International Journal of
INTELLIGENT SYSTEMS AND APPLICATIONS IN ENGINEERING
ISSN:2147-6799 www.ijisae.org Original Research Paper

Integrative Approach for Precision Prediction of Chronic Kidney Disease: Anfis-Based Feature Selection and DCNN Classification

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Submitted: 18/01/2024 **Revised**: 27/02/2024 **Accepted**: 04/03/2024

Abstract: The most dangerous disease in the world is chronic kidney disease (CKD). Identifying the disease is challenging when the doctor conducts various investigations without analyzing the facts. CKD data analysis is important for prediction and risk reduction. Furthermore, prior methodologies failed to pay attention to the mutual relations of the features and increased the dimensionality ratio, so the result produced inaccuracy. To resolve this problem, we propose an efficient approach using an ANFIS (Adaptive Network-Based Fuzzy Inference System) for feature selection and a Deep Convolution Neural Network Classifier (DCNN) for predicting CKD based on a deep neural network model. The Chronic Disease Impact Rate (CDIR) is estimated by taking into account the importance of the features affected by the medical margins identified. Using K-Cross Fold Validation (K_CFV), feature limit patterns are formed and validated to extract feature weight importance. The extracted features are selected with the support of the ANFIS to reduce the feature dimension. The selected features are trained with the Deep Convolution Neural Network Classifier (DCNNC) to classify chronic disease severity. The proposed model utilizes a large dataset of patient information to accurately identify individuals at high risk of CKD. The proposed approach has been demonstrated to be effective and efficient through experiments, outperforming traditional methods and achieving high prediction accuracy. Furthermore, the proposed model shows significant potential for early intervention and prevention of CKD.

Keywords*: Deep learning, Chronic kidney disease, Artificial Neural network, Fuzzy neural network, convolution neural network.*

1. Introduction

Chronic kidney disease (CKD) significantly affects hospitalized patients' morbidity and mortality. Furthermore, CKD is rapidly spreading and has become a significant cause of death globally. Rural regions lack knowledge and understanding of CKD. According to the World Health Organisation, tcontribute to the observed group differences in CKD prevalence, including a small sample size, study period, and cross-sectional study design with an urban-rural geographical distribution [3]. Diabetic complications, hypertension, obesity, and diabetes are among the risk factors for CKD. As a result, severe complications may arise, including heart disease, kidney failure, and premature death. It is imperative that CKD be detected early and treated effectively in order to prevent its progression. Using predictive models is critical for identifying CKD as a serious health problem for individuals at high risk and for providing them with individualized care.

Various medical applications rely on deep neural networks for detecting, predicting, and prognosing diseases. We propose a deep neural network model to predict CKD in this paper. We leverage a comprehensive dataset of patient information and clinical measurements.

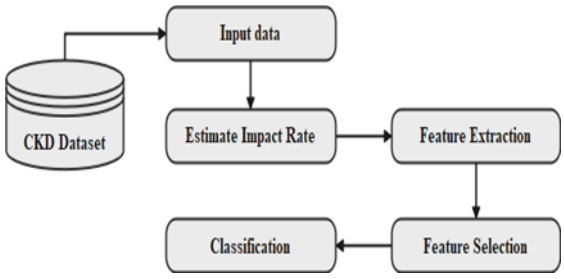

Fig 1. Work process of CKD

Figure 1 illustrates the basic architecture diagram of CKD. This diagram can be used to assess chronic diseases accuracy using impact rate, feature extraction, selection, and classification. However, when patients are in the end-stage of the condition, dialysis or kidney transplantation is often required, CKD can be detected, and biomarkers and risk factors are established. Moreover, diagnostic delays often cause severe outbreaks in many developing countries. As a result, there is an increased need for primary healthcare in rural areas, especially those with limited access to primary healthcare. In addition to the costs to public health, CKD

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treatments like dialysis and kidney transplants also raise the risk of illness and death [4].

In addition, kidney function rapidly declines with a late-stage CKD diagnosis. Early-stage CKD becomes undiagnosed and results in irreversible renal failure. This, in turn, can cause patients to suffer from various other health problems, including but not limited to osteoporosis, anemia, and nerve damage. In view of the erratic and often nonspecific symptoms of this disorder, it is imperative to detect it at its earliest stage [5]. The contribution is, In the past, traditional methodologies have failed to consider the interrelationship of features and the increase in dimensionality ratio, leading to inaccurate results. Using an ANFIS for feature selection and a DNN model for CKD prediction, it is suggested in this study that the two methods can be effectively combined.

