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Smart Diagnostic Model for Chronic Kidney Disease Using Deep Neural Networks

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Abstract

Kidney disease is reported to be the 13 leading causes of death globally, affecting about 10-15% of the global population. Early detection of chronic kidney disease is highly needed to enable clinicians and healthcare providers to be able to mitigate the negative effects it has on patients' health. This study explores the use of predictive models such as the Artificial Neural network in bridging this gap by detecting chronic kidney disease using various physiological variables. The study employed a public dataset from southern India, comprising 25 predictor variables and one target variable that relates to kidney disease diagnosis. It was then analyzed using various statistical approaches, and it uncovers an associating between chronic kidney disease in older patients and a significant correlation between the majority of the physiological features and the diagnosis outcome. The correlation analysis specifically identified strong negative and significant (p-value < 0.05) relationships across factors like specific gravity, hemoglobin levels, packed cell volume, and red blood cells with the diagnosis class. A strong positive and significant relationship was observed between albumin, serum creatinine, and diabetes mellitus with the diagnosis outcome. The proposed model outperformed previous machine learning predictive approaches explored by related authors, with an exceptional performance metrics output of 100% accuracy, specificity, precision, and negative predictive value (NPV) on both training and the unseen (test) datasets. The model kappa score (1.0), and McNemar's Test value (p-value < 0.01) also review the minimal deviation between the ANN

predicted diagnosis classes and the actual disease class. These result findings further show the significance of ANN in driving an optimized approach supported by adequate clinical data in assisting clinicians to make good decisions relating to kidney disease.

Keyword: Chronic Kidney Disease Prediction, Machine learning, Artificial Neural Network (ANN)

1.0 Introduction

Chronic Kidney disease can be described as a non-communicable disease that incapacitates the human body by preventing the passage of waste and fluids via urine, this has made it a major contributor to the mortality and morbidity rate of patients globally (Dibaba and Tilahun, 2022; Ramesh et al. 2022). According to a 23-year report that ranges from 1990 to 2013, it highlighted chronic kidney disease has 13 leading causes of death globally. An estimated population of 850 million people globally reported to have chronic kidney diseases and this could be attributed to factors like aging, hypertension, and diabetes (World Life Expectancy, 2020). Also, a WHO data review revealed that 20% of adults above 60 years are prone to have chronic kidney disease (Ramesh et al. 2022). It has been reported to be prevalent in developing countries where detection, prevention, and treatment are low due to low income (George et al. 2017). Kidney Disease is a serious public health issue in Nigeria which has a discontinuation of dialysis, it is reported that 25 million people have kidney disease (Kidney Disease Nigeria, 2025). Chronic Kidney failure which leads to a reduction of the Glomerular Filtration Rate (GFR) is progressive. Factors such as blood shortage supplies to the kidney, which leads to the hampering in the flow of urine that triggers prostrate, or injuries in the kidneys are associated with chronic kidney disease. The National Kidney Foundation classifies chronic kidney disease into five stages based on kidney functions, stating that stages 1 & 2 are mild stages with few symptoms with stage 5 being total kidney failure. The high cost of Renal Replacement treatment for total kidney failure is expensive mostly in developing countries like Nigeria. Stanifer et al. (2014) and AbdElhafeez et al. (2018) stated issues like shortages in health personnel, poor facilities, and poor health insurance policies. Hence, early detection of chronic kidney disease is crucial in reducing the disease progression and decreasing associated complications. Researchers over the decades have explored different approaches for meeting this gap in the early detection of chronic kidney disease, among these approaches is a predictive analysis approach using Traditional Machine learning and Deep learning algorithms. Agrawal et al. (2018) stated that this approach is efficient for early detection and timely interventions. This study's main objective is to develop an artificial neural network architecture capable of detecting the early stages of chronic kidney disease. This neural network which shares a similar working principle with the human brain, has been reported to be able to uncover patterns and trends from data efficiently (Yadav et al., 2020; Joseph et al. 2024). The structure of this study includes Section 2.0 which explores the machine learning approaches and their performance from recent studies, Section 3.0 explores the data preprocessing and machine learning algorithm evaluating the study objectives, Section 4.0 focuses on the findings and

interpretation of the results, Section 5.0 Discusses this significance results with relation with recent works, and Section 6.0 discusses the conclusion of this study.

