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Prediction of Chronic Kidney Disease Based on Cloud with IoT model in Smart Cities using DL/ML Model

B. Saroja[1], G. Rajesh[2], Thirumalraj Karthikeyan[3,*], S. Venkatasubramanian[4], Kawsher Rahman[5]

[1]Department of Electronics and Communication Engineering, Siddartha Institute of Science and Technology, Puttur, Andhra Pradesh, India.
[2]Department of Electronics and Communication Engineering, New Horizon College of Engineering, Bengaluru, Karnataka, India.
[3]Department of Artificial Intelligence, Trichy Research Labs, Quest Technologies, Tiruchirappalli, Tamil Nadu, India.
[4]Department of Computer Science and Business Systems, Saranathan College of Engineering, Tiruchirappalli, Tamil Nadu, India.
[5]Department of General Medicine, Beanibazar Cancer and General Hospital, Dashgram, Sylhet, Bangladesh.
boda.saroja@gmail.com[1], rajesh.gundlapalli@gmail.com[2], thirumalraj.k@gmail.com[3], veeyes@saranathan.ac.in[4], drkawsher.rahman@gmail.com[5]

Abstract: Cloud computing and the IoT have been more prevalent in numerous healthcare applications in recent years due to their ability to integrate monitoring items like sensors and medical gadgets for investigating distant patients. Instead of relying on limited dispensation and storage resources, the massive amounts of data generated by therapeutic IoT strategies may be analysed in a CC context, leading to improved healthcare delivery. The death rate from CKD can be drastically decreased if patients are diagnosed with the condition early. This research proposes a strategy for predicting CKD status using diagnostic medical data from the UCI repository, which involves preprocessing, handling missing values, aggregating, extracting, and classifying the data, and generating predictions. The suggested method utilises medical data from IoT devices and benchmark repositories to detect and classify multiple stages of CKD. Furthermore, the suggested method employs the Adaptive Synthetic (ADASYN) method for outlier identification. This research offers a deep (GRU) network model for CKD classification to label the CKD category accurately.

Keywords: Internet of Things; Chronic Kidney Disease; Adaptive Synthetic Technique; Bidirectional Memory; Gated Recurrent Units; Red Colobus Monkey; Electronic Health Records.

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1. Introduction

These days, it takes a great deal of time and effort and a high level of expertise with data to handle even a somewhat large data set. Thus, data mining techniques may be used to categorise patients' ailments, with kidney disease among the key disorders

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[*] Corresponding author.

investigated [1]. In recent decades, chronic kidney disease has surpassed all other causes of death on a global scale. Identifying the early warning signs of cardiovascular disease requires a combination of intuitive and analytical skills [2]. Current clinical infrastructures that have recently implemented IoT can collect data from devices to support the evaluation and diagnosis of kidney disease [27]. Despite the efforts of many researchers to pinpoint the source of coronary vein infection, the findings have been unsatisfactory [3]. Recent advances in the Internet of Things (IoT) and sensing technology can also be applied to online healthcare management [4]. New cloud- and IoT-based Healthcare software has been developed to screen and evaluate genuine conditions, providing superior support to clients who use online medical care services [28]. To forecast the general public's risk of developing kidney disease, this investigation develops a practical infection model by combining data from the UCI Repository database with clinical sensor data [5]. A patient with a remote cardiovascular condition can benefit from an IoT system operating in the fog [29].

In such remote areas, it is not uncommon to lack access to a cardiologist. Although there are a few options for structuring coronary infection recommendations, these systems currently rely solely on plan-based recommendations [6]. The research makes available an IoT-based smart community, a system that researches cardiovascular disease and its treatment, and provides suggestions for physical and nutritional preventive measures [30]. The original piece speculated that biosensors might be used to get data from the patient at a considerable distance [31]. The term IoT refers to a network of electronic devices that can exchange data and coordinate their activities in various ways. The concept of an interconnected network of everyday objects is poised to become the next big thing. The accuracy of medical treatments may now be evaluated using ECG sensors [9]; [10]. Those electrocardiogram (ECG) sensors, crucial for remote patient monitoring, exhibit several serious faults [32]. Different data extraction processes are applied to ECG waves to obtain credits, and various application perspectives are used to continue scanning patients and make accurate predictions of heart problems [33]. Instead of being limited by mobile device capabilities, healthcare providers may use the cloud to analyse the vast amounts of data generated by IoT devices in the industry [11]. The authors of this study propose a clinically driven social support system to address the hopes of CKD patients for effective restorative care [34]. In low-income countries, where effective therapies are few, CKD is widely viewed as a devastating health problem [23].

