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

Enhancing Chronic Kidney Disease Diagnosis with an Optimized Fuzzy Deep Neural Network: A Polycystic Kidney Disease Perspective

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Submitted: 15/01/2024 **Revised**: 23/02/2024 **Accepted**: 01/03/2024

Abstract: In recent study, there has been significant interest in developing more effective diagnostics, treatments, and preventive measures to control Chronic Kidney Disease (CKD). This leads to millions of deaths due to increasingly inadequate, untimely, and expensive treatment methods. Kidney function decline affects millions worldwide annually. By constantly affecting kidney function, when both kidneys are damaged, the body's overall health can be negatively impacted. Furthermore, chronic kidney disease impairs the kidneys more than other conditions. Individuals with CKD can live longer even with the disease. However, it may lead to severe medical complications, such as reduced kidney function and kidney damage. To overcome this problem, an Optimized Fuzzy Deep Neural Network (OFDNN) classifier can detect and predict polycystic or non-polycystic kidney disease. Then, we gathered the necessary dataset for Polycystic Kidney Disease (PKD) from Kaggle. Then, a pre-processing step can be applied to ensure satisfactory accuracy of the missing values. As a result, we can use Efficient Multi-Head Self-Focusing Based on Feature Weight (EMS-FW) methods to obtain the average total loss value in the decoder. Next, a feature selection method that relies on Chi-squared based on Mutual Information Gain (Chi2-MIG) can calculate predictive ability by classifying the dependent variable and removing redundant features. Finally, an improved(DL) model based on the OFDNN classifier is proposed to detect and diagnose polycystic or non-polycystic kidney disease. This method suggests that developing DL with predictive modeling is a promising approach to finding effective solutions. Comparison of the proposed OFDNN approach with existing information classifiers shows improved precision, F-measure, and recall accuracy.

Keywords: *Fuzzy, Neural Network, Chi-squared, Information Gain, Deep Learning, Kidney Disease.*

1. Introduction

Among the most important public health concerns in terms of global public health, CKD is one of the most significant issues. As a chronic disease, it can be life-threatening due to the fact that it can cause serious complications. It can be central to malignant kidney tumors or kidney failure. Within humans' retroperitoneal cavity, the kidneys are vital organs that maintain normal bodily functions. The kidneys maintain the proper balance of minerals and substances in the human body, including salt, blood plasma, calcium, chlorine, acid, and other trace elements.

Detecting and treating chronic diseases early can prevent or slow their progression to terminal stages. If the condition reaches a critical point, the patient's life can only be saved through dialysis or surgery. It's essential to seek medical attention promptly to increase the chances of a favourable outcome. Doctors can use routine laboratory tests to detect CKD. As well as preventing disease progression, slowing disease evolution, and improving persistence and life cycle features, explicit therapies reduce the risk of cardiovascular complications. CKD is a non-communicable disease that is highly infectious and adversely impacts patient injury, mortality, and hospitalization rates worldwide.

CKD is one of the leading causes of death in the world today and is rapidly approaching epidemic proportions. This condition interferes with daily life and can lead to heart failure. It is especially prevalent in low- and middle-income countries. CKD occurs when the kidneys cannot filter the blood properly. In the absence of proper control, hypertension can increase the risk of heart disease, stroke, and CKD. Inappropriate analysis may result in kidney disease at the end of treatment and, in extreme cases, death.

This paper aims to develop a promising method to find new solutions using the proposed OFDNN method and improve the classifier's accuracy. To find these, we first collect the PKD dataset from Kaggle. Then, they apply a pre-processing step to ensure satisfactory accuracy of the missing values from the obtained data. Next, the decoder's average loss value can be obtained using EMS-FW methods. Chi2-MIG is the best method for feature selection. Finally,

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a novel DL model based on the OFDNN classifier is introduced to detect and predict PKD or non-PKD kidney disease.

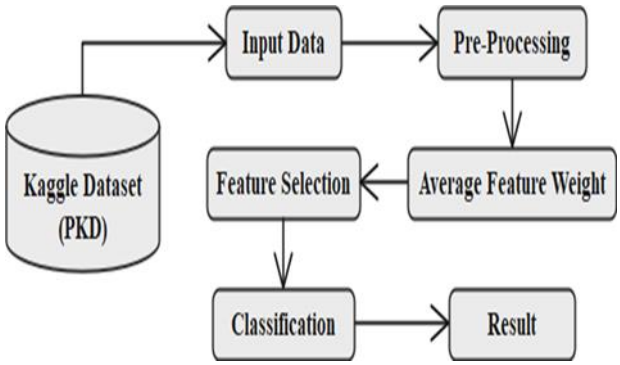

Fig. 1. Basic Architecture Diagram for PKD

This section aims to develop a technique to find new solutions and improve classifier accuracy using the OFDNN approach, as shown in Figure 1. The first step is to gather the PKD dataset from Kaggle. Determine their strengths by implementing pre-processing actions, feature weighting, feature selection, and classification.

