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Efficient Model to detect the kidney Disease through Deep learning

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Abstract: The improvement in various medical facilities has allowed the improvement in the life of a lot of individuals. This has also exposed people that are susceptible to certain illnesses that affect one of the core organs of the human body. This has been one of the most serious medical issues that have put a pressure on the health-care system in recent years. This is a troubling development that has resulted in more complications and deaths as a result of kidney disease. Due to the fundamental nature of these diseases, which necessitates comprehensive testing and diagnosis, these kidney disorders are particularly difficult to detect. The delay in receiving the results causes a delay in delivering prompt treatment to the patient, which is critical for kidney illnesses, as failure to do so can end in a lot of pain for the patient or even death. Therefore, an automatic approach for the diagnosis is needed to achieve prompt kidney disease detection through the use of machine learning methodologies. This research article describes a precise kidney disease detection mechanism that utilizes K Nearest Neighbor and Pearson Correlation along with Artificial Neural Network and Decision Tree. The experimental results indicate a positive performance for the detection that is highly satisfactory.

Keywords— Kidney Disease Detection, K-Nearest Neighbors, Artificial Neural Network, Decision Tree.

I. INTRODUCTION

The global health program of the 21st century is threatened by chronic illnesses; around 10 percent of the worldwide population is Chronic Kidney Disease. The incidence of CKD in China is 10.8% while it is 10% -15% in the United States. In the overall population of adults in Mexico, this proportion has, according to another research, reached 14.7%. The slow deterioration of the renal function, which leads to a full loss of renal function, is characterized in this condition.

In its early stages, CKD has no apparent symptoms. The illness cannot thus be recognized until around 25 % of the renal function is lost. The increased frequency of chronic kidney disease in emerging nations is having major ramifications for health and economic production. The rapid growth of common risk factors, particularly among the poor such as diabetes, BP, and obesity, would lead to an increase in the load that emerging nations are unwilling to cope with.

The world health community's concentration on infectious illnesses and a lack of consciousness have been the main cause for inadequate exposure to chronic illnesses, in particular chronic kidney disease. Chronic kidney disease has increased fast and is associated with excessive cardiovascular risk. Epidemiology is associated with the development of CKD with several additional clinical conditions.

Two procedures, blood testing, and urine testing were often used by nephrologists to screen for CKD. Genetics, diabetes, obesity, and age are factors that might impact CKD. The best timing to start dialysis for CKD in patients is a topic of continuous dispute among nephrologists. The Initiating Dialysis Early and Late research was a randomized controlled experiment that looked at the effect of dialysis scheduling on mortality risk. There were no changes in mortality risk between early and late dialysis in this trial.

Chronic illnesses, particularly chronic kidney disease, have received little attention worldwide. Industrialized countries need to focus on this and establish more inclusive, cost-effective, and prevent chronic illness policies. Many hospitals maintain data in their database on chronic renal disease patients. Various patterns that are useful for decision-making can be uncovered via the analysis of this data. Machine learning is a significant area for research nowadays. Various statistical and machine learning methods are implemented in different fields.
We may utilize machine learning in these areas, such as marketing, medical and health issues, weather forecasts, socioeconomic behavior studies, etc. Many disorders may be recognized either by machine or by machine through the

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application of machine learning algorithms in the medical profession. Using machine learning techniques on these data, it is possible to discover many kinds of knowledge and use this knowledge to predict the chances of having CKD. The major goals of this research are to use a machine-learning algorithm to predict CKD, to warn whether a person is in danger of contracting the disease.

In this research article related works are mentioned in the section 2. The proposed technique is deeply narrated in the section 3. The experimental evaluation is performed in section 4 and whereas section 5 concludes this research article with the scope for future enhancement.

II. LITERATURE REVIEW

G. Chen et al., proposed a system for the identification and diagnosis of Chronic Kidney Disease, known as the Adaptive Hybridized Deep Convolutional Neural Network (AHDCNN). The CNN characteristics were retrieved using the suggested model. It has been supplied to the vector machine with its development as well as renal mitosis. A CNN that has been pre-trained on a big scale to identify kidney carcinoma by the removal of urine CT picture characteristics. Furthermore, the local and global contextual aspects of the CNN model were investigated, and the system boosted speed and effectively diagnosed kidney cancer by employing a fully linked layer within the CNN final layer [1]. A fully convolutional network (FCN) and conditional random fields were utilized to segment renal cancer (CRFs). For FCN model training and conditional random field training, image patches were first used. Finally, the system was calibrated directly utilizing the image slices. In a single pass, a sophisticated CNN model training methodology is integrated with nearby image patches. After the 3D segmentation of images using the CNN modality, the fully connected 3D random field was employed to eliminate false positives. In the classification of renal cell subtypes, the proposed technique, which is dependent on radiologists' ROIs and deeper learning, has shown promising results.