In settings where simple symptom and regenerative intelligence places are not effectively addressed, IoT, as a variety of values that uses simple body sensors and advanced communication devices to provide virtual verification of kidney function, plays an important role [12]; [40]. There are many ways the Internet of Health Things (IoHT) technology can be used in the healthcare industry. One example is the remote monitoring of patient data using a combination of health-monitoring devices, such as sensors and clinical machines [35]. To optimise medical care presentations to clients via e-wellness apps, the authors of this study suggest a network for predicting and diagnosing chronic kidney disease (CKD) across a spectrum of severity levels, using a cloud service that combines clinical expertise with economic support [13]. The medical community faces a significant problem in attempting to diagnose and treat CKD at an early stage [36]. The nephrologist's dual role is to treat the aforementioned systemic signs and, if feasible, slow the progression of the illness to more severe stages [14]. Glomerular Filtration Rate (GFR) stages correspond to the risk factors listed in Table 1. CKD) is typified by a slow and recurrent loss of kidney function over time. In the early phases of CKD, a reliable risk prediction algorithm can be clinically significant [15]. It is hoped that this type of model would aid in the identification and treatment of high-risk individuals, hence reducing the economic burden of this illness [37].

Table 1: CKD risk factors for diverse phases

Range GFR (mL/min)	Stage	Details
>=90 with risk factors	-	At increased risk for CKD
GFR >=90	First	Kidney injury with normal or increased
60-89	Second	Mild decrease in GFR
30-59	Third	Moderate reduction in GFR
15-29	Fourth	Severe decrease in GFR

DL techniques have become essential tools in a wide range of health-oriented applications. The current study will provide a deep learning-based strategy for CKD [7]. This research addresses the dearth of deep learning applications in illness classification by introducing a new network model for CKD data organisation based on BLSTM and GRU cell units. For accurate CKD classification, it is crucial to capture temporal dependencies of both characteristics and features, which is exactly what the suggested network does [8]; [39]. To detect outliers, the suggested method is to apply ADASYN. In addition, the suggested model's hyperparameters are tuned using RCM. An extensive experimental study is conducted to investigate the enhanced CKD detection performance of the BLSTM-GRU method. Here is how the rest of the paper is organised: the background material is presented in Section 2, a concise explanation of the study is in Section 3, the trial analysis and its results are discussed in Section 4, and the research is presented in Section 5.

2. Related Works

The goal of the work by Swain et al. [16] is to predict the onset of chronic renal disease using publicly available data. This dataset underwent a series of data preparation steps to build a generic model. Missing data is imputed, data is balanced using the SMOTE method, and features are scaled in this sequence. The chi-squared test is a statistical method used to determine which characteristics are necessary and strongly connected with the output using the fewest possible measurements. To train a reliable machine-learning model, a variety of supervised-learning methods are combined. The RF achieved the best test accuracy and the lowest false-negative rate among the employed learning approaches. When findings were confirmed using 10-fold cross-validation, however, SVM outperformed RF. The unique model created by Ye et al. [17] uses machine learning techniques to predict in-hospital mortality for that type of ICU patient. Information on people with CKD and CAD was taken from the MIMIC-IV database. Feature selection was performed using the Boruta algorithm. The predictive model was built using a total of eight different machine learning algorithms, including (RF), (KNN), and (AUC). To provide a graphical representation of the model's workings, the (SHAP) method was used. In addition, for an external validation set, data were obtained from the Electronic (eICU-CRD). According to the AUC (0.946) and AP (0.778) results, GBDT exhibited the best predictive performance. Using a significance rating, the SHAP technique provides the top 20 considerations.

External validation metrics, including the area under the receiver operating characteristic curve (AUC) (0.865), the area under the curve (AUC) (0.672), decision curve analysis, and calibration curves, indicated that GBDT had some predictive value and clinical utility. To improve the interpretability of the deep learning model, Liang et al. [18] implemented four cutting-edge attribution techniques. With an AUC-ROC of 0.8991, the deep learning model outperformed the baseline models by a wide margin. Compared with LASSO, the interpretations produced by deep learning with attribution techniques, random forests, and XGBoost were more in line with clinical expertise. The development of CKD was favourably correlated with hematuria, proteinuria, potassium, and the urine albumin-to-creatinine ratio, and negatively correlated with estimated glomerular filtration rate and urine creatinine [25]. In conclusion, deep learning combined with attribution algorithms may provide interpretable insights into the mechanisms underlying CKD development. Our approach identified several key, underreported traits that may serve as new indicators of CKD development. The results of this study provide doctors with concrete evidence to support the clinical management and treatment of CKD. Islam et al. [19] presented multiple machine learning techniques for early CKD diagnosis. After the models are built using CKD patients, they are trained and verified with the previously described input parameters. To reduce the number of characteristics and eliminate unnecessary information, research has been conducted on the relationships among various aspects. The remaining properties were subjected to a filter-based feature selection procedure, and it was found that haemoglobin, albumin, and specific gravity were the most important for predicting CKD [26].