2.0 Related Studies

Ala Kamal R. (2024) used an artificial neural network in detecting chronic kidney disease. The author attained an accuracy of 98%, recall 100%, sensitivity of 1.0, specificity of 100%, and precision of 1.00. Madhusree et al. (2021) utilized the use several supervised Machine learning algorithms in modelling kidney disease. The study reviewed that Random Forest and Extra Trees classifier were efficient models for predicting kidney disease with an accuracy score of approximately 99.36%. Islam et al. (2023) explored a feature selection approach that integrated the use of principal component analysis in selecting the optimal physiological features for predicting kidney disease diagnosis. The explored 12 traditional machine learning algorithms for this use case, and concludes that XGBOOST was more precise and robust with an accuracy of 99.2%. Similarly, Ramesh et al. (2022) explored a feature selection process that integrated Re-cursive Feature Elimination (RFE) and Chi-Square test feature-selection techniques with several Machine learning algorithms. The study results reviews that the Logistic regression + Chi-Square test feature-selection techniques had the highest accuracy of 98.75%. A wrapper approach was integrated alongside several supervised algorithms to streamline the features used in predicting kidney disease (Panwong et al. 2016). The study stated that KNN and Naïve Bayes integrated using wrapper attained a high accuracy of 85%. Pratibha et al. (2019) integrated Decision stump, Rep tree, IBK, K-star, SGD, and SMO in predicting chronic kidney disease. They concluded that the Decision stump, and Rep tree were superior with an accuracy score of 99.3% and a kappa statistic of 0.984, indicating the model capacity to generalized well over the test dataset. Sharma et al. (2018) attained an accuracy of 98.60% and precision score of 100% using tree-based model called the decision tree in predicting the chronic kidney disease. While, Afia et al. (2023) attained 99% accuracy score and 100% precision score using a Light GBM in detecting chronic kidney disease.

3.0 Methodology

3.1 Kidney Disease Dataset Description

This study utilized a publicly available kidney disease dataset in the Kaggle database. The dataset was made up of 400 patients with diagnosis reports from southern India, with 150 with chronic kidney and 250 testing negatives. This dataset includes 25 features, which include a target variable that determines the patient's diagnosis status. Also, 41.7% of the dataset was collected from various blood tests, 29.15% was collated from urine tests, and 29.15% of the dataset features related to scientific factors that caused chronic disease.

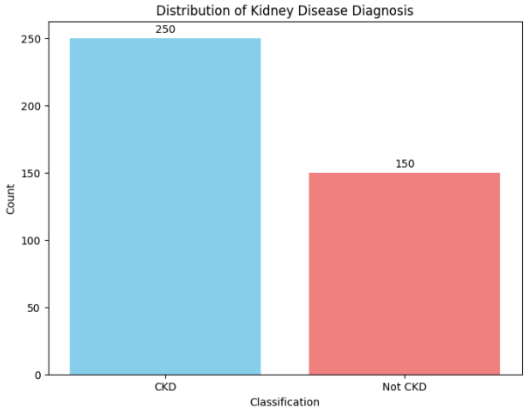

Figure 1: Kidney Disease Distribution

Table 1: Kidney dataset description

Features	Description	Feature type
age	Age	Continuous
bo	Blood pressure	Continuous
sg	Specific gravity	Continuous
al	Albumin	Nominal
su	Sugar	Nominal
rbc	Red blood cells	Nominal
pc	Pus cell	Nominal
pcc	Pus cell clumps	Nominal
ba	Bacteria	Nominal
bgr	Blood glucose random	Continuous
Bu	Blood urea	Continuous
sc	Serum creatinine	Continuous
sod	Sodium	Continuous
pot	Potassium	Continuous
hemo	Hemoglobin	Continuous
pcv	Packed cell volume	Continuous
wc	WBC count	Continuous
rc	RBC count	Continuous
htn	Hypertension	Nominal
dm	Diabetes mellitus	Nominal
cad	Coronary artery disease	Nominal
appet	Appetite	Nominal