The estimation of the Chronic Disease Impact Rate (CDIR) is crucial for identifying the importance of features affected by medical margins. To achieve this, we employ K-Cross Fold Validation (K_CFV) to establish and validate feature limit patterns, extracting feature weight importance. The selected features are then trained with the ANFIS to reduce feature dimensionality. Subsequently, these selected features are trained with the DCNNC to classify chronic disease severity. This approach allows for a more accurate prediction of CKD, as it takes into account the interrelation of features and reduces dimensionality. This leads to more precise results. Finally, the proposed approach offers a comprehensive solution to prior methodologies' challenges by incorporating advanced techniques for feature selection and classification. By leveraging ANFIS and DCNN capabilities, we can improve CKD prediction accuracy and provide more reliable insights into chronic disease severity. This has the potential to significantly impact medical diagnostics and contribute to more effective and efficient patient care

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Table 1. Classification of CKD based on prognosis

Author	Year	Technique	Learning Category	Limitation
P. Yadav [16]	2023	Synthetic Minority Over-Sampling Technique (SMOTE)	ML	However, they face numerous challenges in acquiring crucial datasets.
N. Bhaskar [17]	2021	One-Dimensional Correlational Neural Network (1-D CoNN)	DL	However, analysis takes longer due to the complexity of the process.
S. I. Ali [18]	2020	Cost-Sensitive Ensemble Feature Ranking (CSEFR)	ML	CKD problems can get more destructive if they are not treated early.
Xiaoqing Zhang [19]	2019	CNN	ML	However, it is challenging for medical professionals to make an early diagnosis.
S. T. Himi [20]	2023	Support Vector Regression (SVR)	ML	Visiting the doctor and undergoing a pathology test requires both time and money.

2. Related Work

In the study, [6] applied ML techniques for early CKD diagnosis in developing countries. However, the high costs of treatments such as dialysis and kidney disease result in many deaths. In addition, data from CKD patients can be easily accessed to build Deep Learning (DL) models based on clinical and laboratory characteristics, manipulating end-stage renal disease (ESRD) models to determine public health costs [7]. Similarly, the improved Deep Belief Network (DBN) method can predict kidney-related diseases through an intelligent classification and prediction model

using Softmax as an activation function [8]. A predictive model [9] for determining different patients' clinical characteristics can be developed as part of the CKD approach [9]. Delay in diagnosis can lead to premature death and higher healthcare costs. However, the ML framework can be deployed in clinics with low retention rates of healthcare professionals [10]. Nonetheless, CKD is considered a disease that causes

chronic deterioration of kidney function in global guidelines.

As an additional measure, modified metrics based on machine learning techniques have been employed to evaluate the Composite Hypercube Based on the CHIRP scheme on datasets of kidney patients [11]. To evaluate feature selection methods, we use data from the UCI repository on CKD. It is important to note, however, that CKD may cause many health complications [12]. Utilized CKD clinical features and advanced DL algorithms to predict and classify the disease[32]. Nevertheless, guideline-based prognostic surveillance for CKD remains underutilized due to multiple factors [13]. Afterward, the developed system can use backpropagation ANN (BP-ANN), a method for estimating blood urea and glucose levels in individuals with chronic kidney disease (CKD) [14]. In addition, neural network case-based reasoning (NN-CBR) techniques can establish CKD predictions using techniques to determine explanatory events [15][34]. There have been studies that use ML algorithms for CKD prediction, including Random Forests and SVMs [16].

Table 1 illustrates the CKD predictive model based on classification, with details on techniques, learning type, and limitations provided in the citation.

Table 2. Analysis of Chronic Kidney Disease Prediction

Ref. No	Year	Methods	Advantages	Result Achieved
21	2020	ResNet Neural Network (RNN)	The medical community has reached a consensus that a certain threshold exists.	76%
22	2020	XgBoost	The possibility of various ML approaches for early detection of CKD	90%
23	2020	Multi-Kernel Support Vector Machine (MKSVM)	Processing of selected features in clinical datasets	86%
24	2020	Cost-Sensitive Feature Ranking (CSFR)	The cost of collecting data can be decreased to improve automated detection systems.	74%
25	2021	Random Forest (RF)	The attributes used for classification showed high accuracy in diagnosing CKD	80%

Table 2 can be utilized to estimate the significance of CKD prognostication methods and analyse their benefits and results. Similarly, Decision Tree (DT) models can calculate feature values in CKD datasets and incorporate cost sensitivity into feature rankings [26]. However, most methods focus more on classification models' accuracy. Moreover, by selecting a high-performance base model, the Extreme Gradient Boosting (XGBoost) method can be analysed in the context of CKD [27]. An optimized dataset is generated by analyzing the data and selecting the most relevant features. The dataset can be used to evaluate various classifiers' performance using the K-FCV method. However, patients suffering from CKD experience severe neurological and immune system issues, which significantly affect their quality of life [28]. In addition, a DCNN algorithm could be implemented to objective is to increase the accuracy and quality of the classification model [29]. In addition, ANN and ML algorithms can also be implemented

to predict analytical performance in clinical diagnostics [30]. The novel proposes a classifier, ANFIS, to detect CKD through a neuro fuzzy model. It is important to note, however, that it can also result in kidney failure in the long run. There is, however, a possibility that it could result in permanent kidney damage [31][33].