This is what happened after employing the technique. To diagnose CKD early, this paper proposed a range of machine learning approaches. To ensure the accuracy of the machine learning-based detection algorithms, the original CKD dataset was preprocessed. Then, PCA was performed to identify the most prominent characteristics, which enabled the diagnosis of CKD. After the models are built using the CKD-affected role, they are trained and verified using the previously described input strictures. The precision of such algorithms was the key yardstick for measuring their overall effectiveness. A novel model for CKD has been developed by Saroja and Kalpana [20]. K-Nearest Neighbour (KNN) is used to fill in missing values in this case. Features selected using the (AWDBOA) are well-explored and well-exploited, and they converge to optimal solutions without becoming stuck in local minima, making them FS methods inspired by nature. To improve FS, this study adjusts the operators used in (LSAM) and (BOA), both of which apply adaptive feature weights across generations. At the same time, the researcher pulls an adaptive weight value for FS and adds it to the database. Next, features are classified using one of six MLTs: Logistic Regression (LOG), Support Vector Machine (SVM), K-Nearest Neighbours (KNN), Naive Bayes (NB), and Feed-Forward Neural Network (FFNN). The CKD data sets are from the University of California, Irvine's MLT repository. The classification framework developed in this study is evaluated by comparing its accuracy [38].

Cognitive impairment in patients with CKD may be predicted using structural and functional brain network data, according to a study by Wang et al. [21]. A total of 621 patients with CKD and 625 healthy controls were included in the study from Jinling Hospital, while 57 patients from Hainan Hospital participated. Based on diagnostic criteria, these CKD patients were separated into a CFI group and a non-CFI group. A magnetic resonance imaging (MRI) scan of the brain, together with neuropsychological and laboratory assessments, was performed on all patients. To create an MRI signature for CFI differentiation, a deep MLP was trained on topological features of structural and functional sub-networks. Both the internal and external test sets yielded positive results for the attention MLP model (AUCs of 0.744 and 0.763, respectively). Both the IDI and NRI were significant (all p 0.05) in the external test set, and model performance was significantly enhanced after including the clinical characteristics (AUC: 0.748 and 0.774, respectively). Compared to other common machine learning models. Chronic kidney disease (CKD) is now classified using an Extreme Gradient Boosting (XGBoost) algorithm, as described by Busi and Stephen [22]. The predicted work's conclusion was tested using sensitivity, specificity, and accuracy on four scale datasets, including the Cleveland dataset. The highest classification accuracy on the kidney chronic dataset is 99.06%, which the proposed technique achieves [24]. The clustering method will be used in subsequent studies to improve classification accuracy and reduce misclassifications.

3. Proposed System

The workflow of the projected model is described in Figure 1.

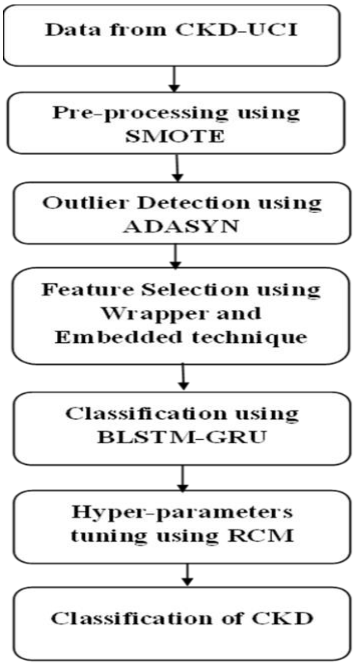

Figure 1: Workflow of the projected model

3.1. Dataset Description

In this investigation, the researcher used data available at www.kaggle.com/datasets/abhia1999/chronic-kidney-disease. There are 400 unique cases in the raw dataset, each associated with 13 input characteristics and one target class feature. Here's a rundown of what those characteristics are:

- What Is Your Diastolic Blood Pressure? The participant's diastolic blood pressure is displayed.
- **Specific Gravity (Sg):** The participant's specific gravity value is recorded here.
- **Albumin (Al):** The albumin level of the participant. There are three levels: "normal," "above normal," and "well above normal" (62.25%, 21.50%, and 6.25%, respectively).
- **Glucose (Su):** This identifier represents the participant's blood glucose concentration. There are three levels: typical (88%), above-average (8%), and exceptional (4%).
- **Red Blood Cell (RBC):** This metric records the participant's RBC count and indicates whether it is within the normal range. The remainder (11.75%) falls into an atypical category.
- **Blood Urea (Bu - mmol/L):** This metric measures the total urea concentration in the study subject's blood. The concentration of urea in blood is expressed in mmol/L.
- * Creatinine in the Blood (Sc - mg/dL) The quantity of serum creatinine in the participant's blood is measured by this function. The unit of measurement for serum creatinine is milligrams per deciliter (mg/dL).
- The participant's blood sodium concentration is measured in milliequivalents per litre (Sod - mEq/L). Sodium is measured in milliequivalents per litre (mEq/L) because it is an electrolyte.
- Potassium (Pot - mmol/L). This characteristic calculates the number of millimoles of potassium per litre of the subject's blood.
- Blood haemoglobin concentration is measured and shown as a value in grammes per deciliter (gm/dL). Haemoglobin (Hb - gm/dL).
- The number of white blood cells (WBC) is a measure of the participant's overall health and is expressed as WBC per microliter of blood.
- Red blood cell count (RBC) is a measurement of the number of erythrocytes (red blood cells) per millilitre of blood.

