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Research Article

# Models of Machine Learning to Diagnose Chronic Kidney disease using a WEKA-based Classifier

Shaymaa Adnan Abdulrahman [1],*, Sameerah Faris Khlebis [2],

[1] *Business Information College, University of Information Technology and Communication, Baghdad, Iraq.*

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## ABSTRACT

In the present day, humans are confronted with a variety of diseases as a result of their lifestyle and the current environmental conditions. Therefore, it is crucial to identify and predict these diseases in their early phases in order to prevent their severe manifestations. Manually identifying maladies is a challenging task for physicians on a regular basis. Predicting chronic illnesses is the aim of this article. This goal is applicable through a state-of-the-art approach to classification correctly identifies people with chronic illnesses. Predicting maladies is also a difficult endeavor. Therefore, disease prediction is significantly influenced by data mining. To get data, a collection of disease symptoms, the individual's lifestyle, and information regarding medical consultations are considered in this general disease prediction. In conclusion, this paper analyzes that model with a variety of algorithms, including (Naiva Bayes) and (RF-Random Forest).

## 1. INTRODUCTION

In The four main organ systems are the gastrointestinal, renal, cardio-vascular, and neuro-muscular systems in the human body that are responsible for essential physiological functions. The organ systems outlined above are in a state of perpetual operation to preserve physiological homeostasis throughout our lifetime. The renal system is crucial in the regulation of blood osmolality and the excretion of debris and toxins. The kidney is the central component of the renal system. Therefore, the kidney's health is justified. The kidneys are afflicted by lifestyle, eating habits, drinking water quality, age-related problems, and late-onset conditions like diabetes, high blood pressure, chronic inflammation, and recurrent microbial infections. However, the life of affected individuals can be extended by managing the illness, provided that they have a prior understanding of the chronic kidney diseases (CKD). The normal output of a healthy kidney is estimated to be 90-60 ml/min/1.73 m2. When creatinine increases, proteinuria, or co-morbidities occur, the eGFR decreases [1]. In India, nephrological care is difficult to access in overcrowded households and in rural areas where patients with kidney illnesses reside [2]. The Uddanam region of Andhra Pradesh, India, is located in the north-central districts and consists of over 100 villages. A significant incidence involving kidney diseases was observed in 150,000 individuals. The incidence of chronic kidney disease unknown etiology (CKDu) in this region ranges from 40% to 60% [3]. In the Srikakulam district, 13% of the population had a higher creatinine levels after being screened in Uddanam [1]. Additionally, it was demonstrated that men are more susceptible to chronic kidney disease than women. Significant CKD prevalence rates were also reported in the neighboring state of Odisha (India), which is situated to the north of Andhra Pradesh [4]. A persistent impairment of renal function is the cause of chronic kidney disease, being a serious medical issue. According to [5], CKD is accounted for global mortalities annually. Additionally, the etiology of an estimated 40% of CKD patients in Maharashtra, India, was virtually unknown. A high frequency of CKDu was reported in Canacona, which is situated in Goa [6]. Community-based data is essential for evaluating the prevalence of CKD. Following Evans and Taal [7], the prevalence of CKD varied from 4.5% to 17.5%, depending on the methodologies used and the sporadic endemic populations that were analyzed. According to patient data regarding albuminuria and glomerular filtration rate (GFR), the estimated prevalence of CKD in USA from late 1980s to mid-1990s and from late 1999s to early-2000s. This increase was classified into five stages and was also attributed to hypertension and diabetes [8]. Medical personnel occasionally depend on machine learning (ML) in preventing and treating diseases. Relying on skilled medical workers is