3. Proposed Methodology

A deep neural network architecture that is specifically designed for analyzing medical data is proposed as the basis for CKD prediction. This architecture captures intricate patterns associated with CKD risk factors. Models consider a variety of patient attributes, including demographic information, medical history, results of laboratory tests, and clinical measurements. It is necessary to preprocess and normalize these input features in order to make sure their compatibility with the architecture of a neural network.

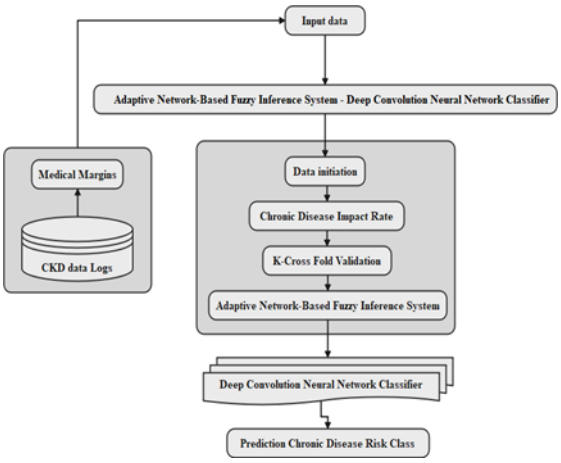

Figure 2: Proposed architecture ANFIS-DCNNC

The DNN model consists of multiple layers, including input, hidden, and output layers, with non-linear activation functions to enable complex feature extraction and representation of input data. When performing classification or regression tasks, SoftMax is used to activate the output layer.

The DCNN model makes predictions on upcoming patient data, accurately estimating the risk of CKD development based on the input features. Figure 2 shows the proposed architecture, ANFIS-DCNNC. Our approach involves estimating the Chronic Disease Impact Rate (CDIR) by identifying the importance of features affected by medical margins. Through K-Cross Fold Validation (K_CFV), we can form and validate feature limit patterns to extract feature weight importance. Our objective is to reduce the feature dimension using ANFIS by selecting the features that are most relevant to us.

Once the features have been selected, they are trained using the Deep Convolution Neural Network Classifier (DCNNC) to classify chronic disease severity. This innovative approach allows us to identify the most significant features for predicting CKD and categorize the severity of the disease. By combining ANFIS for feature selection and DCNN for prediction, we can overcome prior methodologies' limitations and achieve more accurate results. Using this approach could lead to a major improvement in the diagnosis and treatment of chronic diseases as well as a significant advancement in medical prediction. The use of ANFIS and DCNN together provides a comprehensive and robust solution for predicting CKD and other chronic diseases. By leveraging the strengths of both systems, we can effectively address feature selection and prediction accuracy challenges. This will lead to better outcomes for patients and healthcare providers. In conclusion, our approach, using ANFIS for feature selection and DCNN for prediction, represents a major breakthrough in medical prediction. By focusing on the mutual relationship between features and reducing the dimensionality ratio, we can produce more accurate and reliable results. Ultimately, this is likely to lead to improved patient outcomes and better healthcare practices by revolutionizing the way chronic disorders are diagnosed and treated

3.1 Dataset Collection

Data from various patients in India was collected for two months, including characteristics such as red blood cell and white blood cell counts. Recover data from Kaggle, classify their targets as "CKD" or "NOTCKD," and predict the number of 400 sequences among them. Pertinent clinically relevant variables can be utilized in this CKD dataset. In addition, some variables may be interconnected after activation and analysis to improve the model fit. Additionally, the dataset provided within these can be analyzed to determine the most appropriate approach based on individual requirements and objectives.

Table 3. Dataset Collection

Id	Age	BP	SG	AL	SU	RBC	PC	PCC	BGR
0	49	79	1.01	2	1	-	Normal	Not present	121.2
1	7	50	1.02	4	0	-	Normal	Not present	-
2	62	80	1.01	2	3	Normal	Normal	Not present	423
3	48	70	1.005	4	0	Normal	abNormal	Present	117