pe	Pedal edema	Nominal
ane	Anemia	Nominal
classification	Diagnosis of kidney disease	Nominal

3.2 System Architecture

The Chronic Kidney dataset was cleaned and preprocessed to improve the quality and consistency of the dataset (Adekunle et al., 2024). The data was evaluated for missing values and outliers. The missing datapoints were address by using modal approach for the categorical features and a median approach for the numerical features. The categorical features were encoded using the Python map function using nominal scale values of 0 and 1 all the binary factored features in the study. Also, the outliers in the continuous features were evaluated and replaced using the median value of the respective features. For training of the neural network, the features are separated into the predictor variables set made of 25 features and a single target variable. The predictor variables are normalized to boost the training and improve the results of the neural network (Qingjiu & Shiliang, 2017). This was done using the Standard Scaler function in the Scikit-learn preprocessing library. The features are to normalize the predictor variables using the Standard Scaler function in Python. The target variable class balance was addressed using the class weight function from Scikit-learn library to prevent overfitting and bias during the training and testing process (Sihao et al. 2022). This reweighting method assigned more cost to the minority class (Not Chronic Kidney Disease) than the majority class (Chronic Kidney Disease) (Kaidi et al. 2019; Yin Cui et al. 2019). For this study, we employed a train, validation and test split ratio of approximately 80:10:10 to assess the generalization of the model. The trained model is evaluated using selected metrics to validate its performance. The Python libraries used in fitting the neural network models and evaluating its performance includes *Tensorflow, Scikit-learn, Numpy* and *Pandas*. Figure 2.0 shows the overall system work flow for the proposed model.

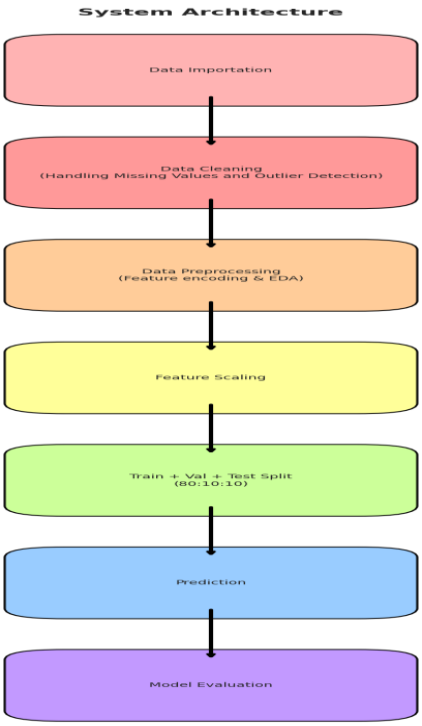

Figure 2.0: The System work flow for the smart chronic Kidney Disease Model

3.3 Artificial Neural Network

The input layer of the ANN is made of 25 features represented by a vector with a length equal to the patient's kidney disease diagnosis records. Each of these features are assigned weights randomly and a bias is initialized for the training process. The neural network used in this study is made up two hidden layers with one output layers. The weight and bias for the first layer are w^I, b^I . The 128 neurons in the first layers performs a sum operation of the input features adding bias, after which is passed through a non-linear activation called ReLu activation function.