2. Literature Survey

The author presented that using the Deep Belief Network (DBN) method to develop intelligent classification and prediction models is the most effective approach to predicting kidney-related diseases. To treat both of these problems, softmax can be used as an activation function, and cross-entropy can be used as a classification loss function to treat these problems [1]. The novel illustrated that Machine Learning (ML) techniques can work for patients with clinical CKD and cardiovascular disease. However, numerous individuals across the globe are impacted [2]. The author presented an innovative method known as SS-MTL method for predicting kidney disease's instant progress by taking advantage of Electronic Health Record (EHR) information acquired from various general practitioners [3]. The author suggested seven advanced DL algorithms to forecast and categorize CKD using different clinical characteristics. Further, the novel described how interpretive data-driven methods could be crucial in providing numerical insights into how certain clinical features contribute to CKD early detection [4, 5].

And they also discussed how ML techniques could be used based on clinical analysis to classify datasets of kidney patients as having CKD or not. In addition, the UCI-CKD dataset serves as an ML repository for diagnosing CKD using ML approaches and demonstrates that many of these values are underrepresented [6, 7]. A review of the recent literature on techniques for segmenting renal images can be obtained in the statement described in this statement. This is after the ML repository has been implemented. In addition, it is necessary to illustrate the inadequacies of the current proposed methods that impede their practical application in a clinical setting [8]. Thus, an ML model can identify specific laboratory characteristics that can help create major pathological categories with the currently described method. Also, to accurately diagnose CKD and save time and money on analytical screening [9].

Similarly, with these, the multi-block Hybrid U-Shape Segmentation Network (HUNet) technique can introduce recurrence rates, stratified residuals, and self-maintenance of multiheads in U-shaped schemes with an efficient flow of information [10]. In addition, urea concentrations in saliva can be monitored using advanced technology that automatically detects kidney disease. However, there is a technique that makes accurate measurements of urea content possible [11]. Although their accuracy is higher when implementing this method, it is still better than the uncertainty-guided Bayesian classification (UGPC) method for accurately classifying Lupus Glomerulonephritis (LGN). Furthermore, these systems were adapted to handle classification tasks related to glomeruli and kidney size [12]. With them, the clinical and laboratory characteristics of CKD patients can be analysed using ML and DL techniques to assess ESRD [13].

It was described that early detection of CKD in developing countries could be prevented using ML techniques. In addition to public health-related costs, CKD treatments, such as kidney transplantation, may increase injury and mortality rates [14, 15]. Based on the above statement, we present a practical approach to ensemble feature ranking, which selects structures based on teams considering cost. It is possible to select features based on different groups, each with its own objectives, in order to achieve different objectives [16]. These can refer to using ancillary data from different categories to accurately diagnose diseases. Combining gene expression data can generate highly accurate fusion networks for renal cell carcinoma (KIRC) [17]. The self-generated classification, therefore, can be used to monitor blood glucose levels and blood urea levels in diabetic patients with chronic kidney disease [18]. Fully automated total kidney volume (TKV) segmentation can be obtained via a DL network while selecting exophytic cysts [19].

In addition, an innovative dynamic pooling method and a network coalition engine are introduced to help select the most suitable features for the classification process [20]. It is proposed to improve the traditional method of diagnosing a patient's likelihood of developing CKD by determining progression from early to later stages. Furthermore, they enable the combination of decision tree and path optimization (DDAPO) and logistic regression (LR) methods [21]. As a result of these functional characteristics, an ANN predictive model can be developed in patients with primary IgAN of developing end-stage renal disease. The

model relies on two tools, classification and regression models, to determine ESKD, according to [22]. The receiver operator's AUC can be used to assess how well the model estimates outcomes. These approaches can be correlated with traditional models such as Cox proportional hazards regression and renal failure hazards equation representations [23]. Various tests are conducted to prove that a certain amount of data is sufficient for predictive models. However, it is essential to determine the exact amount of data needed to establish the reliability of the predictive model [24].