- Whether or not a person has hypertension is indicated by the Hypertension (Htn) characteristic. Approximately 36.75 percent of people here suffer from hypertension.
- Whether the subject has CKD is indicated by this characteristic. Among the participants, 62.5% have been told they have CKD.

Apart from the nominal characteristics of Al, Su, Rbc, Htn, and CKD, all other characteristics are quantitative.

3.2. Data Pre-Processing

To generate minority class (i.e., non-CKD) synthetic data for the present dataset, the researcher used SMOTE and a k-NN classifier with k = 5. To ensure an equal distribution of cases across the CKD and control groups, the non-CKD class is oversampled. In Table 2, the researcher shows a statistical description of the numerical properties after data balancing, including deviation.

Table 2: Statistical explanation of the balanced data

Feature	Max	Min	Mean ± std
Rbcc	8	2.1	4.84 ± 0.82
Hemo	17.8	3.1	13.04 ± 2.68
Sg	1.025	1.005	1.019 ± 0.005
Bu	391	1.5	52.59 ± 45.34
Sod	163	4.5	138.44 ± 8.64
Sc	76	0.4	2.65 ± 5.09
Bp	180	50	75.4 ± 12.6
Pot	47	2.5	4.56 ± 2.53

3.3. ADASYN-Based Outlier Detection

The outliers in this research were eliminated using ADASYN, a variant of SMOTE. Medical imaging applications where ADASYN has proven effective include the identification of preterm delivery, the diagnosis of retinal health, and the diagnosis of localised liver lesions. Although ADASYN relies on SMOTE, it produces different synthetic instances for the minority class based on its tasters, unlike borderline-SMOTE. In addition, in SMOTE, all minority cases have an equal chance of being selected, whereas in ADASYN, selection is based on the proportions of the minority classes.

Using the KNN algorithm, a synthetic instance is constructed from the majority of the closest neighbours. Minority class samples are assigned varying weights in the approach, depending on their complexity during training. It creates more challenging synthetic examples for minority-class samples than for easy training situations. The process begins with an assessment of the existing socioeconomic gap. Then, based on the Euclidean distance in n-dimensional space, it determines how many simulated examples should be generated for the underrepresented group. The method calculates the number of synthetic data examples to generate for the underrepresented group based on the density spread.

3.4. Task of Feature Selection

Unwanted or redundant characteristics in the dataset that do not improve prediction accuracy or may lower model accuracy are being identified and removed using feature and attribute selection strategies. When it comes to feature selection, you may choose between two different approaches.

3.4.1. Wrapper Technique

In this post, researchers utilise the wrapper method to find the optimal combination of 24 features for detecting CKD with high accuracy. In the wrapper approach, subset attribute selection is performed via an induction process, which is a black box. The wrapper employs a 'best first search' search technique, which is both efficient and reliable, to find reasonable parameter values. Select the most promising cluster to proceed. The optimal starting point for a search is when the goal has been reached. This is an optimisation problem; thus, at any time, the search may be halted, and the best solution found so far returned.

3.4.2. Embedded Technique

To make accurate predictions, this study used the embedded method to generate and evaluate features for detecting chronic kidney disease. During the creation process, embedded methods evaluate whether particular aspects improve the model's accuracy.

3.5. Classification using Hybrid Algorithm

The BLSTM-GRU network and the 1D CNN-based system model are described in depth below.

3.5.1. Proposed BLSTM-GRU Network Perfect

The three-layer LSTM network was used to test the proposed network and to assess its performance initially. Each LSTM layer's parameters were determined via experiment. After swapping out the LSTM cell units, the network's efficacy was measured. The recommended values for the proposed network model's hyperparameters are shown in Table 3.