$$x = [age_1, bo_2, sg_3, \ldots\ldots, ane_{25}]^T$$

$$Z^1 = xw^1 + b^1 \quad ------1$$

$$ReLU(z) = max(0, z) \quad ------2$$

$$a^{(l)} = ReLU\left(z^{(l)}\right) = \left(0, W^{(l)} a^{(l-1)} + b^l\right) \quad ------3$$

Where $a^{(l)}$ is the activation function, and l is the layer index. This process is repeated for the two hidden layers made up of 64 neurons and 32 neurons respectively. The output layer of the network was initialize as a single neuron with a sigmoid activation used for predicting the probability of score $\hat{y}$ of binary classification (ckd, notckd). This represented mathematically using equation 4 below:

$$\hat{y} = \sigma\left(Z^{(4)}\right) = \frac{1}{1 + e^{-Z(4)}} \quad -----4$$

Where $Z^{(4)} = W^{(4)}a^3 + b^4$ is the linear combination of both the sigmoid function and the output of the final hidden layer $Z^{(3)}$. This study used a binary cross-entropy function presented in equation 5.0 in minimization of the training loss.

$$L(\hat{y}, y) = -[y * log\ log\ (\hat{y}) + (1-y) * log(1-\hat{y})] \text{ ------ } 5$$

Where y is the true label (0 or 1). To update the weights and bias during the training process so as to minimize the loss we use a process known as back-propagation. This process estimates the gradient of the loss using chain rule formula, updating the weights and bias at each layer along the network. An Adam optimizer was used in this study to control the learning rate. The gradient at the output layer is computed using:

$$\frac{\partial \sigma(z)}{\partial z} = \sigma(z) * \big(1 - \sigma(z)\big) - - - -6$$

The gradient w.r.t the activation function is defined as

$$\frac{\partial Relu(z)}{\partial z}\{1\ if\ z > 0\ 0\ if\ \leq 0\ - - - -7$$

The gradient w.r.t the loss is defined as:

$$\delta^{(4)} = \hat{y} - y - - - -8$$

This loss is propagated backward through each layer to update weights and bias using the gradient descent for learning rate α.

$$W^{(l)} \leftarrow W^{(l)} - \alpha \frac{\partial L}{\partial W^{(l)}} - - - -9$$

$$W^{(l)} \leftarrow W^{(l)} - \alpha \frac{\partial L}{\partial b^{(l)}} - - - -10$$

3.4 Model Performance Metrics

To evaluate the performance of the neural network classification algorithm used in this study, several statistical metrics were utilized. These metrics includes Accuracy, Sensitivity, Specificity, Precision, Negative Predictive Value, Balanced Accuracy, Number of Information Rate (NIR), Detection Rate, and McNemar's Test P-value.

Table 2: Performance metrics and description

	Description	Formula
Accuracy	This is the ratio of correct prediction to the total number	$\frac{TP + TN}{TP + TN + FP + FN}$

	of class instances made by the classification model	
Sensitivity	This measures the ratio of positive instances that actually identified as positives.	$\frac{TP}{TP+FN}$
Specificity	This measures the ratio of negative instances that actually identified as negatives.	$\frac{TN}{TN+FP}$
Precision (PPV)	This measures the ratio of positive instances that are actually true positive.	$\frac{TP}{TP+FP}$
Negative Predictive Value (NPV)	This measures the ratio of patients predicted as not having chronic disease that are actually not diagnose with the disease ().	$\frac{TN}{TN+FN}$
Balanced Accuracy	This measures the mean proportion of the correctly identified classes (Brodersen et al. 2010).	$\frac{Specifity+Sensitivity}{2}$
No Information Rate (NIR)	This measure evaluates the precision of the model in always detecting the majority class (ckd).	
Kappa Statistic	This measures the alignment between the predicted class and actual class label (Jorge et al. 2020).	$\frac{p_o-p_c}{1-p_c}$
Detection Rate	This estimates the ratio True positive cases detected to the total number of diagnosis instances present in the dataset (Jabbar et al. 2017).	$\frac{TP}{Total}$
McNemar's Test P-Value	This statistical test evaluates the disagreement rate of the	

	binary classification model. If the probability value of the test is ≥ 0.05 will conclude no bias towards any class.	