*Corresponding author. Email: dr.shaymaa.adnan@Uoitc.edu.iq

steadily increasing due to the scarcity of knowledge within the prospective patients regarding the ML classifier algorithm [9]. There are numerous public health applications for machine learning technologies. The Chi squared automatic interaction detection algorithm was employed by Osman and Sabit [10] on vaccination. Preterm bradycardia of 30 infants, which involved 3591 hours of ECG at the Royal Hobart Hospital in Australia, was evaluated using ANNs (Artificial neural networks). The mean value of 0.63 AUC was obtained for the predicted bradycardia [11]. (Qezelbash-Chamak et al.) [12] summarized and categorized the diverse ML (Machine learning)-based instruments. Being components of machine learning [14], data analysis and pattern recognition have significant applicability in health intervention programs [13]. Consequently, data mining is a critical prerequisite for identifying the concealed and undetected knowledge within a medical dataset. Data mining techniques can be employed to forecast, categorize, classify, and aggregate data. These processes would evaluate the manner in which the selected algorithm will manage a training set. However, ML techniques are widely implemented worldwide to enhance the precision of diagnosis predictions and predict the recurrence of diseases in the population [6, 8, 15-19]. With automatic hospital dataset expanding at an exponential rate, an increasing number of ML algorithms are incorporated into healthcare applications [20]. Five categories are used to categorize the ML capabilities in healthcare applications, with a particular emphasis on the cardiovascular system: (i) digital image, (ii) electrocardiography, (iii) in-hospital monitor, (iv) mobile and wearable devices, and (v) precise medical care. It has been suggested that the implementation of these algorithms in daily practice may cause annual savings of up to US$600 per individual in the United States [21].

The ML applications are being extensively authenticated and reaffirmed in the healthcare sector, as well as in industrial and small-medium enterprises, which are based on partial least squares [6]. Consequently, ML classifiers are cutting-edge instruments that have applications in industrial, societal, and healthcare research. The local community and community health workers are not yet acquainted. End-stage renal disease (ESRD) is being treated with renal replacement therapy (RRT) in Indian medical facilities. This approach imposes substantial family and national burdens. Some of the known risk factors for CKD include physical, personal, psychological, and socioeconomic conditions. Diabetes and hypertension are synchronized chronic kidney disease (CKD) maladies that are associated with CKD [15].

To stop kidney disorders from developing, it is essential to be aware of the risk factors, disease indicators, and lifestyle choices. Machine learning tools, disease datasets, and accuracy prediction analysis will give the knowledge to health workers at the village and community level well before end-stage renal disease manifests. Given the aforementioned information, the prediction accuracy of the different classifiers chosen for the CKD dataset was assessed in the current study.

## 2. RELATED WORK

In order to diagnose chronic kidney illness, (Hodneland et al). employed image registration to identify changes in renal morphology [9]. Vasquez-Morales et al. used a lot of CKD data to develop a neural network-based classifier. The model's accuracy on their test data was 95% [17]. Furthermore, the CKD data set, which was obtained from the UCI library, was utilized in the majority of the earlier studies. Chen et al. employed k-nearest neighbor (KNN), support vector machines (SVM), and soft independent modeling of class analogies to diagnose CKD. KNN and SVM had the maximum accuracy of 99.7% [2]. Furthermore, they employed fuzzy rule-building expert systems, fuzzy optimal associative memory, and partial least squares discriminant analysis to diagnose CKD, with an accuracy range of 95.5% to 99.6% [1]. Depending on diagnostic categories of the samples, the mean imputation is used in the models indicated above. As a consequence, their approach was no longer applicable when the samples' diagnostic outcomes were unknown. In actuality, there are a number of reasons why patients might not finish some measurements before being diagnosed. Furthermore, for categorical variables with missing values, the data derived by mean imputation may show a notable departure from the true values. For instance, we designate 0 and 1 as the categories for variables with only two categories, even though the variables' means may fall between 0 and 1. An SVM that made use of feature selection technology was developed by (Polat et al.).

Through feature selection, the suggested models decreased the computational cost while achieving an accuracy range of 97.75% to 98.5% [6]. To fill in the missing variables, Using creative multiple imputation, (J. Aljaaf et al). The accuracy of the MLP neural network (MLP) was then 98.1% [6]. Subas et al. used random forest (RF), C4.5 decision tree, SVM, KNN, MLP, and RF to diagnose CKD; the RF had been 100% accurate [4]. In( Boukenze et al). [19], MLP models reported highly accurate rates of 99.75%. SVM and neural networks were used by (Almansour et al.) to diagnose CKD; the models' respective accuracy rates were 97.75% and 99.75% [11].