Table 3: The BLSTM-GRU system model limit setting

Parameter	Value
Learning rate	0.001
Drop out	0.2
Mini-batch	128
Optimizer	Adam

A data sequence serves as the suggested network model's input layer. To provide sequential information about CKD to the network, the first layer. The BLSTM layer comes next, followed by a dropout layer to prevent overfitting. To learn the discriminative characteristics of data at each time step, the BLSTM layer must first understand the relationships. In a deep learning-based approach, the dropout layer is typically utilised to prevent overfitting. To make the network more generalizable, the dropout layer randomly removes neurons. Overfitting in networks is avoided in this way. Following a dropout layer, the proposed model uses GRU cells to perform characterisation at a lower computational cost than LSTM. After that, the researcher uses a standard LSTM unit with 200 hidden units, followed by a fully connected unit with 60 neurons. The last layer is a fully connected (FC) layer with as many neurons as there are dataset classes. Each CKD class's probability is calculated using a Softmax algorithm. By leveraging the network model's ability to precisely label sequences, the proposed approach can provide a comprehensive description of the entire dataset. The function is as follows:

$$\mathrm{Softmax}(z_i) = \frac{e^{z_i}}{\sum_{k=1}^{N} e^{z_k}} \tag{1}$$

Where z represents the input vector, k the sum of classes, N the sum of total tasters, and i the index of a given sample.
These stages outline the suggested algorithm for training models.

3.5.2. Proposed 1D CNN-Based Model

The researcher proposes a 1D CNN-based model for CKD classification and compares its performance with that of the BLSTM-GRU model. Multiple successive convolutional kernels allow a CNN to capture hierarchical characteristics of the data. The following components make up the bulk of a CNN: a set of convolutional filters, an activation function, and a max-pooling layer. An essential part of the CNN design, the convolution layer combines linear and nonlinear operations with activation functions to extract features:

$$f = \sum_{i=1}^{N} (w_i x_i + b) \tag{2}$$

Where i is the input, w is the layer weight, b is the bias, x is the input data, and N is the total sum of tasters. Pooling the maximum values from each convolutional filter is known as maximum pooling. The following is how the patch's current feature is highlighted in the resulting down-sampled or pooled feature map:

$$\hat{c} = \max(c) \tag{3}$$

Where c is the final value of the convolution layer. To introduce more nonlinearity in the CNN feature maps, the ReLU activation is used; its calculation is as follows:

$$g(i) = \begin{cases} 0, & \text{if } i \leq 0 \\ i, & \text{otherwise} \end{cases} \tag{4}$$

Batch normalisation is a technique for refining the performance and consistency of artificial neural networks by determining the average and standard deviation of all input variables simultaneously. To extract features from the data, the projected 1D CNN network uses three parallel paths. Two 1D convolution layers are shadowed by batch normalisation, ReLU, and dropout layers in each of the three distinct paths (see Table 3). To minimise data dimensionality, the retrieved features are fed into a max-pooling layer. Each of the two paths had 64 and 128 convolutional filters. Therefore, a layer is fed into the process. The likelihoods for each category are calculated using the Softmax function. The suggested values for the 1D CNN are shown in Table 4.

Table 4: Limits for tuning the projected 1D CNN system perfectly

Pathway	**2**	**3**
Convolution filters	64/128	64/128
Kernel size	3	1
Dropout	0.2	0.2
Stride	2	2
Padding	0	0

```
Algorithm 1 Projected BLSTM-GRU Network Perfect
1. Input: the sequence of the CKD data.
2. Output: corresponding class of the CKD.
3. Learning rate, batch size, embedding dimension.
4. BLSTM (hidden unit size, batch size)
5. Drop out Layer (0.2)
6. GRU (hidden unit size, batch size)
7. Drop out Layer (0.2)
8. LSTM (hidden unit size, batch size)
9. Drop out Layer (0.2)
10. FC (60 neurons)
11. FC (number of classes)
12. Softmax
13. Return Output
```

The weight of the 1D-CNN, as described in Eq. (2), is optimally selected by RCM, as follows.

3.6 Mathematical Model of RCM

The RCM method and underlying mathematical model are presented in this section.

3.6.1. Group Division

The RCM algorithmic programme operates like the red monkey. Each cluster in the monkey area needed to move around the search area for their interactions to be modelled. It has been established that when monkeys are separated into groups, each group contains at least one male, though this does not necessarily mean the male is the leader. Instead, the strongest monkey is selected as the group's leader based on their physical prowess and ability to win fights. Additionally, male Cercopithecus mitis rarely engage with young. Due to the territorial nature of Cercopithecus mitis, young males need to go out immediately if they hope to be successful when facing off against dominant males from other families. If they succeed in vanquishing that guy, they will assume leadership roles in the family and provide shelter, food, and social opportunities for the younger men.