TN= True Negative, TP = True Positive, FN = False Negative, FP = False Positive, p_o=the proportion of observed agreement.

4.0 Result Findings

This section of this study focuses on exploratory statistical carried out on the chronic kidney disease dataset and the model performance report in predicting the chronic kidney disease across the selected metrics stated in this study. Figure shows the dataset

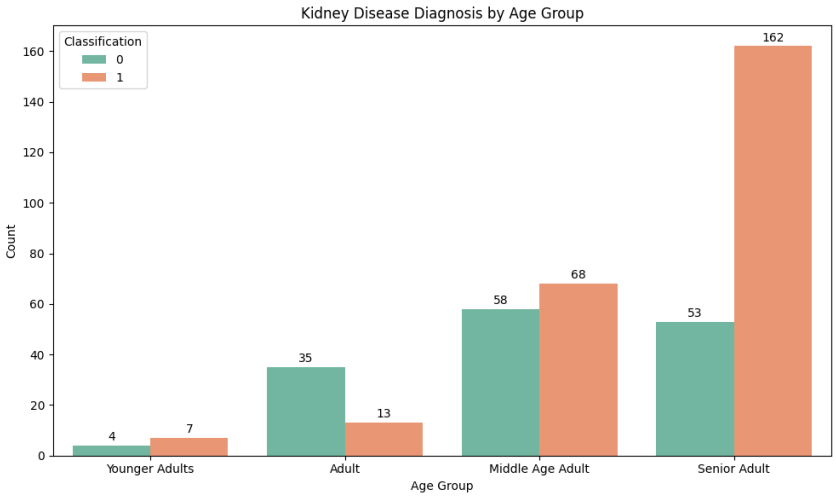

Figure 3.0: Distribution of the kidney disease diagnosis by age group

Figure 3.0 shows the distribution of chronic kidney disease across different age groups. It reviews that senior adult shows higher chances of having kidney disease followed by middle-aged adults. The lowest counts of individuals with kidney disease were observed in children and teenagers. This reflects that older people show higher chances of having chronic kidney disease [1]