J. Qin et. al., explains that in terms of data imputation and sample diagnosis, the suggested CKD diagnostic approach is practical. The integrated model could obtain adequate accuracy after unsupervised imputation of missing values in the data set using KNN imputation. Therefore, they believe that adopting this technique to the practical diagnosis of CKD would have a positive outcome. Furthermore, this technology might be used to clinical data from various disorders in real-world medical diagnosis. However, due to the restrictions of the settings, the available data samples for creating the model are quite little, with just 400 samples. Therefore, the model's generalization performance may be restricted [2]. Furthermore, because the data set contains only two types of data samples (CKD and notckd), the model is unable to determine the severity of CKD.

M. U. Emon et al., explains that Chronic kidney disease (CKD), commonly known as chronic kidney failure, is characterized by a severe decrease in kidney function. The wastes and surplus blood fluids in the blood are filtered by the kidneys and eliminated in the urine. When chronic kidney disease progresses, dangerous quantities of fluid, electrolytes, and waste can accumulates in the body. End-stage renal disease (ESRD) and cardiovascular disease are both increased by CKD, and additional risk factors for heart disease, such as high blood lipids, are also seen in people with CKD. Cardiovascular disease, rather than renal failure, is the leading cause of mortality in people with CKD [3]. The authors took few attributes to measure their analysis of chronic kidney disease. They used Weka tools to analyze eight machine learning classifiers: Logistic Regression(LG), Naive Bayes(NB), Multilayer Perceptron (MLP), Stochastic Gradient Descent(SGD), Adaptive Boosting(Adaboost), Bagging, Decision Tree(DT), and Random Forest(RF). Using principal component analysis, they can extract all properties (PCA). They analyzed that the Random Forest(RF) method has the maximum accuracy of 99 percent, and the ROC (receiver operating characteristic) curve value is likewise the greatest among other algorithms.

N. Bhaskar et al. suggested a deep learning network that is based on a modification of the classic CNN algorithm's structure. Correlation and sub-sampling layers are followed by bidirectional LSTM layers and a fully linked classification layer in the design. The correlational layer is the most important part of the architecture. The feature extraction operation is performed by the correlation layer and the sub-sampling layer to extract the best features from the input signal. The CNN will learn local attributes, while the LSTM network will learn signal sequences. Experiments with the hardware sensing module are carried out to test the capabilities of the suggested approach. Patients will be more accepting of the saliva-based technique proposed in this research since the sample extraction process is stress-free and painless [4]. The numerous performance parameters are used to evaluate the performance of the built networks. In the automated identification of CKD, the suggested hybrid model showed encouraging results. The suggested technique achieves a prediction accuracy rate of 98.08 percent, which is greater than other standard approaches. This research indicates that combining LSTM with a neural network model can improve the efficacy of 1-D signal processing. Furthermore, the authors conducted clinical validation, with the results showing a strong connection with their experimental findings.

Haya Alasker et al. used six different machine learning algorithms to predict renal illness and then compared their results. CKD is a chronic kidney disease that causes kidney function to deteriorate over time (NHS). The goal of this

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project is to use data mining classification tools and intelligent algorithms to estimate renal function failure. The sensitivity, specificity, positive predictive values of classification precision, and the area under the ROC that each classifier produces for distinct groups of CKD data sets were used to evaluate each classifier's performance [5].