4	51	80	1.01	2	0	Normal	Normal	Not present	106
5	60	90	1.015	3	0	-	-	Not present	43
6	68	70	1.01	0	0	-	Normal	Not present	100
7	24	-	1.015	2	4	Normal	abNormal	Not present	410
8	52	100	1.015	3	0	Normal	abNormal	Not present	138
9	53	90	1.02	2	0	abNormal	abNormal	Not present	70
10	50	60	1.01	2	4	-	abNormal	Not present	490
11	63	70	1.01	3	0	abNormal	abNormal	Not present	380
12	68	70	1.015	3	1	-	Normal	Not present	208
13	68	70	-	-	-	-	-	Not present	98
14	68	80	1.01	3	2	Normal	abNormal	Present	157
15	40	80	1.015	3	0	-	Normal	Not present	76
16	47	70	1.015	2	0	-	Normal	Not present	99
17	47	80	-	-	-	-	-	Not present	114
18	60	100	1.025	0	3	-	Normal	Not present	263
19	62	60	1.015	1	0	-	abNormal	Not present	100
20	61	80	1.015	2	0	abNormal	abNormal	Not present	173
21	60	90	-	-	-	-	-	Not present	-
22	48	80	1.025	4	0	Normal	abNormal	Not present	95
23	41	70	1.01	0	0	-	Normal	Not present	-
24	42	100	1.015	4	0	Normal	abNormal	Present	-
25	61	60	1.025	0	0	-	Normal	Not present	108
26	75	80	1.015	0	0	-	Normal	Not present	156
27	69	70	1.01	3	4	Normal	abNormal	Not present	264

This dataset can be used for predictions, and by analyzing Table 3, datasets obtained from hospitals and CKD can be analysed. Some features include RBC, al-Albumin, BGr, pc-Pus cells, pcc-Pus cell clumps, and hemoglobin. These features are crucial for identifying and predicting CKD. These features are crucial for identifying and predicting CKD accurately.

3.2 Chronic Disease Impact Rate (CDIR)

The Z-transform of the normalized variable can be employed to determine the impact ratio using the CDIR method to specify the value of the Z-score of the normalized variable based on the mean and standard deviation. The CDIR method predicts a normalization value that equals the average of all feature values. CDIR can identify the

proportion of negative or positive numbers that affect values below the mean and above the standard. Furthermore, the patient's feature values can be standardized to determine the maximum possible impact ratio of the data. The CDIR method can be implemented to identify potential new patients by observing the patient impact rate in the patient's medical data. And compare it to the predetermined threshold to determine whether the patient qualifies as a potential new patient.

Estimate the normalized impact variable using the Z-transform as shown in Equation 1. Let's assume $a'(u)$ −normalized data value, a-score, μ −mean, ς −standard deviation

$$a'(u) = \frac{\mathfrak{a}-\mu}{\varsigma} \quad (1)$$

Calculate the patient characteristic values with max-min normalization as illustrated in Equation 2. Where F_o −normlized data, $a_{(u)}$ −original data value, $m^{\mathbb{im}}(u)$ −the minimum data value, $M_{ax}(i)$ −maximum data value.

$$F_o = \frac{\mathfrak{a}_{(\mathbb{m})}-m^{\mathbb{im}}(u)}{\mathbb{m}_{ax}(\mathrm{u})-m^{\mathbb{im}}(u)} \quad (2)$$

As shown in Equation 3, calculate the minimum and maximum similarity between the new patient and the other patient data. Where a-value of the feature, N- represents the feature index data, $\mathbb{l}$ -new patient data, M-feature health data store, N- new patient similarity value, i,j-values, $Q_{u,v}$ −similarty data's.

$$q_{u,v} = 1 - \sum_{u=1}^{\mathbb{l}} \sum_{v=1}^{f} \sum_{N=1}^{e} \sqrt{\left(A^{u,v} - \mathfrak{a}_{N,v}\right)^2} \quad (3)$$

As shown in Equation 4, Estimate the impact rate of weight on patient health records. Where P^u −represents the feature impact rate, P-feature value, K-Number of specific type chronic disease, P_u^v −feature value of new and previous patients, $\bar{p}_v$ −average feature value, G-weight, G_u −new feature weight, G_u^v −new and previous feature weight.

$$q_{u,v} = \sum_{p=1}^{e} \left(\mathcal{p}^u + \frac{\sum_{v=1}^{k} (\mathcal{P}_u^{\mathfrak{v}} - \bar{p}_V) * \mathcal{g}_u^{\mathfrak{v}}}{\sum_{\mathfrak{v}=1}^{\mathbb{k}} |G^v| + |\mathcal{G}_u|} \right) \quad (4)$$

In this section, the new patient's impact ratio weighting can be normalized according to clinical data. It can also be compared to the impact ratios of other patients in the same database.

3.3 K-Fold Cross Validation (K-FCV)

The K-FCV method can be used to partition the data into subsets for training and measuring the models. The K-FCV technique is typically trained on an existing dataset with class labels for predictive analytics. After building the model, evaluate its performance and test the dataset with updated data with unknown output labels. Furthermore, the K-FCV method separates data into multiple K-folds based on repeated tests and training. After that, a template can be used to evaluate the model in other areas. The K-FCV model repeats itself by generating and testing each fold. Finally, the mean of all k cross-validation test errors is computed. The ability of the model to generalize can be determined by assessing its performance and generalization abilities.

Algorithm 1: K-FCV

Input: Chronic Impact rate $\mathcal{P}^u$

Output: Accuracy of cross-validation

Start

Step 1: Divide the K data into equally sized validation folds.