3.6.2. Position Update

Each red monkey in a group receives a position update relative to the best red monkey in the group, as described by the following formulae:

$$\mathrm{PB_{i+1}} = (\mathrm{PA_i} \times \mathrm{PB_i}) + (\mathrm{W_{leader}} - \mathrm{W_i}) \times \mathrm{rand} \times (\mathrm{X_{best}} - \mathrm{X_i}) \tag{5}$$

$$\mathrm{X_{i+1}} = \mathrm{X_i} + \mathrm{PB_{i+1}} \tag{6}$$

$$\mathrm{PB_{i+1}} = \mathrm{PA_i} \times \mathrm{rand} \tag{7}$$

Were,

- PB signifies the monkey form power (a random sum among [−5, 5]).
- PA signifies the monkey combat power (a randomly selected sum among [0, 1]).
- $\mathrm{W_{leader}}$ signifies the leader's weight.
- $\mathrm{W_i}$ signifies the monkey's weight (random statistics from the range [4, 6]).
- X signifies the site of the red monkey.
- X best signifies the location of the leader. In contrast, rand signifies any number between [0, 1]. To update the location connected to the children of the red monkey, the subsequent reckonings have been utilised:

$$\mathrm{PBch_{i+1}} = (\mathrm{PA_i} \times \mathrm{PBch_i}) + (\mathrm{Wch_{leader}} - \mathrm{Wch_i}) \times \mathrm{rand} \times (\mathrm{Xch_{best}} - \mathrm{Xch_i}) \tag{8}$$

$$\mathrm{Xch_{i+1}} = \mathrm{Xch_i} + \mathrm{PBch_{i+1}} \tag{9}$$

$$\mathrm{PBch_{i+1}} = \mathrm{PBch_i} \times \mathrm{rand} \tag{10}$$

Were,

- PBch signifies the power degree of the child's body.
- PAch is on behalf of the child's battle power degree.
- $\mathrm{Wch_{leader}}$ on behalf of the heaviness of the child of the front-runner
- $\mathrm{Wch_i}$ on behalf of the child's heaviness, where all the weights were stated as chance statistics in the range of [4, 6].
- Xch represents the site of the child.
- $\mathrm{Xch_{best}}$ signifies the site of the leader's child, and “rand” signifies a random sum in the variety of [0, 1]. Also, this site must be rehabilitated in all repetitions.

Notably, RCM allows all parameters to be set experimentally or tailored to the problem being solved. In addition to balancing the exploitation and exploration phases, RCM's few parameters also make it a good fit for solving a wide variety of optimisation problems.

4. Results and Discussion

Experiments were run on a computer with the following stipulations: an 11th Gen Intel(R) Core System and an x64-based CPU, and the Weka tool was used to evaluate our proposed model. To evaluate the presentation of the representations on the 500-instance balanced dataset after SMOTE, the experimental results were obtained using a validation split. The initial dataset has been split into a training and a test set. The test-to-training data ratio is 70:30.

4.1. Evaluation Metrics

The researcher uses typical measures from the relevant literature to evaluate the DL models' results. Accuracy, in particular, is a summary measure of the classification task's success; it is the fraction of data instances correctly predicted. The proportion of CKD cases that were accurately labelled as the recall metric captures CKD. Accuracy reveals the percentage of CKD patients that fall into this category. The F-measure is a summary statistic for a model's prediction accuracy; it is a calculated statistic. The following is a definition of the metrics mentioned above:

$$\mathrm{Precision} = \frac{\mathrm{TP}}{\mathrm{TP+FP}}, \tag{11}$$

$$\mathrm{Recall} = \frac{\mathrm{TP}}{\mathrm{TP+FN}} \tag{12}$$

$$\mathrm{F-Measure} = 2\,\frac{\mathrm{Precision.Recall}}{\mathrm{Precision+Recall}} \tag{13}$$

$$\text{Accuracy} = \frac{\text{TN+TP}}{\text{TN+TP+FN+FP}} \tag{14}$$

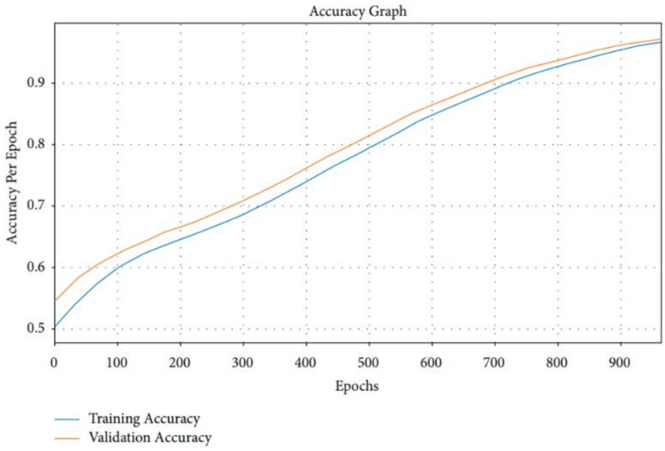

Figure 2: Accuracy graph analysis of the BLSTM-GRU-RCM method

Accuracy analysis for the suggested model is shown in Figure 2, and loss analysis is shown in Figure 3.