K. Thirunavukkarasu et al. suggested approaches that were utilized to compare Logistic Regression, K-nearest Neighbor, and Support Vector Machine classification accuracy. The data must first be cleaned. After filling in the missing data, the nominal attribute is converted to a binary attribute. The next stage is to choose the optimal characteristic for a subset of features, which is called feature selection. A pivot table was used to visualize the connection between the qualities and the predictor variable in this study. The qualities have been chosen based on the findings. Data transformation is the third phase, in this technical data is normalized using Gaussian distribution with a mean of 0 and a standard deviation of 1. The classification model is trained in the fourth stage to predict results in unknown data. In the last stage, the optimal model for predicting liver illness is chosen based on the accuracy of several categorization models [6]. All of these algorithms were compared based on classification accuracy, which was determined using a confusion matrix. Logistic Regression and K-Nearest Neighbor had the best accuracy in the experiment, while logistic regression has the best sensitivity.

Yashuang Mu, et al., proposed PCC-Tree and its parallel counterpart MR-PCC-Tree that are decision trees that are based on Pearson's correlation coefficient [7]. Using the Pearson correlation coefficient, the optimal splitting attribute and the splitting points inside the tree node splitting rule are chosen during the inaugural of decisions. The percent of samples covered by a node will meanwhile be utilized as a stopping condition for the over partitioning problem. The MR-PCC-Tree version is developed within the map reduction framework to meet major obstacles in the categorization of data and it exceeds the unprecedented model concerning the time complexity and memory limitations. The practicality and parallelism of the experimental research are the two most important factors. On 17 data sets, the viability of the proposed PCC-Tree is evaluated by comparing it to 5 typical decision tree classifiers in terms of testing accuracy, tree scale, and running time. In terms of parallelism, the parallel MR-PCC-Tree model is tested on further eight data sets to ensure its validity in terms of computational time and memory constraints. Furthermore, three assessment indices, Speedup, Scale up, and Size up, confirm the strong parallel performance.

Kriplani et al. suggested a technique that depends on a deep neural network that has 97 percent accuracy in predicting the presence or absence of chronic renal disease. The model they developed outperforms other available techniques, and it is implemented utilizing the cross-validation methodology to protect the model from over fitting. This automated chronic kidney disease treatment slows the course of kidney damage, but it requires early identification of chronic kidney disease [8].

Using machine learning methods, Tahsin M. Rahman et al [9], created a classification-based model to diagnose renal illness at an early stage using digitized ECG. Two key criteria are necessary to identify CKD in patients with 97.6% accuracy: the QT interval and the RR interval. The fundamental benefit of this approach is that it gives a safe and non-invasive technique to assess patients' kidney health. Based on the patient's ECG, any sort of cardiovascular illness may be identified, and since each patient with any form of cardiovascular illness must have an ECG test, the same test code may be transmitted to the sample to assess whether or not the patient's kidneys are impacted.

A technique based on the automatic identification of ultrasonography (US) flaws in kidney pictures was proposed by S. Sudharson et al. The input photos are divided into two categories: ordinary and aberrant photos. This paper suggests using a pre-trained AlexNet CNN for automated feature extraction and then combining it with a Multiple Support Vector Classification Model (MSVM) for the classification of anomalies on renal ultrasonography. This categorization system is based on the idea of the totality. Set techniques were successfully utilized to combine the findings of several classifiers. To combine the findings of the MSVM model, the majority procedure is used [10].

Mohan, Vijayarani suggested a data mining technique to categories renal illnesses into four categories. The data was gathered from a variety of medical labs, centers, and hospitals. The synthetic kidney function test (KFT) dataset was developed from this for renal disease analysis. This comparative study is based on a dataset with 584 cases and age, gender, urea, creatinine, and glomerular filtration rate are the characteristics in this KFT dataset (GFR). This dataset contains information on renal diseases that are impacted. The performance factors classification accuracy and execution time are used to compare the Support Vector Machine (SVM) and Artificial Neural Network (ANN) algorithms [11]. Based on the findings, it can be stated that the ANN improves classification performance and produces accurate results, making it the top classifier when compared to the SVM classifier method. SVM classifiers can potentially classify data with little execution time.

To predict CKD at an early stage, the researchers Pasadana, I. A et al. used decision tree algorithms such as Decision Stump, Hoeffding Tree, J48, CTC, J48graft, LMT, NBTree, Random Forest, Random Tree, REP Tree, and Simple Cart. These algorithms produce a variety of experimental outcomes depending on Accuracy, Mean Absolute Error, Precision, Recall, Kappa Statistics, and Runtime [12]. The effectiveness of these strategies was assessed and contrasted. According to the experimental findings, Random Forest surpasses other algorithms and achieves a 100% accuracy rate. The use of a decision tree to forecast CKD will aid in maintaining one's health.