In the methods indicated by (Gunarathne et al.), decision forests performed best, with an accuracy of 99.1% [18]. Image registration was used by (Hodneland et al.) to identify changes in renal morphology [14].

A neural network-based classifier was constructed by (Vasquez-Morales et al.) using a substantial amount of CKD data. The model achieved an accuracy of 95% on their test data [13]. (Chen et al). used soft independent modeling of class analogies, k-nearest neighbor (KNN), and support vector machines (SVM) to identify chronic kidney disease. At 99.7%, KNN and SVM showed the highest accuracy rate [7]. Additionally, they used partial least squares discriminant analysis, fuzzy optimal associative memory, and fuzzy rule-building expert systems to diagnose CKD; the accuracy of these models ranged from 95.5% to 99.6% [1]. Their studies have produced positive findings for CKD diagnosis.

Mean imputation has been utilized to reach certain aims, contingent upon the diagnostic categories of the data. Consequently, the procedure cannot be implemented. For a variety of reasons, patients may actually disregard certain measurements prior to making a diagnosis. Additionally, the true values of missing values in categorical variables may differ substantially from the data obtained through mean imputation. For variables that have only two categories, we assign the categories to 0 and 1, although average variables may vary between 0 and 1. (Polat and others). An SVM was developed using feature selection technology; the accuracy of the suggested models ranged from 97.75% to 98.5%, and the computational cost was reduced through the use of feature selection [6]. The MLP neural network (MLP) achieved an accuracy of 98.1% when (J. Aljaaf et al.) implemented new multiple imputation [28]. To detect CKD, (Subas et al.) implemented MLP, SVM, KNN, C4.5 decision tree, and random forest (RF), which achieved a 100% accuracy rate [2]. In the models developed by( Boukenze et al.) [5], MLP exhibited highly accurate rates of 99.75%. The research of [8] primarily focused on innovative tools to get optimum findings. In order to diagnose CKD,

(Almansour et al.) implemented SVM and neural networks; the models' respective accuracy rates were 97.75% and 99.75% [22]. Approaches proposed by( Gunarathne et al). demonstrated the highest level of accuracy when used to make decisions, with a score of 99.1% [16].While (Park et al.) designed the SHapley method to predict clinical features linked to ten diseases, such as pulmonary tuberculosis, end-stage renal disease, infectious colitis, unstable angina, acute pyelonephritis, acute pancreatitis, hepatitis, liver cirrhosis, malaria, and acute myocardial infarction. They suggested predicted association models based on laboratory tests and clinical characteristics. In conclusion, the majority of the CKD diagnostic models that were previously developed were either limited in their applicability due to the approach used to impute missing values.

## 3. BACKGROUND

### 3.1. Chronic Disease.

Chronic diseases are defined as conditions that persist for a prolonged period, typically exceeding three months. Neither vaccines nor medications are effective in treating or preventing these diseases. The primary causes of chronic diseases are tobacco use, as well as other unsuitable living conditions. Additionally, this condition was frequently precipitated by the aging process [5]. Heart disease and stroke are cardiovascular diseases that are frequently fatal. The utilization of tobacco, inadequate nutrition, and inadequate physical activity are the primary contributors to the development of this condition. Persistent conditions like arthritis lead to joint inflammation, discomfort, and stiffness that worsens with age. Although there are affordable ways to lessen the effects of arthritis, they are not frequently employed. Regular moderate exercise can help lessen the effects of arthritis.

Diabetes is a severe and costly condition. Self-care and early detection of diabetes can mitigate its effects [5]. This disease, notably type 2 diabetes, affects approximately 7 million individuals who are 65 years of age or older. Obesity has become increasingly prevalent among adults of all ages since 1980. Individuals who are overweight or obese may develop some blood-related diseases. Certain varieties of cancer can also be caused by obesity. The treatment of epilepsy and seizures is exceedingly expensive [23]. This condition is prevalent in all age categories, with a particular prevalence among the elderly and young. The health of elderly individuals is particularly affected by oral health issues, which are a critical concern. This is a severe concern, as it impacts an individual's daily activities, including the ability to communicate, chew, swallow, and adhere to a nutritional diet.