For each H in value (0, h) do

Step 2: $H \leftarrow N^h$ in data

Step 3: $Z \leftarrow {}^{O}/_{J}$ (5)

Step 4: Training T

Step 5: $X_H \leftarrow j$ Utilize trained models for assessment

End for Each

Step 6: Accuracy validation $\leftarrow \frac{1}{K}\sum_{\mathbb{k}=1}^{H} \mathcal{X}_{\mathbb{h}}$ (6)

Step 7: Return X_H

End

As presented in Algorithm 1, we can assess the prediction model for the dataset and compute the mean experimental error. Let's assume H-validation folds, J-validation, Z-trained model, O-data, F-fold, X_H − accuracy validation.

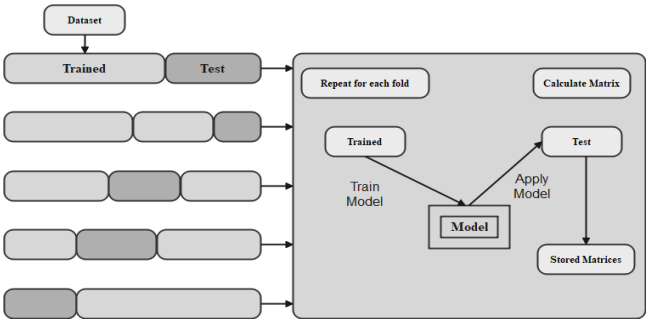

Fig 3. K-FCV Architecture Diagram

K-folds can be divided into validation and approximation of the data set as test and training sets for model building, as depicted in Figure 3 blow.

3.4 Adaptive Neuro-Fuzzy Inference System Prediction (ANFIS)

The ANFIS method integrates linguistic variables into fuzzy logic to implement computer capability in fuzzier rules for inferential systems. The ANFIS method utilizes supervised algorithms to establish a rule base based on neural network strategies. Furthermore, the ANFIS method is applied to inference-based CKD systems and uses learning processes continuously to update the system parameters. The output function coefficients are modified using the least squares method, while the fundamental factors of the CKD system are determined through the ANFIS prediction method. The ANFIS prediction method combines fuzzy logic and neural networks to make accurate predictions.

Calculate the input variables generated at each node using the membership function as illustrated in Equations 7 and 8 to obtain the final result. Where x and y-input variables, u-number of nodes, P and q-terms of linguistic, ℓ -layer, S-Generate node.

$$S_1^{\ell} = X_H\ \mu_{p^{\ell}}(x),\ U = 0,. \tag{7}$$

$$\mathcal{S}_2^{\mathbb{I}} = \mu_{q^{l}}\,(y),\ u = 0,1,..3 \tag{8}$$

Calculate using the bell-shaped membership function as described in Equation 9. Where a,b and t- varies membership parameter,

$$\mu_{P^{\mathrm{I}}}(x) = {}^{1}/_{[1 + |(x-t)/A|2b_{\mathbb{L}}],}\quad \mathfrak{u} = 1,2,3 \tag{9}$$

Calculate the firing strength of each node in the output layer using Equation 10. Let's assume G^{ℓ} −ouput layer of strength.

$$S_{2,l} =\ G^{\ell} = \mu_{\mathcal{s}^{\mathbb{L}}}[x] * \mu_{\mathcal{s}^{\mathbb{I}}}[\mathcal{y}],\quad \mathbb{u} = 1,..3 \tag{10}$$

Calculate the normalized firing strength of the output layer as depicted in equation 11.

$$\mathfrak{s}_{3,\mathbb{I}} = \bar{G}_L = \frac{(g^{\mathbb{I}})}{(\mathcal{g}_1+\mathcal{G}_2+\mathbb{g}_3)},\ \mathcal{u} = 1,..3,4 \tag{11}$$

As demonstrated in Equation 12, calculate the output exponential product of the normalized firing strength. Where $\bar{W}_f$ −firing strength, p, q, and r- identify parameters training process.

$$S_{4,\ell} = \bar{\mathcal{G}}_N = \overline{\mathcal{g}}(r_u(x) + \mathbb{S}_u(y) + p^{\mathfrak{x}}),\quad \mathfrak{u} = 1, \ldots 2,3 \tag{12}$$

Calculate the sum of all inputs and output layers as shown in Equation 13.

$$\mathfrak{s}_{4,l} = \sum \overline{\mathbb{g}}_{n_{\mathbb{L}}},\quad \mathbb{U} = 1,..3,4,5 \tag{13}$$

The coefficients of the output function may be estimated using the least squares method and updated using the essential factors of the CKD system.