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III. PROPOSED METHODOLOGY

The presented technique for the purpose of enabling chronic kidney disease detection which has been achieved through the use of Artificial Neural Networks has been depicted in the system overview in figure 1 .

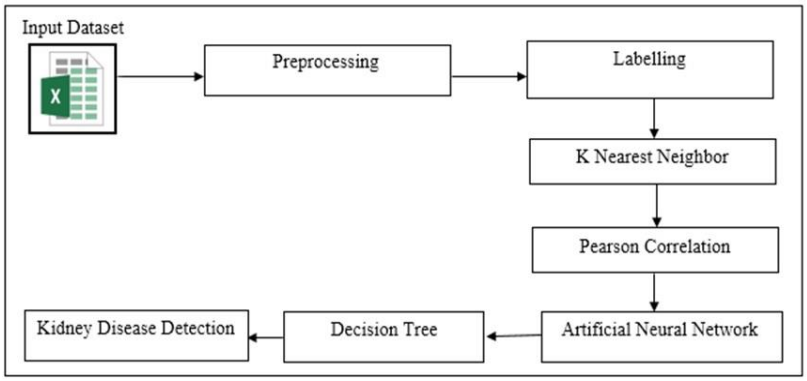

Figure 1: Proposed model System Overview

The steps being used to achieve the proposed system are elaborated below.

Step1: Dataset collection, preprocessing and Labeling : The presented technique utilizes an intensive dataset for the purpose of achieving the kidney disease detection. The dataset containing the various attributes related to kidney diseases has been downloaded using the URL - https://www.kaggle.com/mansoordaku/ckdisease. This dataset is downloaded and provided to the system as an input.

The dataset extracted from the URL given above contains a collection of kidney disease related data for a large number of patients. This dataset is in the form of a workbook format. This workbook is interfaced into the java code through the use of the JXL library, which converts it into a double dimensional list. This dataset consists of various attributes such as, age , bp (blood pressure), sg (specific gravity), al(albumin), su (sugar), rbc (red blood cells), pc (pus cell), pcc (pus cell clumps), ba (bacteria), bgr (blood glucose random), bu (blood urea), sc (serum creatinine), sod (sodium), pot(potassium), hemo (hemoglobin), pcv (packed cell volume), wc (white blood cell count), rc (red blood cell count), htn (hypertension), dm (diabetes mellitus), cad (coronary artery disease), appet (appetite), pe (pedal edema), ane (anemia), and class (class of kidney disease).

The attributes extracted from the dataset provide in-depth information about the patient's physical well-being. This allows for a much greater accuracy for the purpose of providing the achieving the kidney disease detection. Not all of the attributes are being considered for use in our implementation of the proposed methodology. The selected attributes are age, bp, sg, al, wbc, bgr, bu, sc, hemo, htn, and dm. These attributes are extracted into a list and labeled to achieve the integer representation before providing it to the next module for processing.

Step 2: K Nearest Neighbor Clustering: The list of patient details that is preprocessed and labeled in the previous step is provided as an input to this step of the procedure. This step performs the clustering of the input attributes provided for the kidney disease detection with respect to the dataset attributes. The clustering of the dataset is achieved through the use of the following steps.
Distance Evaluation – The Euclidean distance is evaluated between the attribute values entered by the user and the dataset entries. This is done for each of the attribute in the row and the respective row distance is stored at the end of the same row. This is performed for all of the rows in the input preprocessed and labeled list through the Euclidean distance equation given in the equation 1 below.

$$ED = \sqrt{\sum(ATi - ATj)^2} \quad \text{_____ (1)}$$

Where,
ED=Euclidian Distance
A_{Ti}=Attribute at index i
A_{Tj}= Attribute at index j

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Centroid Estimation – The list achieved as an output is provided as an input to this step of the procedure. The list is first sorted into ascending order and then the data points are selected randomly. The indices are k in number achieved through the respective data points. These data points are utilized to attain the respective row distances which are then considered as the Data Point. The centroids along with the average row distance are used to achieve the boundary for cluster formation.