### 3.2 K-Nearest Neighbor (KNN)

One of the strategies employed in the supervised learning method is the utilization of K-Nearest Neighbors for grouping. By identifying the k adjacent neighbors of a data item, the concept of this method is to determine its classification. In order to quantify the distance, Euclidean geometry was implemented.

$$EUC\ DISTANCE\left[X_I - X_J\right] = \sqrt{\left(\sum_1^N X_I - X_J\right)^2} \tag{1}$$

Where ($X_{I1}$, $x_{I2}$, $x_{I3}$,…………., $x_{In}$) and ($X_{J1}$,$X_{J2}$,$X_{J3}$………., $X_{Jn}$)

### 3.3 Convolutional Neural Network (CNN)

Because CNNs are superior to traditional ANNs and can retain the original spatial context of processed images, they have attracted a lot of interest in the field of medical image analysis. In CNN, the main components are the convolution layers, non-linearity layers, pooling layers, and fully connected (FC) layers. Inspired by deep ANNs, the convolutional neural network (CNN) is a machine learning model that uses a series of learnt filters for convolution. Deep ANN served as the inspiration for the CNN machine learning model in the area of medical image analysis. CNNs have gained popularity over traditional ANNs as a result of their ability to preserve the original spatial relationships between processed images. The basic building blocks of CNNs are convolution layers, non-linearity layers, pooling layers, and fully connected (FC) layers. As shown in Fig. 1, the "convolution" layer first applies a set of learnt filters to the input image or volume. The convolution layer creates feature maps with the same dimension as the number of filters. The concentrated activations linked to a particular filter are depicted in each map. The convolution operation between an image Mi of size Ni and a filter Wi of size Ai × Bi, which yields a feature map $\gamma$, is defined by the following dot product.

$$y = \sum a \sum bI(a.b)w1(m1 - a, n - bi) \tag{2}$$

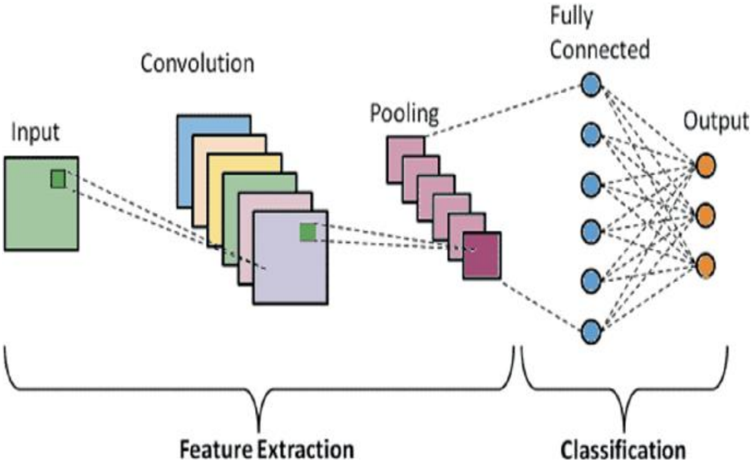


Fig. 1. Convolutional Neural Network (CNN)

## 4. PROPOESED METHODOLOGY

This section offers a comprehensive account of the development of data sets, the development of models, and the prediction of maladies. Data collection is the initial step. Structured and unstructured data are collected from a variety of sources by our proposed system. Subsequent to data acquisition, they undergo preprocessing. The constructed model is prepared for testing after several epochs, once the intended goal has been reached. At this stage, new data that wasn't used during training is used to test the model and confirm its performance. The proposed model can reach the desirable accuracy in test data, as illustrated in Fig. 2.