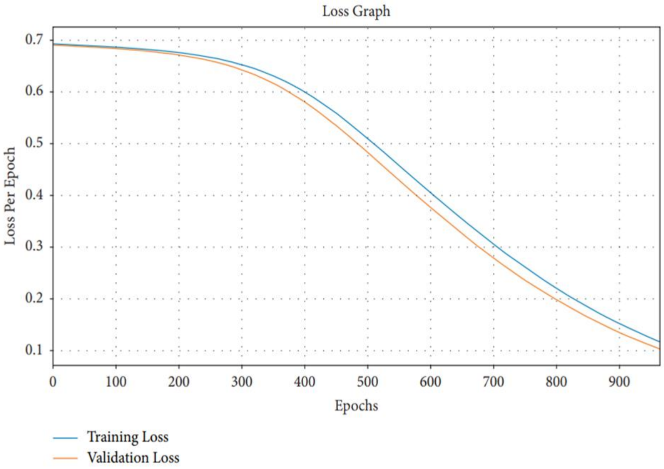

Figure 3: Loss graph analysis of the BLSTM-GRU-RCM method

4.2. Validation Analysis of Proposed Model with Existing Techniques

In Table 5, the hyperparameter for the 1D-CNN is determined by RCM, and different optimisation models are used to evaluate its efficiency. All models are tested for hyperparameters, and results are averaged.

Table 5: Analysis of proposed RCM model

Models	Sensitivity	Specificity	Accuracy	F-score
Butterfly	0.8664	0.7665	0.7732	0.7634
ACO	0.7680	0.7702	0.7691	0.7902
Whale	0.8618	0.8686	0.8643	0.8651
FFA	0.8501	0.7653	0.8627	0.8659
RSO	0.7599	0.8424	0.9111	0.9060
CSO	0.8251	0.9305	0.9265	0.9324
DMO	0.9060	0.8944	0.9026	0.9241
RCM	0.9610	0.9487	0.9778	0.9573

When the models are tested for accuracy, the proposed model achieved 97%; RSO, CSO, and DMO achieved 90% to 92%; FFA and whaleachieved 86%; and ACO and butterflyachieved 76% to 77% (Figure 4).

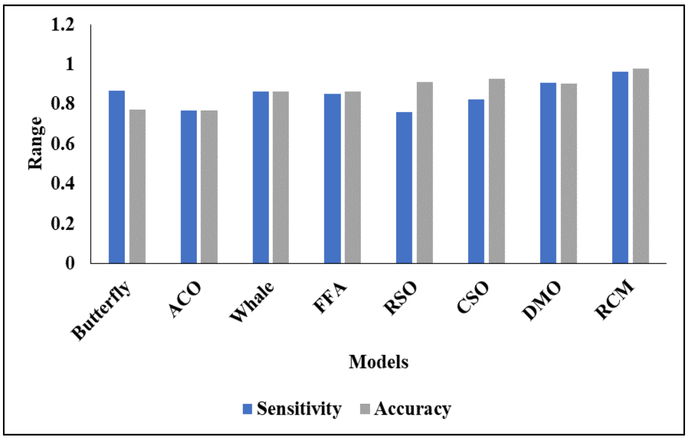

Figure 4: Analysis of the projected model

When the models are tested with sensitivity, the RSO achieved low performance, i.e., 75%, ACO has 76% of sensitivity, Butterfly has 86%, FFA has 85%, CSO has 82%, DMO has 90% and the proposed model has 96% of sensitivity (Figure 5).

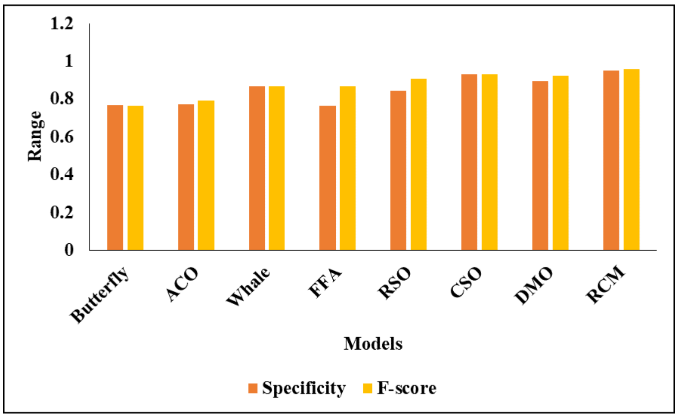

Figure 5: Comparative investigation of various optimisation models

The proposed RCM has 94% specificity and 95% F-score, whereas the existing techniques achieved 76% to 93% specificity and 76% to 93% F-score (Table 6).