Their determinations can be described using a method of feature extraction to predict the early stages of DKD progression. However, using complex techniques such as CNN is challenging due to data limitations [25]. The most accurate classifiers can evaluate various ML classification techniques to determine this complexity. However, they also recognize that challenges can affect performance outcomes [26]. Although various problems are mentioned and discussed above, ML techniques for clinical treatment can provide reliable and timely diagnosis.

Furthermore, these can be implemented based on the CKD prediction discussion [27]. Hybrid approaches were used to develop the presented model [28]. A novel DL model coupled with a fuzzy deep neural network (DNN) method can diagnose and predict kidney diseases. However, CKD can lead to persistent kidney function decline, leading to kidney damage and failure [29]. An ML technique can accurately predict the development of sepsis-induced acute kidney injury (AKI) and AK disease (AKD) in patients [30-33] to prevent dysfunctions in these segments.

3. Proposed Methodology

A method will be developed here in order to evaluate the functional utility of the OFDNN method for identifying and predicting PKD or non-PKD by utilizing DL models. We first collect the required PKD dataset from Kaggle to handle these methods. Then, a pre-processing step can be used to ensure the correct accuracy of the missing value from the obtained dataset. Then, we applied the EMS-FW method to find the mean of the total loss value. After that, predictive ability can be calculated by selecting the features based on Chi2-MIG and removing the redundant parts of the dependent model. Finally, for the purpose of evaluating their robustness and improving accuracy, the proposed OFDNN method can be applied and evaluated.

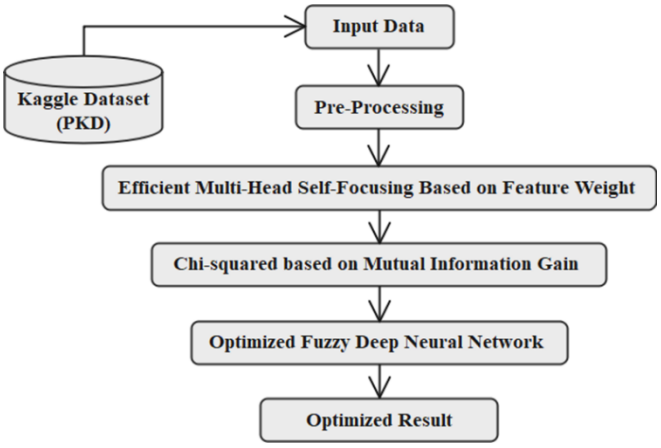

Fig. 2. The Proposed Architecture Diagram for PKD

Figure 2 describes the proposed method's architecture. Based on this framework, we developed a procedure to evaluate the robustness of the OFDNN method using DL models. This was done to detect and predict PKD or non-PKD and achieve accuracy.

3.1. Dataset

A study was conducted on the PKD dataset, which consists of 400 rows and 14 columns. The output column "type" can have a value of "1" or "0". If the value is "0", it means the patient is not suffering from PKD, when a patient's problem is PKD, they receive a value of "1", indicating that they have this disease. The total number of PKD and non-PKD inputs is displayed in the output column before pre-processing. There are 250 PKD and 150 non-PKD data points, making 400 rows and 25 features such as red blood cells, sugar, and more. These are used to classify patients into polycystic or non-polycystic groups. This classification is determined by an attribute called "classification" called "PKD" or "Non-PKD." We clean the dataset by converting text to numbers and performing various transformations to ensure accuracy. As a result of using the model, the dataset can be divided into training and test sets for the purpose of measuring the performance of the classification process. Then, the confusion matrix, classification report, and accuracy can be implemented.

3.2. Pre-Processing

In the pre-processing step, data values can be manipulated based on their distribution to ensure sufficient accuracy and check for non-uniformity of data values. Missing data were imputed using multiple imputations with five replicates to create imputed datasets. The incorrect values were randomly selected from a predicted distribution based on the observed data. The models were trained and tested on each evaluation set using a five-fold cross-validation procedure. Preprocessing results in the model deviating from the correct training set due to unnecessary noise and outliers. Possible bias due to missing data is determined by the mechanism driving the missing data. To enhance prediction

accuracy, raw medical data undergoes data pre-processing that eliminates incorrect values.