3.5 Convolutional Neural Network (CNN)

CNN is the most popular DL model, with three layers: convolutional, pooled, and fully connected. Furthermore, the information layer categorizes the image data into multiple layers, widths, and channels while specifying the input map type. Moreover, feature maps can be approximated through CNN techniques by utilizing various convolution kernels for the convolutional layers. It is necessary to experiment with CNN parameters in order to ensure that each neuron in the feature map is primarily connected to neighboring neurons in the layer preceding it. In addition, each CNN consists of multiple layers, with the convolutional and subsampling pooling layers being particularly crucial. As an option, CNN can be used to calculate the output feature estimates for the final layer. A CNN method can be used to make predictions or classifications based on the output feature estimates of the final layer.

As shown in Equation 14, compute the feature map of the homogeneous channel range of convolutional layers. Where $O_{u,u,v}$ −convolution's output, ℓ -layer, R, S-channel range, E-feature map, $K_{RS^{hE}}$ −Convolutional weight applied, Y_{uv_E} − represents bias applied to the convolution.

$$\mathcal{O}_{u,\mathfrak{u},\mathbb{v}} = Q_{4,l} \sum_{h=0}^{H-1} \sum_{R=0}^{K-1} \sum_{S=0}^{\mathcal{K}-1} \mathcal{U}_{u+r+s,h}^{\ell-1} K_{RS^{hE}} - + Y_{uv_E} \tag{14}$$

Calculate the padding and striding layers as described in Equation 15. Let's assume G-weight, N-feature, R-padding, Q-striding.

$$([G - N + 2_R]/Q) + 1 \tag{15}$$

Evaluate the layer used to construct the ReLU activation function as depicted in Equation 16 and 17. Where $\mathcal{RELU}$ −rectified linear unit, $N(a)$ −represents the ReLu parametric function, $\sigma_{u,h}$ −Connotes the convolutional channel and feature map, and O-disease convolutional layer.

$$N^{\mathcal{RELU}}(\sigma_{u,h}) = \mathbb{m}_{ax}(0, \mathbb{O}_u^{\mathbb{k}}) \tag{16}$$

$$N(a) = \begin{cases} X_a\ for\ \mathfrak{a} < 0 \\ \mathfrak{a}\ for\ a \geq 0 \end{cases} \tag{17}$$

Calculate the predicted Softmax activation for the subsection depicted in Equation 18. Where T- feature activation.

$$(T) = \frac{\mathcal{E}_{\mathcal{X}^{\mathcal{P}}(\sigma)}}{\sum e_{xp}(d)} \tag{18}$$

Compute the stack of related values in the feature map as illustrated in Equation 19. Let's assume $T_{x,y,\mathbb{C}}^{\ell}$ −corresponding feature value, $G_x^{\mathbb{I}^z}$ −denotes the

weight, ℓ -layer, $\mathbb{C}$ -feature map, (X, y)-centered location, $Y_{\mathbb{C}^l}$ −bias filter corresponding layer.

$$T^{\ell}_{x,y,\mathbb{C}} = G^{\mathbb{I}^z}_{x} J^{\mathbb{I}}_{x,y} + Y_{\mathbb{C}^l} \quad (19)$$

Calculate the activation value for the functional feature as shown in Equation 20. Let's assume $A^{l}_{a,b,c}$ −activation function.

$$A^{l}_{a,b,c} = a\left(Z^{l}_{a,b,c}\right) \quad (20)$$

As shown in Equation 21, calculate the assessment expressed in the pool function. Where $I^{\mathbb{L}}_{x,y,c}$ −value, P^{l} −pooling layer, $X^{\ell}_{E,h,\mathbb{c}}$ −corresponing pooling function, P^{y}_{x} −rectified location.

$$I^{\mathbb{L}}_{x,y,c} = R^{\ell}\left(X^{\ell}_{E,h,\mathbb{c}}\right), \forall (e,H) \in P^{y}_{x} \quad (21)$$

Calculate the classification of the target label in the output layer as described in equation 22. Let's assume $\mathbb{L}$ -loss, H-input feature, ϑ −overall parameter, $I^{(h)}$ −target labels, $D^{(h)}$ −corresponding output layer.

$$\mathbb{L} = \frac{1}{H}\sum_{\mathbb{h}=1}^{h} \ell\left(\vartheta; I^{(h)}, D^{(h)}\right) \quad (22)$$

The convolution kernel of the convolution layer can be used to approximate the feature map of the output layer in this category. An activation function is applied to the feature map of the previous layer in order to generate the final output of the neural network.

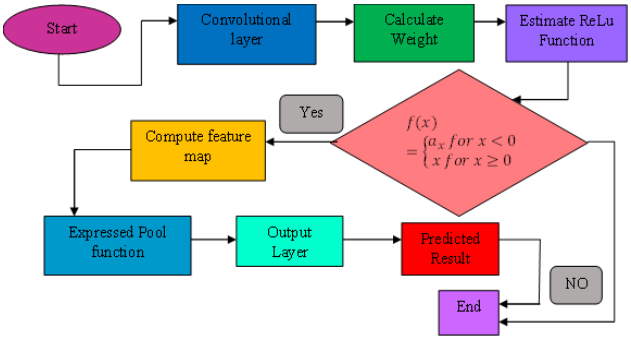

Fig 4. DCNN Flowchart Diagram

Based on the convolutional layer, a DCNN flowchart can be used to estimate the value of the feature map. Figure 4 illustrates how this can be done. Through the use of convolutional layers and pooling layers, the spatial information and patterns underlying the input are extracted and transformed.