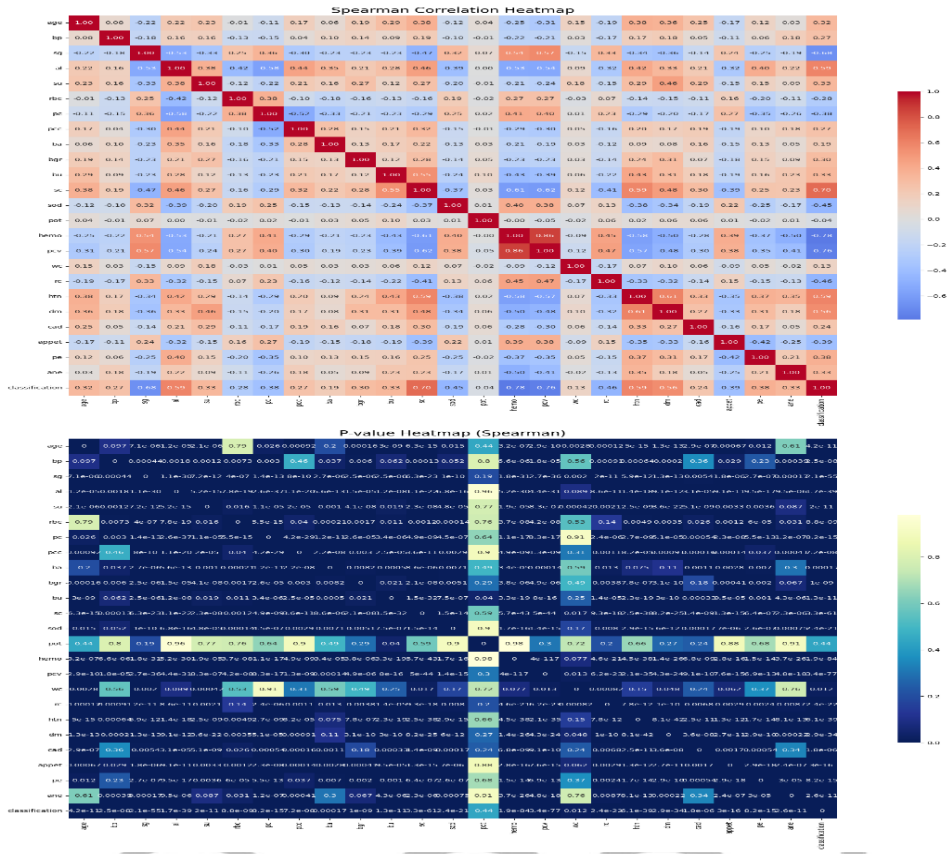

Figure 4.0: Correlation Plot

Figure 4.0 shows the correlation plot which shows the linear relationship between the predictor variables and the target variable. For this study we considered only variables with correlation within the scale of -0.5<r<-1 or 1< r < 0.5 as strongly correlated. The following features which include age, bp, su, pcc, ba, bgc, bu, wbc, coronary artery disease presence, pe, and ane all show a weak positive and significant (p-value< 0.05) correlation with kidney disease (0.32, 0.27, 0.33, 0.27, 0.19, 0.30, 0.33, 0.13, 0.24, 0.38, 0.33). While, rbc, pc, pot, sod, appet and red blood cell all shows a weak negative and significant (p-value < 0.05) relationship with the kidney disease, except pot which relationship was not statistically significant (-0.46, -0.38, -0.01, -0.04, -0.45, -0.39, -0.28). At the same time, alb, sc, and dm were observed to have a strong positive and significant (p-value < 0.05) with kidney disease (0.59, 0.70, 0.56), while sg, hemo, and pcv have a strong negative and significant (p-value < 0.05) relationship respectively (-0.68, -0.78, -0.76, -0.61).

Table 3: Summary statistics of chronic kidney disease diagnosis continuous features

	Kidney Disease	Average	Min	Max	Standard Deviation
age	notckd	46.57	12.000	80.000	15.59
	ckd	56.53	11.00	90.00	13.87

bgr	notckd	108.25	70.00	140.00	18.37
	ckd	128.52	70.00	220.00	33.02
bp	notckd	71.47	60.00	80.00	8.54
	ckd	77.08	60.00	90.00	9.18
bu	notckd	33.17	10.000	50.00	11.36
	ckd	48.76	1.50	113.00	23.64
hemo	notckd	15.09	12.65	17.80	1.35
	ckd	11.09	5.50	16.10	2.03
pcv	notckd	46.17	40.00	54.00	4.21
	ckd	35.44	19.00	52.00	6.18
pot	notckd	4.34	3.30	5.00	0.58
	ckd	4.37	2.500	47.000	0.55
rc	notckd	5.35	4.40	6.50	0.59
	ckd	4.64	3.70	5.60	0.36
sc	notckd	0.88	0.400	1.30	0.26
	ckd	1.90	0.5	5.30	1.01
sod	notckd	141.61	135.00	150.00	4.78
	ckd	136.95	126.00	147.00	3.41
wc	notckd	7719.33	4300.00	11000.00	1797.12
	ckd	8174.00	3800.00	12800.00	1714.71

Based on the results in Table 3.0, those with chronic kidney disease are older on average (54.53 years) compared with those without kidney disease (46.57 years). This result is consistent with the findings reviewed using Figure 2.0. Additionally, patients diagnosed with kidney disease were observed to show higher mean blood glucose levels (128.52 vs 108.25), blood pressure (77.08 mmHg vs 71.47 mmHg), blood urea (48.76 vs 33.17), potassium level (4.37 vs 4.34), serum creatinine (1.90 vs 0.88), and WBC count (8174.00 vs 7719.3). On the other hand, lower hemoglobin levels were noticed for patients with chronic kidney disease (11.09 vs 15.09).