Using Equation 1 of the class model, calculate the synthetic event that has recently occurred within the class model for the most recent period.

$$x = 2 * (q - c) + c \quad (1)$$

Using Equations 2 and 3 as a guide, find the distance between the original minorities in order to remove outliers based on sample reconciliation for each pair of minorities.

$$Min_{Rap}(\hat{R}_a, \hat{R}_y) = \sum_{D=1}^{c} \sum_{b=1}^{y} \sqrt{\left(\hat{R}_a^{(b)} - \hat{R}_{yD}^{(b)}\right)^2} \quad (2)$$

$$K = \sum_{a=1}^{x} \left(Min_{Rap}(\hat{R}_a,\ R_y)\right) \quad (3)$$

Calculate the distance between the original majority and each other using equation 4 to find out the distance between them.

$$Maj_{Rap}(\hat{R}_a, R_u) = \sum_{a=1}^{q} \sum_{b=1}^{y} \sqrt{\left(\hat{R}_a^{(b)} - R_{uK}^{(b)}\right)} \quad (4)$$

By exploiting the compromise method shown in Equation 5, we can obtain the original majority model derived from the majority model.

$$G = \sum_{a=1}^{x} \left(Maj_{Rap}(\hat{R}_a, R_u)\right) \quad (5)$$

$$G(w) = -\sum(J_a * \log_2 J_a) \quad (6)$$

Calculate the connection between probability and diversity as shown in Equations 6 and 7.

$$F\ (J) = \sum_{a=1}^{x} J_a \log_2 J_a \quad (7)$$

Let's assume q-majority class sample, c-minority class sample, x-newly created synthetic instance, Maj_{Rap} and Min_{Rap} sample rapprochement, y-measure, k-link, J-probability link, F-entropy, and G-heterogeneity. There is a correlation between probability and heterogeneity in this category. Values seem missing for all features except the diagnostic category.

3.3. Efficient Multi-Head Self-Attention Based on Feature Weight (EMS-FW)

This section provides the feature-weighted average total loss value based on the EMS-FW method. The EMS-FW design aims at learning long-range biases. The approach involves using EMS-FW to acquire long-range correlation information while concurrently utilizing convolutional layers to extract local intensity features. With this approach, we can avoid extensive focusing mechanisms during the pre-training phase. The EMS-FE is made up of multiple self-monitors that operate independently. The output results of each self-monitor are linked in a channel to create integration. As a loss function sample, it overcomes the imbalance between positive and negative examples, speeding up model convergence. We utilize the weighted average approach to arrive at the total loss value of the network.

In order to determine how many channels there are on a feature map, use Equation 8 to calculate the number of channels.

$$w \in q^{z \times G \times E} \quad (8)$$

A two-layered reduced transform embedding process can be demonstrated using equations 9 and 10 because two reduced transform layers are used.

$$D \in q^{\frac{GE}{R^2} \times z} \quad (9)$$

$$M \in q^{\frac{GE}{R^2} \times z} \quad (10)$$

Based on the statement explained in Equations 11, 12, and 13, according to estimates, each self-monitor output result is then combined into a channel in order to maximize the integration effect of the output results to the greatest extent possible.

$$Attention(r, D, M) = softmax\left(\frac{rD^T}{\sqrt{z}}\right) M \quad (11)$$

$$EMSA = Conv\big(concat(head_1, head_2, \dots, head_h)\big) \quad (12)$$

$$head_i = Attention(r, D, M) \quad (13)$$

The equation 14 is capable of effectively calculating the sampling loss function and the imbalance between positive and negative sampling can be addressed as a result of this equation.

$$K_{Dice} = \frac{2|M_{seg} \cap M_{gt}|}{|M_{seg}| + |M_{gt}|} \quad (14)$$

Compute the Hausdorff distance loss function in Equation 15.

$$\left(W_{seg}, B_{gt}\right)_{HD} = max\left[\max_{w \in W_{seg}} \min_{b \in B_{gt}} \|W - B\|, \min_{b \in B_{gt}} \max_{w \in W_{seg}} \|B - W\|\right] \quad (15)$$

As shown in Equation 16, the weighting parameters are calculated using the total loss function to equalize different loss terms.

$$K_{seg} = \lambda K_{Dice} + (1 - \lambda) K_{HD} \quad (16)$$

Using Equations 17 and 18, we can get a total loss value for the entire network by using a weighted average calculation that utilizes the entire network value.

$$\mathrm{K}_{\mathrm{total=K1_{seg}+ConsineDecay\left(K2_{seg}+K3_{seg}+K4_{seg}\right)}} \quad (17)$$

$$Decay = \frac{1}{2}\left(1 + cos\left(\frac{T\pi}{t}\right)\right)\alpha \quad (18)$$

Let's assume w-encode, q-input feature map, c-convolutional, G, and E-spatial height and width. r - query, D - key, v - value, R2 - kernel size, k - loss value, Mseg -

denotes the predicted segmentation; Mgt - labeled segmentation, Wseg, Bgt - denotes prediction surface is represented as a set of point sets corresponding to the ground truth; λ - weighting parameters; There is a relationship between the second-term weight and cosine decay. T is the current step; t is the number of steps in the entire training; α - initial weight. There is a weighted average method that can be employed to balance out the various loss items found in a given network in order to calculate the overall loss value for the entire network.