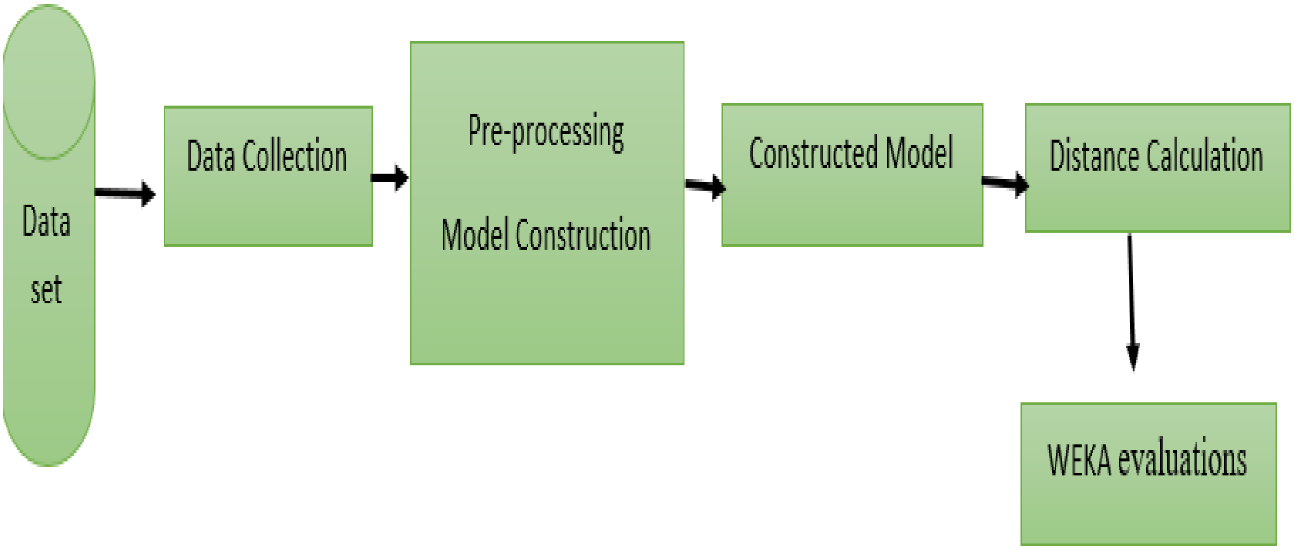


Fig. 2. Architecture of proposed disease and risk prediction system

### 4.1. Data Collection

Structured information, which encompasses patient fundamental information including medical, social, economic, environmental, and personal indicators, which includes patient's consultation with the doctor and the symptoms of the disease, are real-world data. The data set does not contain private information, including name, identification number, and address, in order to protect their privacy.

### 4.2. Pre-processing

The majority of the structured data is preprocessed to account for the presence of absent values. Compilation Test Data for Model Construction Developed a model for disease prediction using CNN and KNN to calculate distance. Figure 2 illustrates the architecture of the proposed disease and risk prediction system. Additionally, the preprocessing phase eliminates white spaces, punctuations, and commas. After the data has been preprocessed, it is subsequently subjected to feature extraction and disease prediction.

### 4.3. Model Description

The data set is composed of both structured and unstructured data, as previously mentioned. The structured data is presented in a tabular format and includes patient demographics, laboratory test results, their living habitat, and the disease they are affected by, as well as details about the disease's cause, including height, weight, age, and gender. The symptoms of the patient's illness and the textual information about the doctor's questioning are examples of unstructured data. Another advantage of the prediction assignment is the unstructured data, which makes it possible to provide more accurate findings.

### 4.4. Disease Prediction Using CNN

The CNN algorithm is implemented in the prediction of chronic diseases by the proposed system. The data set is initially converted to vector form, and then word embedding is performed to assign zero values to the data in order to fill it. It is then transferred to the convolution layer. The pooling layer, which gets input from the convolution layer, carries out the max pooling procedure. The output of max pooling is sent to the fully connected layer, which then sends the classification results to the output layer. Figure 3 depicts the convolutional neural network's block diagram.

### 4.5. Distance Calculation Using KNN

Features that are similar to the K value are referred to as the nearest neighbor in K-Nearest Neighbor (KNN), when the value of (K) is known. The closest distance between them is calculated after choosing the neighbor that is closest to the known K value. The final disease prediction output is the feature with the lowest distance value, which is referred to as the exact match. Euclidean distance is implemented in the proposed system due to its superiority over other distance calculation methodologies. It is a nonparametric algorithm, as it does not make decisions based on the original data. In

KNN, the test data are situated in the plots of the X and Y axes, while the training input data are situated in the X and Y axes. subsequently, the graphs of test data with the least distance are selected and regarded as the desired target. Selecting the adjacent K point is crucial, as it must always be odd.