Table 4: Model evaluation result

Metrics	Train	Test	All
Accuracy	1.0000	1.0000	1.0000
95% CI	(0.9881, 1.0000)	(0.9124, 1.0000)	(0.9894, 1.0000)
Kappa	1.0000	1.0000	1.0000
Sensitivity (TPR)	1.0000	1.0000	1.0000
Specificity (TNR)	1.0000	1.0000	1.0000
Precision (PPV)	1.0000	1.0000	1.0000
NPV	1.0000	1.0000	1.0000
Prevalence	0.625	0.625	0.625
Detection Prevalence	0.625	0.625	0.625
Balanced Accuracy	1.0000	1.0000	1.0000
Number Information Rate	0.625	0.625	0.625
Detection Rate	0.625	0.625	0.625
P-Value [Acc > NIR]	4.80e-66	6.84e-09	3.29e-74
McNemar's Test P-Value	1.0000	1.0000	1.0000

The model performance metrics in Table 4.0 show that the model accuracy on train, test, and all (train+test) was 100% showing the model has a high generalization capacity. Also, the 95% confidence for the accuracy shows that the confidence bound for the train and train+test was a bit narrow between >0.98 to 1.0, while the test shows a wide range which could be attributed to its sample size. The kappa statistics show that the model-predicted instances align with the actual instances in this study. The sensitivity, specificity, precision, and NPV all aligned, indicating the model's capacity to accurately predict the disease status of each individual. The prevalence, detection prevalence, and detection rate all aligned, indicating that there is no bias in the prediction process aligning with the Balanced accuracy of the model. The NIR indicated that the model significantly outperforms random chance (62.5%, p-value< 0.01). The McNemar's Test value which was 1.000 across all sets, indicated that there is no difference in residual rates of the two classes predicted by the ANN model in this study.

5.0 Discussions

This study provides credible insight relating to the predictive capacity of Neural Networks in predicting chronic kidney disease using various clinical factors. The initial exploratory statistical analysis displayed in Figure 3.0 indicates a prevalence of renal failure with an increase in age, particularly in older adults. This was also consistent with results presented in Table 2.0 which shows that on average chronic kidney diseases are associated with older patients (54.56 years). This result was consistent with findings made by Ramesh et al. (2022), who also stated that this prevalence is associated with patients with pre-existing cases of high blood pressure (HBP) or diabetes mellitus (DM). Other factors such as bg 167.15, bp (79.64 mmHg), bu (70.80), pot level (4.72), sc (4.27), and wbc (8646) were observed to be associated with chronic kidney disease on an average. Figure 4.0 displays the correlation analysis results between the target variables and physiological features. It reviews that features such as age, bp, su, pcc, ba, bgc, bu, wbc, cod, pe, and ane all show a weak positive and significant (p-value < 0.05) relationship with kidney disease. Though this relationship was observed as weak, but still indicates that an increase in these factors is associated with renal failures. Rbc, pc, sod, and appet all show a weak negative and significant (p-value < 0.05) relationship with the kidney disease, except the pot of which its relationship was not statistically significant. The potassium shared a weak negative relationship with kidney disease that was not statistically significant (p-value > 0.05). Additionally, alb, se, and dm were observed to have a strong and significant positive relationship with kidney disease. This indicates that patients with preexisting cases of dm, a higher ratio of alb in their blood, and se show higher chances of having chronic kidney disease. Sg, hemo, pcv, and red blood cell counts show strong and significant correlation values with chronic kidney disease, indicating a fall in any of these factors is associated with a higher chance of renal failure. The neural network performance displayed in Table 3.0 shows significant performance across all metrics. The model accuracy on train, test, and train + test had a perfect accuracy score of 1.0. Similar values were observed for Kappa, Sensitivity, Specificity, Precision, and NPV, indicating the model's capacity to predict the kidney disease