3.4. Chi-squared Based on Mutual Information Gain (Chi2-MIG)

This feature selection method based on Chi2-MIG calculates predictive ability by classifying the dependent variable and removing redundant features. When analysing clinical data, it is essential to identify the most significant risk factors. The process involves eliminating unnecessary elements, ensuring data consistency, shortening training time, and enhancing prediction accuracy. As a result, various techniques for choosing desirable characteristics and eliminating less significant ones have gained popularity. The Chi2-MIG approach identifies the most beneficial features. Implementing efficient feature selection techniques allows for accurate predictive models while removing less valuable attributes. Additionally, information not directly related to the target variable can also be analysed. As a result, these properties can also increase the computational costs of the model, preventing it from achieving optimal performance.

This method of analysing information is based upon Equation 19, statistical correlation measures the relationship between two variables based on how they interact with each other and is calculated by an equation.

$$IG(W|B) = G(W) - H(W|B) \tag{19}$$

In order to calculate the entropy of the target variable across all the variables in a dataset, such as entropy and conditional entropy, we need to fit an equation, as shown in equation 20, to each variable in the dataset.

$$G(W) = -\sum_{w \in W} J(W) \log_2(w) \tag{20}$$

Based on equation 21, the purpose of determining if there is a correlation between the information acquired and the later conclusions and the target variable based on the information gain equation.

$$G(W|B) = -\sum_{w \in W} J(W) \sum_{b \in B} J(W|B) \log_2\big(J(w|b)\big) \tag{21}$$

Using Equations 22 and 23 to determine the marginal distribution and the joint distribution due to mutual information, multiply the marginal distributions as specified in each equation.

$$W_z^2 = \sum \frac{(e_a - F_a)^2}{F_a} \tag{22}$$

$$a(W;B) = \int_W \int_B J(W,B) \log \frac{J(W,B)}{J(W)J(B)} dWdB \tag{23}$$

By removing unnecessary elements, equations 24 to 28 evaluate subsets that contain essential features. These subsets can be analysed to identify patterns and make predictions. They can also be used to filter out irrelevant information and find the underlying structure of a set of data. Finally, they can be used to test hypotheses and measure prediction accuracy.

$$\lambda_1 = \{\epsilon_E\} - [\varepsilon_{correlation} \tag{24}$$

$$\varepsilon_E = \{W | W \in Chi^2 \cap MIG\} \tag{25}$$

$$\varepsilon_{correlation} = \{W | W \varepsilon \, High \; correlation \; in \; features\} \tag{26}$$

$$Chi^2 = \{a | a \; important \; feature \; found \; from \; the \; Chi^2 \; test\} \tag{27}$$

$$MIG = \{a | a \; important \; feature \; found \; from \; the \; MIG\} \tag{28}$$

Pearson's correlation matrix is calculated in Equation 29. Basically, it is a measure of how strongly two variables are associated with one another. Pearson's correlation matrix can be used to identify relationships between variables and test hypotheses about relationships.

$$R = \sum \frac{(W_a - \widehat{W})(B_a - \hat{B})}{\sqrt{\sum (W_a - \widehat{W}) \sum (B_a - \hat{B})}} \tag{29}$$

Using Equation 30 as a basis for determining the model's constant values is the method that was used.

$$\omega = \frac{(\mu - \nu)}{\phi} \tag{30}$$

Let's assume w and B are two variables: the G-entropy variable, J - potential value, z -degree of freedom, e - observed value, F - expected value, $J(w|b)$ - density function, λ_1- impart feature subset, R - correlation matrix, ω - omega, μ - Mu, ν - Nu, ϕ - Phi variant. In this category, we eliminate redundant features by providing a subset of essential elements.

3.5. Optimal Fuzzy Deep Neural Network (OFDNN)

This proposed OFDNN method can detect and determine PKD or non-PKD based on classifiers. Among these, inflammatory processes in PKD have been implicated in disease, cachexia, and renal osteodystrophy. However, PKD also increases stroke risk. To ensure accuracy during the PKD process, the OFDNN is carefully managed and monitored. Using a predictive model, we can calculate strength and endurance values. This approach, which utilizes the latest advances in DL and predictive modelling, has the potential to lead to new solutions in OFDNN.