Cluster Formation – The centroid values along with the average row distance are used to derive the values of the boundary used to cluster the input dataset. The boundary is created by adding and subtracting the value of the average row distances with the row distance of the centroids to achieve the maximum and minimum boundaries for clustering. The achieved clusters are then provided to the Pearson correlation for the purpose of correlation estimation.

Step 3: Pearson Correlation: This step of the procedure utilizes the cluster attained in the previous step are used to evaluate the correlation between the user input. The Pearson correlation technique is used to achieve the correlation which utilizes the user input for the attributes as the value of x [ ]and the attributes of the cluster as the y [ ]values. These values are subjected to the equation 2 given below for the calculation of the correlation value.

The clusters achieved in the previous step have been utilized as an input in this step of the approach. This is combined with the user input provided as the value of x which is then used to correlate with the cluster values y[ ]. The Pearson correlation utilizes the clusters and extracts the individual row values for the measurement of the correlation of each of the rows of the cluster with respect to the input provided by the user. This is performed through the use of the equations illustrated below.

$$r = \frac{\sum xy - \frac{\sum x \sum y}{n}}{\sqrt{(x^2 - \frac{\sum x^2}{n})}\sqrt{(y^2 - \frac{\sum y^2}{n})}} \quad \text{(2)}$$

Where,
x is the user input attributes
y is the attributes extracted from the dataset
n is the total number of entries
r= correlation value in between -1 to +1.

The correlation is measured for each of the rows in the cluster. This is repeated for all the clusters and their respective rows for the user input values. The correlation values of all of the rows of the cluster are added and a mean is evaluated to get a Pearson correlation value of the entire cluster. The attained values of correlation are stored in the form of a list. These correlation values are in the range of 1 to -1. The cluster list is then sorted in the descending order of the correlation values. The top 3 clusters from the list are then selected and provided to the Artificial Neural Networks in the next step to achieve the Kidney disease detection.
This process of Pearson Correlation can be depicted using the below mentioned algorithm 1.

ALGORITHM 1: Pearson Correlation Estimation for each of the Clusters

```
//Input : K-NN Cluster List KNC_L
// Input : User attribute list X[]
//Output:Correlation List PCR_L
pearsonCorrelationEstimation(KNC_L)
1: Start
2: CR_L =∅
3:    for i=0 to Size of KNC_L
4:      S_GCL= KNC_L [i] [S_GCL = Single Cluster]
5:    for j=0 to Size of S_GCL
6:          ROW = S_GCL [j]
7:          Y[]→ROW
8:          PR_C=pearsonCorrelation(X,Y)
9:          ROW= ROW+PR_C
10:         S_GCL = S_GCL +ROW
11:   end for
12:      PCR_L = PCR_L + S_GCL
```

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13: ***end for***
14: return PCR_L
15: **Stop**

Step 4: Artificial Neural Networks: The clusters with maximum amount of correlation are considered as an input in this step for Artificial Neural Network evaluation. The ANN approach utilizes input layer and hidden layer to achieve the output layer values. This is achieved through the assignment of the cluster values based on the attributes a set of random weights and a single bias weight to form the hidden layer. This is achieved through the use if the equations 3 and 4 given below.

$$T=\left(\sum_{=0}^{} AT * W\right) + B \quad \text{(3)}$$

$$H_{LV} = 2\left(\frac{1}{(1+\exp(-T))} X\ 2T\right) - 1 \quad \text{(4)}$$

Where,
n- Number of attributes
A_T- Attribute Values
W- Random Weight
B- Bias Weight
H_{LV} – Hidden Layer Value

The probability values from the input are achieved through the use of the ReLU activation functions and the 8 hidden layers that are formed. These scores are added to an ANN list and the resultant list is subjected to the sorting in the descending order. This allows the elements with the highest probability with the user input to come up on top. This is then provided to the next step for the classification of these probability values for accurate selection of the prediction.

Step 5: Decision Tree: The probability scores achieved from the Artificial Neural Network execution in the previous step are being utilized as an input for classification purposes. The Decision Tree approach attains precise classification of the relevant probability scores for an accurate output. The If-then rules provide effective realization of the segregation of the probability scores. The realization of the Decision tree also serves as an improvement in the Kidney Disease Detection Methodology by reducing the instances of false positives that can reduce the accuracy of the output. The detection of detected kidney disease is then displayed to the user.