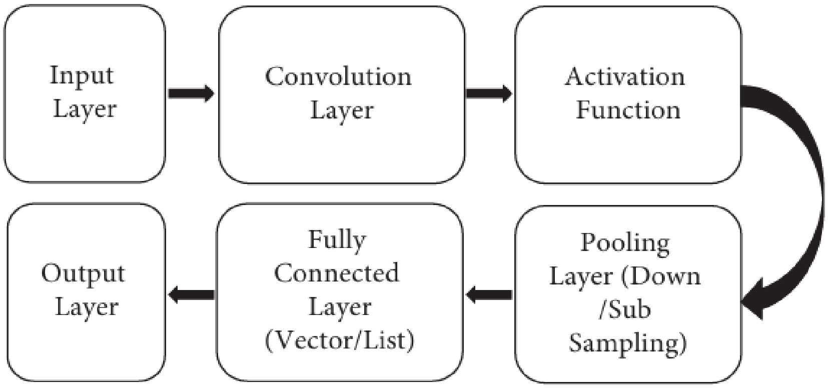
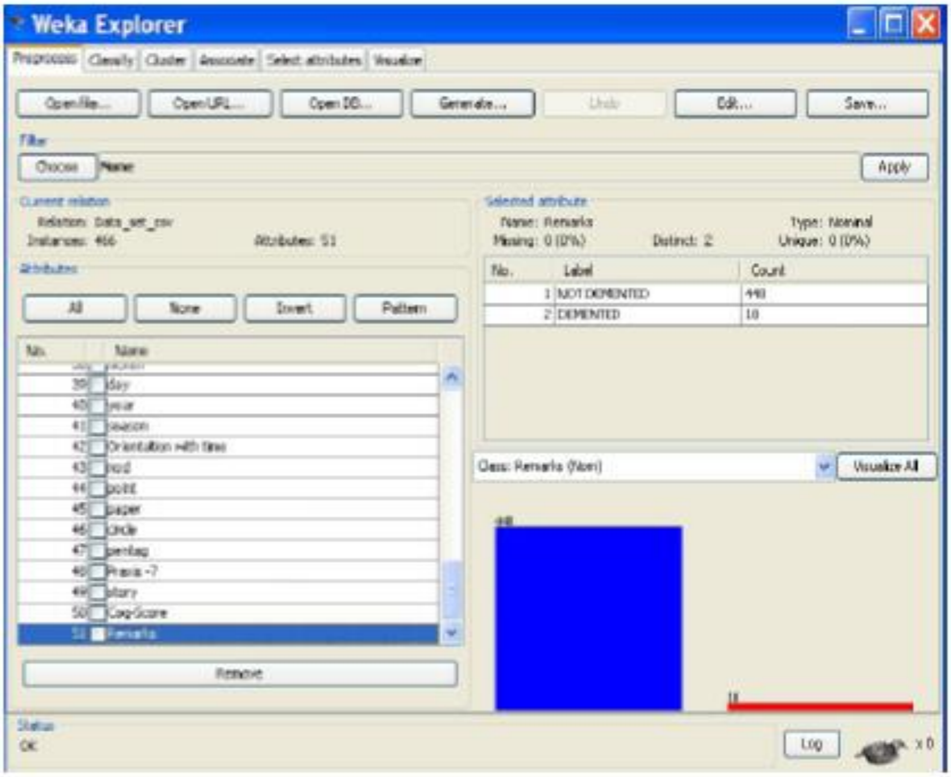


Fig. 3. Block diagram of convolutional neural network

## 5. PERFORMANCE EVALUTION

In this investigation, we implemented utilization. Two (2) learning performance evaluations are incorporated into WEKA[5].

