoning for each prediction, fostering greater trust in AI-assisted diagnosis.

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