As illustrated in equation 31, here is a description of an equation for evaluating a fuzzy rule unit based on a set of fuzzy rules and the organization of those rules.

$$Y'(D) = d(y(D), h[D, D+1]) \quad (31)$$

Input data is processed in accordance with Equations 32 and 33 and then evaluated using the output data.

$$h = R_a x_a, a = 1{,}2 \quad (32)$$

Equation 33 shows the evaluation of the fuzzy logic output based on the fuzzy logic input

$$FL = h_1 + h_2 = R_1 D_1 + R_2 D_2 \quad (33)$$

Using Equation 35, it is shown that the sigmoid function can be calculated using the neuron's work transfer.

$$y = o(FL) = o(R_1 D_1 + R_2 D_2) \quad (34)$$

Using equation 36, it is possible to determine the entry points and the spectrum available for data transmission.

$$R_a^h = \alpha_a r \log\log\left(1 + \left|h_{a,x}\right|^2 W_{a,x} h^{-x}\right) \quad (35)$$

Calculate the efficiency of the data transmission in the data link model as shown in equation 36 by using data transmission efficiency.

$$d_a^D = \beta_a V \log\log\left(1 + \frac{|h_{x,a}|^2 W_x h^{-v}}{\sigma^2}\right) \quad (36)$$

As shown in Equation 37, different geographical regions will have different delays in finishing jobs due to a variety of factors.

$$W_a^x = \frac{h_a}{h_a^D} \quad (37)$$

Equation 38 can be used to calculate the cumulative time delay between the two events.

$$h_a^y = \sum_{y \in h} (1 - \alpha_a) h_a^y \quad (38)$$

Using Equation 39, we can calculate the information that arrives at the neuron using the coupling described in this equation.

$$h_a^x = \frac{y_a}{h_a^x} \quad (3)$$

To determine the relationship between the amount of received information and the network performance of data transmission, refer to Equation 40 and calculate the bandwidth-delay time ratio.

$$h_a^x = \frac{h_a}{V_a^D} \quad (40)$$

Calculate the proportional value of server computation time to data volume and server computing power, as shown in Equation 41.

$$v_a^o = \frac{o_a}{w_a} \quad (41)$$

In order to calculate the time, it takes to upload tasks assigned to the network edge, you must plug the value into Equation 42.

$$R_a^x = R_a^z + R_a^G + R_a^o \quad (42)$$

Using equation 43, we estimate the time delay associated with offloading tasks on the edge device as a function of time.

$$w_a^x = \sum_a^x (\alpha_a \, d_a^x) \quad (43)$$

The pulse rate calculation is shown in Equation 44 as a clinically significant indicator of psychological, physical, and behavioral health as well as general well-being.

$$minh = \sum_{a=1}^x (h_z^a + d_a^x) \quad (44)$$

This equation evaluates the output voltage of a 5-volt direct supply according to equation 45.

$$R.T.O1: \sum_{G_{a \in d}} y_a \leq y_w \quad (45)$$

Based on the fuzzy logic system structure in Equation 46, it can be seen that the calculations are enhanced by using fuzzy logic systems.

$$O2: \sum_{h_{a \in d}} \alpha_a \leq 1 \quad (46)$$

This equation shows an improved method for evaluating firms based on information and fuzzy decision-making based on equation 47.

$$O3: \sum_{h_a \in d} \beta_a \leq 1 \quad (47)$$

According to Equation 48, the delay time for an energy field decreases by a given percent, corresponding to a higher intensity.

$$O4: y_a^x > 0, \forall a \in d \quad (48)$$

This equation calculates strength and endurance based on equation 49.

$$d_a = \frac{1}{h_a} \quad (49)$$

Let's assume Y' (D) - fuzzy rule unit, d(y(d)) - gains a unit, d - denoted value, Ra - signal, xa - large number of materials, d+1 - framework condition, a - access to internet bandwidth, R_a^h – web access transmit, ha,x - scaling factor between access point and terminal, terminal products, h-x - node facility distance, v - represent loss, σ2 - noise level, h_a^x - capacity of the terminal, ha - information process, Ra - Uploading task, O1 to O4 - input data panel, O -sigmoid function, O(B) - work transfer sigmoid function, βa - Fraction of power transmission. In this category, we use a fuzzy decision-making process to assess entities. The predictive model calculates strength and tolerance values by evaluating the decrease in energy field delay time linked to high intensity.

