

A Neural Network based Model for Predicting Chronic Kidney Diseases

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Abstract: Chronic kidney infection is a huge and rising problem among developing populations. It is one of the critical known health concerns with rising demand for early detection for prosperous and sustainable care. Many factors (such as Haemoglobin, Blood Pressure, diabetes, obesity) contribute to the continuous decline of kidney function over time. Chronic kidney disease has many stages for the criticality of the disease. Hence, a better diagnosis of chronic kidney disease is required to prevent continuous progression. This work gives a comprehensive study of the bio-clinical phenotype of cases with high-risk of Chronic kidney disease and will repeatedly assess victims over the long term and helps in classifying the stage of chronic kidney disease and then provides better recommendations (food, medicine) to prevent the rise of chronic kidney disease.

Keywords--- Chronic, comprehensive, prosperous, obesity, phenotype, bio-clinical.

1. INTRODUCTION

Kidney infection is a growing problem. Globally more than 8 million people die because of kidney diseases. The Identification of kidney disorders is difficult because of various hidden causes. This infection has an indirect result on whole world morbidity and fatality rate by developing the risks associated with other major killers (cardiovascular

disorders, diabetes, hypertension, contamination with human immunodeficiency virus (HIV), and malaria). Cases with chronic kidney disorder manage to develop heart disorders and additional organ failures if neglected. The progression of chronic kidney disease is a very important factor in a person's health. So maintaining a good kidney function is very important for overall health.

In many cases, kidney injury happens gradually, frequently because of diabetes or an increase in hypertension. This damage is termed as chronic kidney disorder. CKD includes a condition that affects the kidney and if the kidney becomes more critical, infections can develop to great levels in the haemoglobin, which damages both kidneys and leads to loss of life.

If there is an unexpected development in kidney function because of sickness, or trauma, or consumed any medicines—it is known as vital kidney injury. Critical kidney injury happens when kidneys quickly lose the ability to reduce excess salts, liquids, and garbage substances from the haemoglobin. It develops over a few hours or a few days to weeks.

Kidney infection occurs despite age or class. The principal determinants for generating kidney infection are:

Polygenic disease, Increase in Hypertension, heart disease, decrease in the blood vessel, and related records of kidney malfunction.

Kinds of Kidney Infection are:

Acute Perennial Kidney Malfunction

Deficient plasma movement to the organs has the ability to produce vital perennial kidney malfunction. The kidney organs cannot separate wastes from the serum without sufficient haemoglobin movement.

Acute Intrinsic Kidney Malfunction

Acute Intrinsic kidney malfunction is generated by immediate injury to the organs, such as a natural consequence of a disaster.

Chronic Perennial Kidney Malfunction

If a person doesn't have enough blood flowing to the kidneys for the long term, then they begin to narrow and suffer while filtering the blood.

Chronic Intrinsic Kidney Malfunction

This Infection is because of natural kidney disorder which results in long term injury in kidneys. An Inherent kidney infection is obtained because of the primary wound in the kidneys.

Chronic Post-Renal Kidney Malfunction

In this kidney injury occurs if there is any obstacle in the urinary region. Because of obstacles it generates high pressure in the body.

In the healthcare industry, the patient's data which represents their medical status is highly required. There are millions of such records. This data can be utilized to find patterns and meaningful insights. By observing these patterns, this proposed research work can analyze and provide better suggestions to the people. To do this, a machine learning algorithm is used to predict the results accurately.

The existing system is based on the corresponding outline of the immediate foresight of Chronic Kidney Disease and Dietary forecast for victims with Chronic Kidney disorder applying Classification algorithms. They haven't provided the desired accuracy in predicting chronic kidney disease. When compared to different machine learning algorithms, the algorithm built shows a better result which is implemented using the univariate statistical and wrapper techniques to keep the algorithm safe from the overfitting difficulty. This spontaneous system helps physicians to provide therapy that serves to diminish kidney damage improvement, but before performing this chronic kidney disease discovery at a beginning stage is important.

2. LITERATURE SURVEY

S. Shah.et.al [1] performed research to predict the appearance or nonexistence of chronic kidney disorder. To discover the connection between chronic kidney disorder and chosen properties, a data mining approach is applied in this research.

S.Bala.et.al [2] presented a summary of data mining classifications procedures practiced for

chronic kidney disorder Identification. The goal was to examine several data mining algorithms used in the Identification of chronic kidney infection.