1. **Training. Configure:** In this case, the classifier divides the dataset into test and training sets.
2. **Cross-Validation:** WEKA generates (T) models when employing n-fold cross validation. Subsequently, it computes the average of these (T) models and displays the results. The models that remain are eliminated. The model is analyzed using Explorer. The process of loading the {CSV. file } into the WEKA is illustrated in Figure 4. The data set contains (390) instances and 51 attributes. Furthermore, there are (290) negative (N-) instances and (31) positive (P.+) instances.



Filter: None

Relation: Data_set_csv
Instances: 466
Attributes: 51

| No. | Name |
|---|---|
| 39 | day |
| 40 | year |
| 41 | season |
| 42 | Orientation with time |
| 43 | word |
| 44 | point |
| 45 | paper |
| 46 | Circle |
| 47 | pentag |
| 48 | Praxis -7 |
| 49 | story |
| 50 | Cog-Score |
| 51 | Remarks |

Name: Remarks
Type: Nominal
Missing: 0 (0%)
Distinct: 2
Unique: 0 (0%)

| No. | Label | Count |
|---|---|---|
| 1 | NOT DEMENTED | 448 |
| 2 | DEMENTED | 18 |

Class: Remarks (Nom)

OK

x 0

Fig. 4. CSV. file loaded to ^Weka explorer.[12]

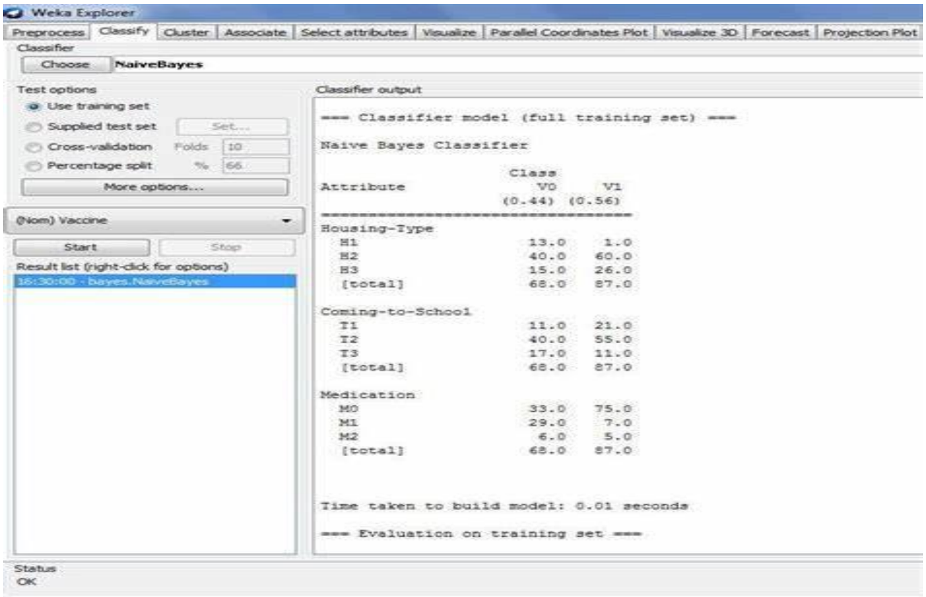
A dataset on CKD that is publicly accessible at the UCI Machine Learning Repository (https://archive.ics.uci.edu/ml/datasets/Chronic_Kidney_Disease) [24] has been used. Four hundred individuals in the dataset were classified as having CKD and not having CKD. For each patient, twenty-five disease-related data were collected (see Table 1).

TABLE 1: ATTRIBUTES IN KIDNEY DISEASE DATASET AS GIVEN IN UCI MACHINE LEARNING REPOSITORY

| **Symbol** | **Description** | **Symbol** | **Description** |
|---|---|---|---|
| age | Age | Sod | Sodium |
| bp | Blood Pressure | Pot | Potassium |
| sg | Specific gravity | Hemo | Hemoglobin |
| al | Albumin | Pcv | Packed Cell Volume |
| su | Sugar | Wc | White Blood Cell Count |
| rbc | Red Blood Cells | Rc | Red Blood Cell Count |
| pc | Pus Cells | Htn | Hypertension |
| pcc | Pus Cell Clumps | Dm | Diabetes Mellitus |
| ba | Bacteria | Cad | Coronary Artery Disease |
| bgr | Blood Glucose Random | Appet | Appetite |
| bu | Blood Urea | Pe | Pedal Edema |
| sc | Serum Creatinine | Ane | Anemia |
| | | Class | Class |

The information-data utilized in this investigation was. While [*ARFF] is WEKA's native data storage format, it is presented in the form of a datasheet. Eleven The data from the spreadsheet will be converted to a CSV format. Subsequently, the CSV file is converted to an ARFF file [12].