classes accurately. The model used in the study was superior in terms of accuracy compared to those used by Mohammed et al. (2019) (95.00%), Madhusree et al. (2021) (99.36%), Md. Ariful Islam et al. (2022) (98.33%), Ren et al. (2019) (92.7%), J.Qin et al. (2019) (99.7%), Ebiaredoh - Mienye SarahA. et al. (2017) (98.5%), Ramesh et al. (2021) (98.75%), Khamparia et al. (2020) (99.7%), Elias D. and Maria (2022) (99.20%); Pankaj et al. (2021), and Pankaj et al. (2021) (98.86%). While existing recent studies used similar data explored ML algorithms such as Logistic Regression, Decision Tree, Naive Bayes, Support Vector Machine, Bayesian Network, J48, AdaBoostM1, Stochastic Gradient Descent, Ensemble Learning, Rotation Forest, and others, the proposed approach achieved a high accuracy of 100%. This could be attributed to a more refined approach which includes employing feature encoding for the categorical features, feature scaling the predictor variables, and the use of class weighting to balance the target variable during the training process. This enables the model generalization well over the test dataset (Unseen data).

This study enables clinicians to be able to validate patients who need follow-up interventions and those who don't need them based on the neural network's high capacity to differentiate positive and negative cases by looking at the NPV values (See Table 3.0). It shows a reliable and accurate approach to early diagnosis approach that supports targeted interventions. This underscores the potential of effectiveness that comes with the integration of Artificial neural networks into healthcare systems for tackling chronic kidney disease.

The limitations observed in this study includes the generalization of the neural networks under other context which factors patients from a different geographical zone, selected physiological features used in the training and development of the model, also the exclusion of other critical factors that relates closely to the lifestyle of the actual patients. These factors, we believe, could increase the generalization of the model to cover more diverse cases if they are explored. We also recommend the retraining neural architecture using various feature selection approaches to streamline the model predictive attention to features that holds greater weight, use of (Big) larger dataset for training, the and exploration Advance Generative Artificial Intelligence[2] modelling techniques in improving the robustness of the model to perform under different technique clinical cases in relation to addressing kidney related issues of patients.

6.0 Conclusion

This study shows the efficiency of Artificial neural network in predicting chronic kidney disease using several clinical and physiological features. The exploratory statistical analysis reviews a trend between older patients having a high prevalence of kidney disease, and also significant (p-value < 0.05) relationship between the physiological variables and target variable. However, we noted the relationship between the potassium levels and kidney disease has not been statistically significant (p-value > 0.05). The proposed neural network was capable of generalizing well over the test data, with an accuracy of 100% across the train, test and (train + test) dataset. This balance could be attributed to use of rigorous data preprocessing

techniques employed in this study which includes evaluation of missing values, outlier detection, feature encoding, feature scaling and class weighting to address the distribution of the target classes. Also, we observed 100% across other metrics like sensitivity, specificity, precision, and negative predictive value. This proposed ANN architecture was able to outperform previously stated approaches used by various authors who utilize Supervised Machine Learning algorithms in predicting chronic kidney disease. In summary, the results demonstrate the potentials of predictive models like ANN in driving medical diagnostics, specifically in the early detection of chronic kidney disease. Its high precision can be supportive to clinicians in enabling them narrow cases that would require adequate follow up or intervention proactively. The adaptation of such a smart system into the healthcare workflows will be supportive in enabling clinicians detecting chronic kidney disease proactively, this will increase the robustness of healthcare centers in dealing with patients care. We advise healthcare policy makers, researchers, stakeholders and centers to drive more resources in the development of Machine learning driven systems for optimizing the care of kidney related diseases.

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