Anusom Charleonnann.et.al [3] exhibited diverse machine learning techniques. The algorithms used were binary regression, decision-tree, K-Nearest-Neighbors, and SVM (Support Vector Machine) classifiers to recognize Chronic Kidney disorder. The performance of these algorithms is analyzed mutually to pick the most reliable classifier to Identify chronic kidney infection.

Gunarathne W.H.S.D.et.al [4] proposed a model for prognosticating the patient's status of Chronic Kidney disorder. The machine learning classification algorithms have been used for the forecast of chronic kidney disorder. The classification algorithms which were used are decision-forest and DAG.

M.M. Luck.et.al [5] explained how to use a data mining algorithm that in-depth search in the characteristic attributes for foretelling chronic kidney infection grades considering the proton Nuclear Magnetic-Resonance (1H) data. They examined acquired predictive design including a conventional model, connecting traditional univariate statistical feature collection methods with an L2LR, and a prototype combining global and local characteristics.

S. Dilli Arasu.et.al [6] has handled the missing values in chronic kidney disease health records. Missing values in the health records will degrade the efficiency in the forecast outcome. To skip the disappeared states they have worked on a recomputation method of chronic kidney disorder stages and the hidden states are chosen by using the prepared states.

Zeinab Sedighi.et.al [7] implemented a collection of filter and wrapper methods supported by machine learning procedures to analyze chronic kidney infection. They confirmed that feature collection methods let us deliver well-defined classification in the minimum time applying fewer dimensions.

Asif Salekin.et.al [8] projected twenty-four related parameters and designed a machine learning model to discover Chronic Kidney disorder. They worked on a cost-accuracy trade-off examination to recognize a new Chronic Kidney disorder exposure strategy with high efficiency and minimum cost.

In order to implement a more conventional dietary clarifications Anonnya Banerjee.et.al [9] proposed

a design considering the victim protein level in haemoglobin. Analysis of the victims is executed to suggest a diet for subjects suffering from a kidney infection and then more applying queries for matching, they prescribed the diet for the recognized stages by considering the weight of the condition.

Asif Salekin Stankovic.et.al [10] performed research on chronic kidney disease with the help of classifiers kNN, random forest, and Backpropagation to determine an appropriate answer. Applying a feature selection method they implemented a characteristic compression examination to observe specific properties to expose chronic kidney disorder with great efficiency.

Uma N. Dulhare.et.al [11], proposed a prototype by applying Naive Bayes including a 1R characteristic selector for discovering chronic kidney infection. At every stage, rules have been generated accordingly to proceed for further treatment.

M. S. Wibawa.et.al [12] implemented a prototype in which they applied a machine-learning algorithm for a quick judgment of chronic kidney disorder by applying characteristic choice and aggregate training. In order to enhance the kind of chronic kidney disorder, Correlation-based characteristic Choice was applied for feature collection and Adaptive Boosting was employed for aggregate training. Classifiers such as the KNN algorithm, Bayes, and SVM algorithms were adopted.

JIONGMING QIN.et.al [13] proposed a machine learning methodology for discovering chronic kidney infection. They used a combined prototype that connects logistic regression and random forest utilizing a perceptron.

3. PROPOSED SYSTEM

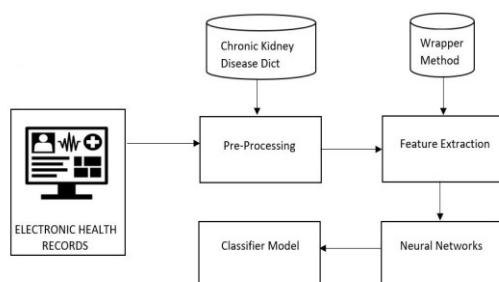


Fig 1: Identification of Chronic Kidney Disease

Chronic Kidney Infection is proved to be fatal when it is not diagnosed or treated properly. Diagnosing a chronic Kidney disease at the correct time is more important in order to stop its progression. The proposed system will predict the chronic kidney disease with better classification of the CKD stage, accuracy, recommendations and with less overfitting problems. For that, the

proposed research work has developed a machine learning model with artificial neural networks. There were several steps involved in creating the desired machine learning model which include

1. Data Pre-processing
2. Feature Selection
3. Splitting the data
4. Applying the neural network algorithm.

DATA PREPROCESSING

The data pre-processing mainly consists of two major steps which include:

-Removing noisy data – In this process, the undesired data is removed from the health records, because certain attributes consist of unstructured and meaningless data. To eliminate that, the min-max scalar method is performed to keep the data in the min-max range. The whole data is then divided into segments of equal size and replaced all values in a segment by its mean.