IV. RESULT AND DISCUSSIONS

The proposed system for the identification for the presence of the kidney Diseases has been deployed using Java programming language. The NetBeans IDE has been utilized to achieve the development of the methodology on a laptop. This development laptop is powered by an Intel Core i5 CPU with a RAM of 4GB and 500GB of Hard drive storage.
The performance of the described detection mechanism for the kidney Diseases needs to be measured to extract efficiency of the execution. The assessment has been performed for the error introduced through the execution of the presented technique. The error is calculated by the evaluation of the RMSE or Root Mean Square Error. The error of the detection is useful in understanding the overall precision of the prescribed system.
The RMSE approach utilizes a pair of continuous and correlated variables for the assessment of the error achieved between these entities. The variables selected for the assessment of error in our approach are the expected kidney disease detections and the obtained kidney disease detections. This has been demonstrated mathematically in the equation 5 given below.

$$RMSE = \sqrt{\frac{\sum_{i=1}^{n}\left(x_{1,i} - x_{2,i}\right)^2}{n}} \quad \text{(5)}$$

Where,

$\sum$ - Summation
$(x_1 - x_2)^2$ - Differences Squared for the summation in between the expected kidney disease detections and the obtained kidney disease detections

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n - Number of samples or Trails

Extensive evaluation has been performed and the results of the experimentation have been recorded in the table given below.

Experiment No	No. of Expected Kidney Disease Detections	No. of obatained Kidney Disease Detections	MSE
1	13	11	4
2	11	9	4
3	14	10	16
4	9	8	1
5	8	6	4

Table 1: Mean Square Error measurement

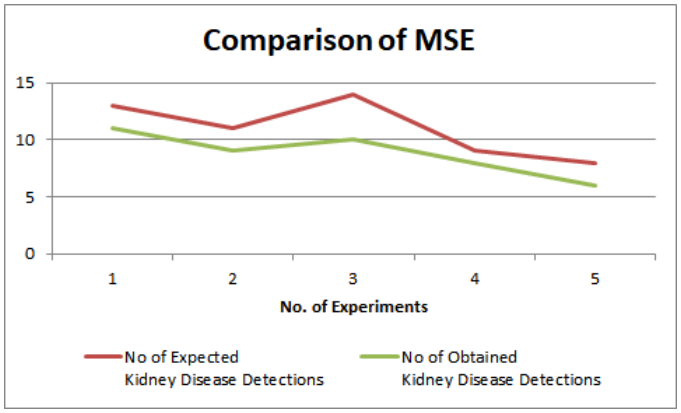

Figure 2: Comparison of MSE in between No of Expected kidney disease detections V/s No of obtained kidney disease detections

The output values tabulated in the table have been deployed to attain the line graph provided in the figure 2 above. These outcomes have been attained for 5 trials of experimentation carried out for the kidney disease detection with different user inputs. The error measured between the expected kidney disease detection and the achieved kidney disease detection has been assessed for each of the trials. The assessment results have attained a value of MSE and RMSE as 5.8 and 2.40 respectively. This is indicative of a satisfactory performance of the detection technique which is well within the expectations. The experimentation has been considerable in the determination of the outcome that the ANN and Decision Tree modules have be precisely implemented.

V. CONCLUSION AND FUTURE SCOPE

The presented system for the kidney disease detection has been illustrated in this research article. There has been a considerable increase in the number of people suffering from kidney disease. The kidney problems have been extremely problematic to deal with due to the large amount of time and resources required to accurately diagnose the disease. These diagnostic abilities have been effectively useful in determination of the kidney diseases. This research article achieves the determination of the kidney disease through the use of a dataset containing parameters of patient. This dataset is preprocessed, labeled and provided to the K Nearest Neighbors for the purpose of achieving the clusters. The KNN approach utilizes distance evaluation and centroid formation to achieve the clusters. These clusters are provided to the Pearson Correlation for the purpose of determining the correlation between the user input and the clusters. The obtained clusters are then provided to the Artificial Neural Networks for the evaluation of the hidden layer and the output layer. The resultant values are then subjected to the Decision Tree approach to achieve the classification of the probability values resulting in accurate kidney disease detection. The experimental evaluation has resulted in a highly satisfactory performance.

The future research approach can be made in the direction of enhancing the kidney disease detection system into an API for easier integration into existing systems.

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