4. Results and Discussion

CKD prediction models based on DNNs are tested on a comprehensive dataset of patient records. Based on experiments, this approach has demonstrated to be highly accurate and outperforms traditional methods. CKD outcomes can be captured effectively with DNN models due to their robustness and generalization abilities. Using cross-validation, the model is further validated, with superior accuracy, sensitivity, and specificity in terms of measuring CKD outcomes compared to existing predictive models.

The proposed model for chronic kidney disease is based on DCNN prediction appears to offer several advantages over conventional methods, including its ability to handle high-dimensional, heterogeneous medical data, to learn complex patterns, and to provide accurate and personalized predictions. A large-scale deployment of this model is suitable in clinical settings since it is efficient and scalable. It is therefore possible to identify at an early stage individuals who are at high risk of developing CKD and timely interventions and individualized healthcare plans can be provided. Furthermore, the interpretability of the DNN model allows healthcare professionals to gain insights into the key risk factors and features contributing to CKD prediction. This enhances clinical decision-making and patient management.

Classifiers are evaluated using precision, sensitivity, error rate, F-measure, root mean square recall, and log loss. Compared to alternative systems, the proposed model provides much higher accuracy than alternative systems and outperforms them in terms of overall performance.

Table 4. Simulation Parameter

Simulation Limit	Variable
Name of the dataset	Kaggle
The number of datasets	4982
Number of Training Data	3556
Number of Testing Data	1426
Language	Python
Tool	jupyter

To detect CKDs using Python and Jupyter Notebook, Table 4 lists the proposed simulation parameters. The kidney CKD dataset was collected from Kaggle and includes a bulk dataset that can be used for training and testing to achieve accurate CKD detection. A variety of characteristics are included in the dataset, including age, blood pressure, specific gravity, albumin, sugar, red blood cells, pus cells, and so on. This information provides comprehensive information for analyzing and predicting CKD.

4.1 Performance Matrix

A number of performance metrics are analyzed in this section of the paper, including precision, sensitivity, precision, F1 score, and recall, to evaluate the CKD detection classifier. Classifiers are evaluated based on their ability to recognize and classify congenital kidney disease through the use of metrics. Data from the training and testing phases is used to calculate the metrics. To determine whether the proposed classifier is accurate and effective at detecting and categorizing CKDs, a comparison is made between the proposed classifier and existing state-of-the-art classifiers.

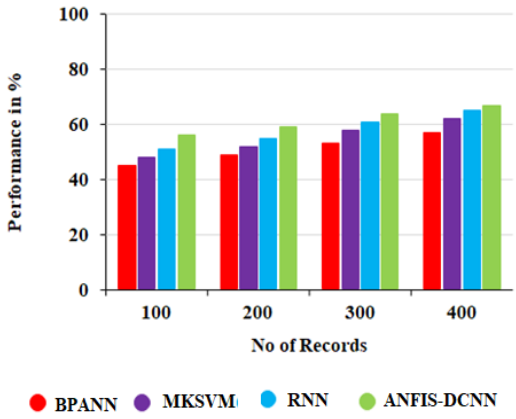

Fig 5. Analysis of Sensitivity

In Figure 5, we illustrate how the ANFIS-DCNN approach suggested by our method can be used to determine the accuracy of sensitivity analysis for detecting kidney CKDs. According to literature analysis, the proposed method achieves a higher accuracy of 69% than the existing methods of BPANN, MKSVM, and RNN. There is an accuracy rate of 43% for these methods. In addition to outperforming these, the proposed method is also more accurate and reliable in terms of precision and recall than other methods.

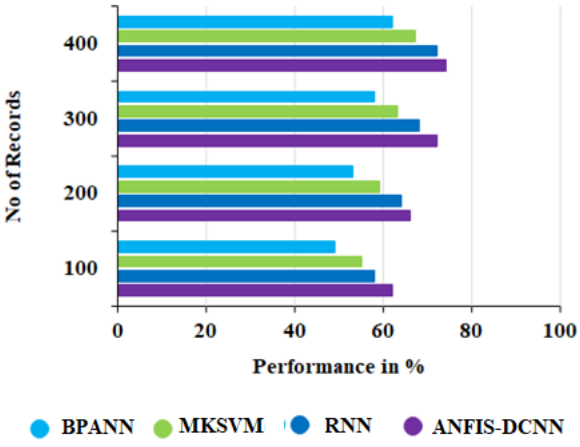

Fig 6. Analysis in Precision

In Figure 6, the proposed method of using ANFIS-DCNN for CKD detection shows a significant increase in accuracy. This method involves obtaining CKD data from a dataset and conducting training and testing analyses to determine its accuracy. Compared to other techniques, such as BPANN, MKSVM, and RNN, the accuracy is less than 52%. However, the proposed method improves accuracy by up to 73%. In conclusion, the developed method shows a significant improvement in accuracy compared to other techniques, with an increase of up to 73%.