-Replacing the missing values – There are some attributes such as red blood cells, blood glucose random, sodium, and potassium, which consist of NaN value instead of a numeric value. It is later eliminated by replacing NaN values with the mean.

FEATURE SELECTION

This work uses a univariate statistics approach, which selects features based on univariate statistical tests between each feature and the target variable. The intuition is that features that are independent of the target variable, are irrelevant for classification. The chi-squared test is used for feature selection. Then the attributes are selected based on the chi-square scores.

The features extracted from the dataset are specific gravity, albumin, serum creatinine, haemoglobin, packed cell volume, and a class label.

Separation the health records into Training and Testing data set

The health record is separated into training and test record. In the learning phase of a health record there is a column which contains a class variable and the algorithm is trained on this data to be generalized for any other records.

The health records are selected randomly for 80% training and 20% testing health records, and shuffle the records before learning.

After the records are separated into testing and training collection. The learning records are trained subsequently.

NEURAL NETWORKS

The model architecture is created, then the proposed model has added 2 layers, the first layer with 256 neurons and the 'ReLU' activation function with a normal distribution initializer for the weights. Since that, layer is the first layer, which must also specify the number of features in the data set.

The second layer which happens to be the last layer as well, will have 1 neuron and use the 'hard_sigmoid' activation function.

Compile the model, and give it the loss function called 'binary_crossentropy' which is a loss function used for binary classification, It estimates how well the algorithm did on training and then tried to increase the efficiency on it using the optimizer.

First, the forward propagation is applied. In forward propagation, the inputs are considered and then multiply those with weights which are initially obtained in random order.

Equation (a):

$$Y = W1I1 = W1I1 + W2I2 + W3I3$$

The equation (a) represents the weighted sums of inputs. This is also called the linear transformation of weights with respect to given inputs.

To determine a node amount, the equation "Y" is passed with the result through a sigmoid formula. To normalize the result between [0,1] Sigmoid function is used.

Equation (b):

$$\text{Sigmoid Function} = 1 / (1 + e^{-Y})$$

The equation (b) represents the activation function.

The loss rate is obtained by considering the variation among the original yield and the predicted yield. Upon examining the error, the weights have been adjusted by multiplying the loss rate with the information. The same step is performed with the slope of the sigmoid trajectory:

Equation(c):

$$\text{Weight} += \text{loss} * \text{NeuronInput} * \text{NeuronOutput} * (1 - \text{NeuronOutput})$$

In the above equation(c), $\text{NeuronOutput} * (1 - \text{NeuronOutput})$ is a derivative of the sigmoid trajectory.

ADAMS OPTIMIZER

The optimizer that deployed here is called the 'Adam' optimizer. It is also required to observe how well the model does, so some metrics will be obtained on the model's accuracy. Train the model using the training data sets (X_{train} and y_{train}).

Adam is designed specifically for learning dynamically and optimizing the weights of an algorithm for training deep neural networks. Adam is an adaptive training scale classification, it calculates unique learning measures for various parameters. Adam's name is obtained from adaptive moment evaluation, and the reason it's called because Adam practices evaluations of primary and secondary consequences of the gradient to adjust the learning degree for every specific weight of the neural channels.

Equation (1):

$$M_n = E[X^n]$$

m =moment X =random variable

Here the moment is called mean and the random variable is the variance. It utilizes exponentially shifting aggregates, measured on the gradient estimated on the prevailing mini-batch.

Equation (2):

$$\begin{aligned} m_t &= \beta_1 m_{t-1} + (1 - \beta_1) g_t \\ v_t &= \beta_2 v_{t-1} + (1 - \beta_2) g_t^2 \end{aligned}$$

m, v = moving averages g = gradient on current batch

The equation (2) estimates the moments by utilizing the exponentially moving averages computed on the gradient and squared gradient analyzed on the current batch.

The pattern for the value of m has been decided after observing a few iterations of $m_0, m_1 \dots m_t$.

Equation (3):

$$m_t = (1 - \beta_1) \sum_{i=0}^{t-1} \beta_1^{t-i} g_i$$

m = moment g = gradient of the particular batch

The equation (3) represents the estimated value of m . In order to optimize, the gradient is modified as follows to obtain a higher-quality step gradient to update the weights with momentum level before measuring the gradient.

Equation (4):

$$\begin{aligned} g_t &= \square f(w_{t-1} - \beta m_{t-1}) \\ m_t &= \beta m_{t-1} + \eta g_t \\ w_t &= w_{t-1} - m_t \end{aligned}$$

m = moment w =weight g =gradient

Before computing the gradient it is required to take a higher quality gradient step direction by taking updated parameters using the equation (4).