Table 6: Analysis of proposed classifier with existing technique

Models	Recall	F-Measure	AUC	Accuracy	Precision
BLSTM-GRU	0.974	0.974	0.989	0.98	0.974
ELM	0.860	0.835	0.867	0.84	0.812
DBN	0.791	0.791	0.877	0.79	0.791
AE	0.916	0.915	0.943	0.81	0.818
CNN	0.791	0.791	0.791	0.88	0.791
RNN	0.909	0.909	0.927	0.91	0.909
LSTM	0.881	0.881	0.929	0.92	0.884
GRU	0.93	0.93	0.93	0.93	0.93
BLSTM	0.966	0.966	0.956	0.97	0.966

In the accuracy analysis, the proposed model achieved 98%; BLSTM, 97%; GRU, 93%; LSTM, 92%; RNN, 91%; CNN, 88%; AE, 81%; DBN, 79%; and ELM, 84%. When tested for precision, the proposed model achieved 97%; the existing models, such as BLSTM, GRU, and RNN, achieved 90%-96%; and other models achieved 79%-88%. The improved performance is due to the hybrid GRU and BLSTM configurations, as shown in the results for CKD classification.

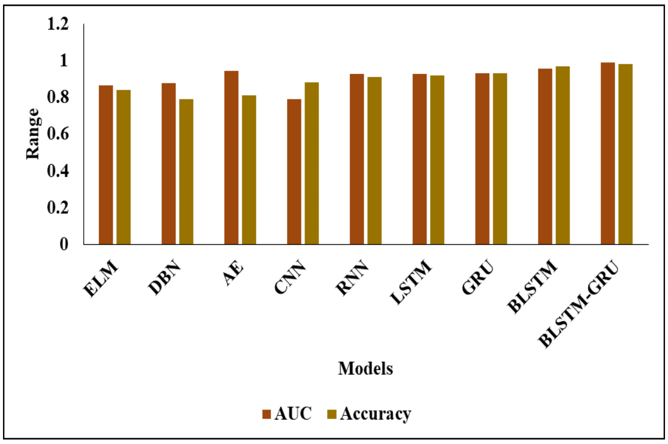

Figure 6: Analysis of various DL classifiers

In addition, the proposed model has 97% recall and F-measure, and 98% AUC, whereas the existing models achieved 79% to 95% recall and F-measure, and 80% to 96% AUC. Figures 6 and 7 present the various metrics.

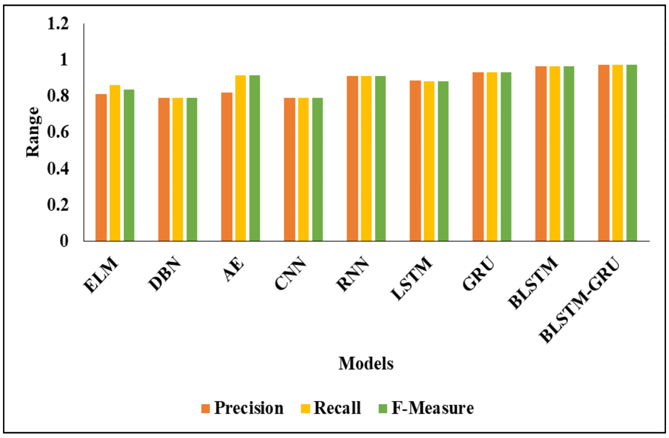

Figure 7: Validation Analysis of different techniques

5. Conclusion

Kidney illness affects a large number of people nowadays. Therefore, the fundamental objective of this work is to classify and diagnose chronic kidney disease using various computational methodologies. Our research used publicly accessible information about chronic renal illness. This research presents a unique BLSTM-GRU method for detecting and classifying CKD in an IoT-enabled cloud setting. Data collection, pre-processing, ADASYN-based outlier identification, hybrid classification, and RCM-based hyper-parameter tuning are all separate steps in the proposed BLSTM-GRU method. To do this, the researcher combined the Wrapper Method with LASSO Regularisation, two well-established feature reduction techniques. These techniques helped isolate the most important predictors of CKD while also decreasing the likelihood of overfitting. The classification procedure uses a BLSTM-GRU model combined with a 1D-CNN, with the latter's hyperparameters optimised using RCM. Numerous simulations are conducted, and the results are evaluated using various metrics to examine the BLSTM-GRU approach's enhanced CKD detection performance. In-depth comparison results showed that the BLSTM-GRU method outperformed the competition. As a result, the suggested BLSTM-GRU method is a useful instrument for detecting CKD. The suggested model could be used in the future to diagnose a wide variety of ailments.

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