4. Result and Discussion

This research developed a model using data from different scenarios. To achieve accuracy in the PKD process, we collected the necessary datasets from Kaggle. We then verified the accuracy of the missing values and selected the features by computing the average total loss value. In addition, we are exploring promising methods to enhance classifier accuracy based on the proposed approach. These can be evaluated using the Python programming language in a Jupyter notebook with the correct precision.

Table 1. Simulation Model

Simulation	Value
Dataset Name	PKD
No of Records	1100
Training	854
Testing	246
Language	Python
Tool	Jupyter

Using the Python language-based Jupyter Notebook can improve the accuracy of the total score estimation of the dataset given in Table 1 on the training and test data.

4.1. Evaluation of Matrix

To determine the accuracy of our model, we set the PKD category value as positive and the PKD or non-PKD category value as negative. We then optimized the confusion matrix and evaluated performance based on True Positives (TrPo), True Negatives (TrNe), False Positives (FaPo), and False Negatives (FaNe). If a specimen was correctly classified as PKD, it was considered a True Positive (TrPo). When the test correctly determines a PKD sample, it is called a True Positive (TrPo). However, the FaNe test shows that some PKD samples were misclassified. The test could not accurately identify FaPo, PKD, or non-PKD samples. Only TeNa samples were accurately identified.

$$\text{Accuracy} = \frac{TrPo+TrNe}{TrPo+FaNe+TrNe+FaNe} \quad (50)$$

$$\text{Precision} = \frac{TrPo}{TrPo+FaPo} \quad (51)$$

$$\text{Recall} = \frac{TrPo}{TrPo+FaNe} \quad (52)$$

$$\text{F-Measure} = 2 * \frac{Precision*Recall}{Precision+Recall} \quad (53)$$

$$\text{Specificity} = \frac{TrNe}{TrNe+FaPo} \quad (54)$$

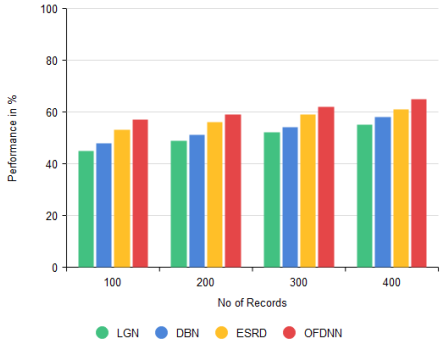

Fig 3. Analyse of Precision Measurements

Figure 3 shows that the proposed OFDNN method enhances accuracy. This means that other LGN, DBN, and ESRD techniques discussed in the literature review can be compared to the suggested OFDNN method. This will provide better than 65% accuracy in PKD analysis. Out of all the methods, the proposed method has shown the most significant improvement in accuracy.

Figure 4 demonstrates multiple studies aimed at improving recall accuracy in PKD analysis. It was determined that the proposed method would be accurate by evaluating the PKD dataset. In comparison to other methods that have been studied in the literature, DBN, LGN, and ESRD had the lowest accuracy of 51%. The proposed method's accuracy was the highest among the other methods. However, the OFDNN method achieved 78% accuracy in recall content analysis.

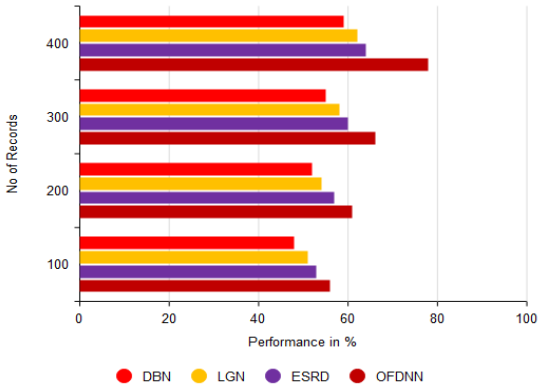

Fig 4. Analysis of Recall

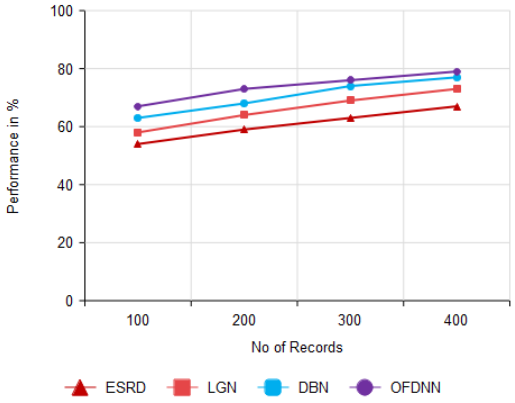

Fig 5. Analysis of F-Measure

Figure 5 shows that the accuracy of the OFDNN method proposed can be enhanced through F-measure analysis. Upon comparing the performance of ESRD, LGN, and DBN methods from literature analysis with the OFDNN method proposed in F-Measure, it is clear that the accuracy has been 79% improved.