Finally, Function f gives the loss function to optimize and then the gradient is measured to make a correction that helps in classifying the chronic kidney disease.

4. EXPERIMENTAL RESULTS

Each of the above modules have their own significance. The end results of each are shown below:

Data Pre-processing

The result of this module is that the noisy data is filtered from the health records and all the disappeared states were replaced by the mean of all the records.

Feature Selection

```
df.head()
```

	sg	al	sc	hemo	pcv	htn	classification
0	1.020	1.0	1.2	15.4	28	1	0
1	1.020	4.0	0.8	11.3	22	0	0
2	1.010	2.0	1.8	9.6	15	0	0
3	1.005	4.0	3.8	11.2	16	1	0
4	1.010	2.0	1.4	11.6	19	0	0

Fig 3: Attributes selected through feature selection

After the data preprocessing is done, few features or attributes that subscribe to the forecast of chronic kidney disorder are selected. The features that are selected are shown in Figure 3.

Applying the Neural Network algorithm

TEST RESULT	CHRONIC KIDNEY DISEASE		
		Predicted NO	Predicted YES
	Actual NO	31	0
	Actual YES	2	25

Fig 4: Confusion Matrix

To evaluate the performance of the deep neural network on a collection of test records, a confusion matrix is generated. In the confusion matrix, the correct values are identified. The True Positive (+) value is 31, False Positive (-) value is 0, False Negative (-) value is 2 and True Negative (+) value is 25. The example of a confusion matrix is shown in Figure 3.

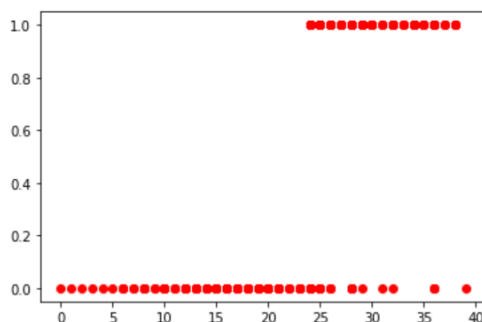


Fig 5: Data points of PCC after data preprocessing

Fig 5 represents the graph where the PCC points after performing the data preprocessing on the data records. To measure overall correctness externally considering what set of failures are made, this research work has used Percent Correct Classification (PCC) metric to assess the model

accuracy.

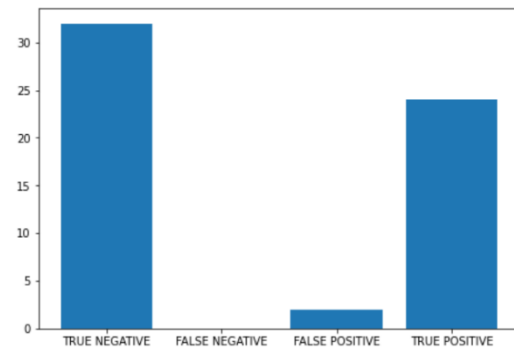


Fig 6: Confusion matrix results

The confusion matrix outcomes are presented in picture 6. PCC and the confusion matrix metrics are useful when a complete group needs are composed.

```
2/2 [=====] - 0s 3ms/step - loss: 0.5315 - accuracy: 0.9655
Original : 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 1, 0, 1, 1
Predicted : 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 0, 0, 1, 0, 1, 0, 1, 1
Scores : loss = 0.5315239429473877 acc = 0.965517228813171
```

Fig 7: Comparison of original value and the predicted value with accuracy

Fig 7 represents the final result of our model after performing the prediction on a testing dataset.

The proposed work presents the classification accuracy, sensitivity, and specificity for chronic kidney Infection applying deep Neural Networks. The best accuracy of 96% is obtained using deep Neural Network.

5. CONCLUSION

Chronic Kidney Infection is one of the health problems which needs better diagnosis. Prognostication of this disease in the early stages may stop the progression of this disease. This paper has worked on artificial neural network algorithms. The 14 different properties are analyzed and linked to chronic kidney disorder victims and foretold accuracy for a machine learning algorithm named Artificial Neural Network. After analysing the outcomes, it is recognized that the algorithm gives correctness of 96. The advantage of this system is that the prognostication method finishes in a shorter period. This application will encourage physicians to commence specific surgeries ahead to chronic kidney disorder victims and also serves in diagnosing the higher cases in a shorter time.

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