We used two classifier folders in our study such as ((RF-Random Forest) and Naive Bayesian) shown Figure 5. Various algorithmic models are included with each one. They are distinctive in their ability to test, validate, and develop models using the dataset. They are a diverse array of models, including statistical-based learning models, neural network models, multiple training subsets, association rules for correlation models, and decision trees with nodes representing a test.



Classifier: NaiveBayes

● Use training set
○ Supplied test set
○ Cross-validation Folds 10
○ Percentage split % 66

(Nom) Vaccine

16:30:00 - bayes.NaiveBayes

```
=== Classifier model (full training set) ===

Naive Bayes Classifier

                       Class
Attribute                 V0      V1
                      (0.44)  (0.56)
====================================
Housing-Type
  H1                    13.0     1.0
  H2                    40.0    60.0
  H3                    15.0    26.0
  [total]               68.0    87.0

Coming-to-School
  T1                    11.0    21.0
  T2                    40.0    55.0
  T3                    17.0    11.0
  [total]               68.0    87.0

Medication
  M0                    33.0    75.0
  M1                    29.0     7.0
  M2                     6.0     5.0
  [total]               68.0    87.0


Time taken to build model: 0.01 seconds

=== Evaluation on training set ===
```

Status
OK

Fig. 5. Random Forest and Naive Bayesian with Weka

The experimental data set was divided into two groups: 20% for assessment and 80% for training. The results of the suggested approach that was evaluated and trained upon are presented in Table 2. Among several criteria, our suggested system method assesses false negative rate, false positive rate, and precision. Consult equations 3, 4, and 5 to assess system performance.

Where: TP, TN, FP, and FN denote the number of True Positive cases, True Negative cases, False Positive cases, and False Negative cases, accordingly. The percentage of papers returned that are relevant to the query is known as precession.

Recall is the number of documents that were retrieved that are pertinent to the query.

Our system achieved 81% accuracy as a detector of kidney disease when applied naïve Bayesian while 89% when used

Random Forest algorithm. in addition in this study, decreased the rates of false positives and false negatives in comparison to previous research, as indicated by [20]. The precision achieved in [20] was inferior to that of the proposed method. Previous research has also employed partition-based approaches or conducted tests having not removed first noise from images or uses. When employing the naïve Bayesian algorithm, the proposed system obtains an accuracy of 81%. However, when employing the Random Forest algorithm, the accuracy is 89%.

TABLE II. THE EFFICIENCY OF THE SUGGESTED SYSTEM IS DEMONSTRATED IN TESTING AND TRAINING

| Method | Accuracy | Recall | Precession | F-Measure |
|---|---|---|---|---|
| Random Forest | 89% | 1 | 1 | 1 |
| Naïve Bayesian | 81% | 0.91 | 0.90 | 0.90 |

## 6. CONCLUSIONS

This research offers a method for diagnosing renal disease through the use of a Convolutional Neural Network model, which will assist physicians in their diagnostic procedures. In order to achieve this, we employed CKD information that is publicly accessible on UCI ML repository. (https://archive.ics.uci.edu/ml/datasets/Chronic_Kidney_Disease) .These medical images have been transformed into a spreadsheet for the purposes of this investigation. The proposed method produced favorable results when compared to the existing methods. It was 89% accurate. Naive Bayesian achieved 81% accuracy in comparison to random forest. Our research can assist medical professionals or the institution in making more informed decisions.

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### Conflicts Of Interest

The author's disclosure statement confirms the absence of any conflicts of interest

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