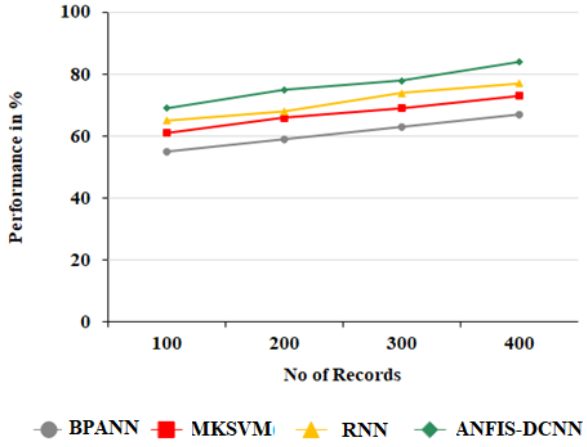

Fig 7. Analysis in F1-Score

Figure 7 shows an estimate of F1-score analysis using the proposed ANFIS-DCNN approach to detect kidney CKD accuracy. The data can be collected from the dataset and processed to obtain kidney lateralization accuracy using training and testing. The F1 score can be analyzed using this. Also, the ANFIS-DCNN method increased to 78%. However, the accuracy of the BPANN, MKSVM, and RNN methods determined from literature analysis is less than 55% compared to the suggested method.

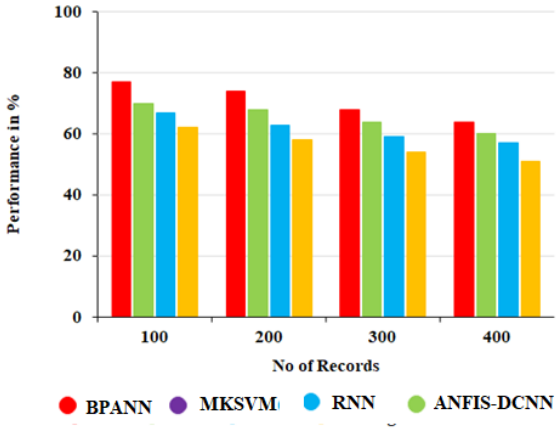

Fig 8. Analysis of Error Rate

In Figure 8, it was demonstrated that CKD accuracy can be achieved through the use of error rates. The accuracy of BPANN, MKSVM, and RNN techniques increased by 79% due to reduced error rates. When testing the proposed ANFIS-DCNN method, the error rate accuracy was less than 57%.

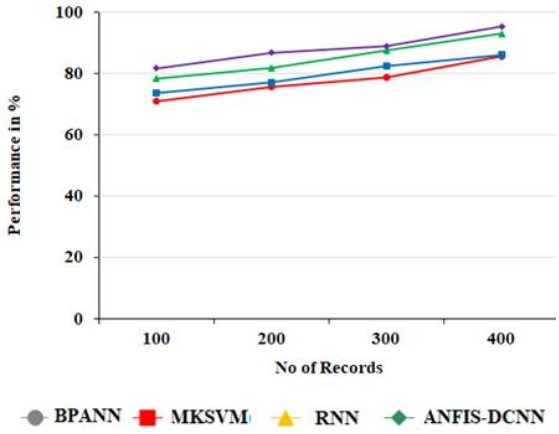

Fig 9. Analysis in Accuracy

Figure 9 presents a method for collecting CKD data called ANFIS-DCNN. This method has been trained and tested for accuracy. When compared to other methods like BPANN, MKSVM, and RNN, the proposed method has shown an improvement in accuracy to 95.30%.

5. Conclusion

In conclusion, the proposed approach to efficient CKD prediction based on deep neural network modelling holds significant promise for preventing CKD and improving its management. In terms of accurate identification of people at high-risk for CKD, the DNN model performs admirably. This is done by leveraging a diverse set of patient attributes and complex relationships. The model's effectiveness, efficiency, and interpretability make it a valuable tool for healthcare professionals. It enables personalized healthcare strategies and proactive interventions to mitigate the burden of chronic kidney disease. Future work may involve further refinement and validation of the DNN model using diverse patient cohorts and real-world clinical data, as well as integration into clinical decision support systems for widespread adoption and impact. Overall, the proposed DCNN-based CKD prediction model represents a significant advancement in leveraging deep learning techniques for proactive and personalized healthcare solutions.

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