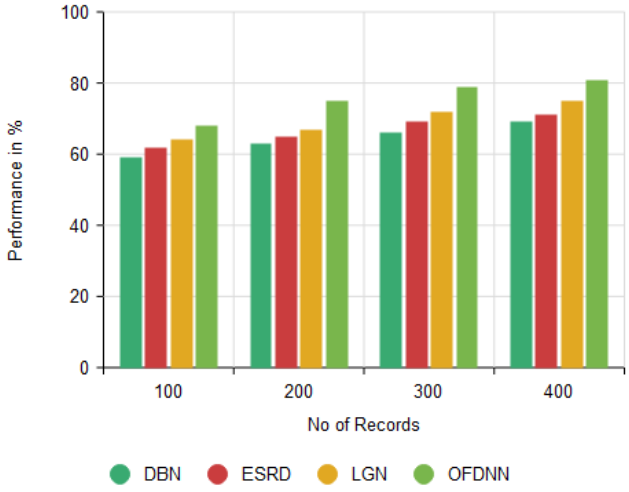

Fig 6. Analysis of Specificity

Figure 6 shows that PKD detection can be accurately achieved with high specificity. However, when using the ESRD, DBN, and LGN methods analysed in the literature, the specificity accuracy can be as low as 59%. Using the proposed OFDNN method for testing, feature analysis accuracy increased to 81%.

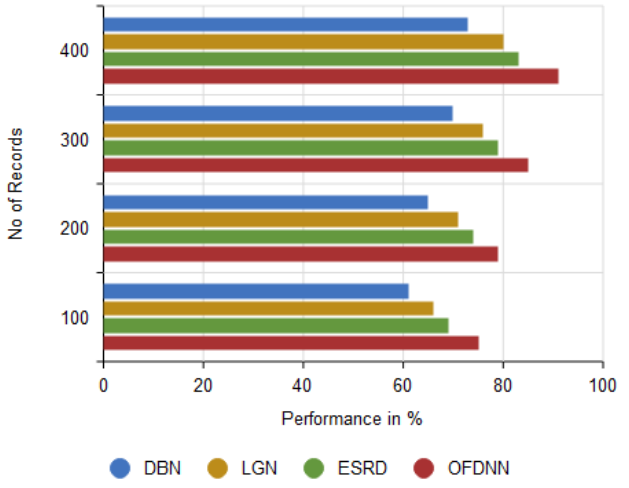

Fig 7. Analysis of Accuracy

Figure 7 illustrates that the proposed OFDNN method has been tested using the DBN, ESDR, and LGN methods found through literature analysis. This has been done to enhance accuracy. As a result of using these methods, the accuracy of the proposed OFDNN method has improved to 91% compared to other methods.

5. Conclusion

This approach utilizes DL algorithms to predict PKD by identifying crucial risk factors for early detection. The method involves employing the proposed OFDNN approach and Chi2-MIG feature selection techniques and implementing the EMS-FW method to determine their feature weights. Pre-processing is also performed to ensure missing value accuracy based on DL models. This research aims to devise a technique for discovering fresh solutions by utilizing the suggested OFDNN method. Firstly, we conducted a pre-processing step on the PKD dataset to guarantee missing values accuracy. Following this, we employed the EMS-FW method to determine the average feature weight of the total loss value. We then evaluated the predictive ability of the dependent variable by utilizing the Chi2-MIG method and eliminating redundant components. This was done to select features for this analysis. Lastly, we implemented the OFDNN classification method, which enabled detection and prediction of PKD or non-PKD kidney disease. The results of these can determine the model's accuracy using TP, TN, FP, and FN. This is done by setting the PKD type value as positive and the PKD or non-PKD type value as negative. The OFDNN method proposed has shown an improved accuracy rate of 91% in detecting and predicting PKD. OFDNN exhibits the highest level of accuracy among all classification algorithms based on the results of all experiments. This proves that using advanced DL techniques can benefit clinical decisions.

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