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Performance based Evaluation of Algorithmson Chronic Kidney Disease using Hybrid Ensemble Model in Machine Learning

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In medical data science, data classification, pattern generation, data analysis and improving classification accuracy are the important issues in the recent scenario. The main objective of this research to enhanced classification accuracy by four combinations of features technique separately with Neural Network classifier approach. The neural network is analyzed for chronic kidney disease with the help of features reduction and relevant techniques. In experiment, we used neural network as ensemble model with different features techniques as: Pearson Correlation, Chi-Square, Extra Tree and Lasso regularization. In this research paper, we have prepared training model on 300(75%) instances of chronic kidney disease attributes and testing on 100 (25%) instances. We test the dataset on different applied epochs and calculated accuracy with error rate. The summary of this experiment, we used400 instances with 26 attributes of Chronic Kidney Disease and evaluated highest accuracy calculated (99.98%) with less error rate on passing several epochs by Neural Network ensemble with Lasso model.

Keywords: Correlation Features Selection Method: Extra Tree Chi-Square; Epoch; Error Rate Accuracy; Features Important; Neural Network; Pearson Correlation; Variable Selection and Regularization: Lasso Model.

Chronic kidney failure is not known until its function deteriorates. Kidney function can only be assessed if it is too bad, then kidney transplantation will be only one way to safe human life.

Transplantation will be only one way remains by which can be avoided in this fatal situation. Some symptoms arise when the kidney is unhealthy such as:

- Frequent nausea
- Frequent vomiting
- Loss of appetite
- Fatigue
- Excessive weakness of sleep
- Lack of sleepiness
- Frequent urination changes
- Mentally weak muscles
- Spasms, feeling of tension
- Tension, swelling of feet
- Persistent itching in the body[1].

On the basis of our previous analysis[2-6], we calculated high accuracy on the basis of ensemble method and majority of voting. The machine learning algorithm provides an environment that makes the study of the data set very easy for the analyst. Machine learning has different algorithms for different property patterns. Some algorithms describe the relationship between attributes and what types of attributes are present in the data set, and some algorithms identify their distribution intensity etc.

Nithya A et al. [2020], discussed about normal and abnormal kidney disease by neural network. Authors used ultrasound image, neural network, multi-kernel k-means clustering, GLCM features, segmentation, classification and bilateral filter for better prediction. They used linear and quadratic based segmentation for find better accuracy (99.61%) compare with other machine learning algorithms[7].

Verma AK et al. [2020], analyzed about skin disease by six different machine learning algorithms. Authors used bagging, AdaBoost, and gradient boosting Meta classifiers to predict class level variable prediction. They find accuracy (99.68%) after the applied features selection method, gradient boosting trained algorithms[8].

Harimoorthy K and Thangavelu M [2020], observed that the hidden pattern in the Chronic Kidney Disease, Diabetes and Heart Disease by different SVM method with Random forest and decision tree. They calculated accuracy (98.7%) by SVM-Radial bias kernel technique on diabetes medical dataset[9].

Nazari M et al.[2020], considered tumor patients CT images by different preprocessing machine learning techniques. Authors used three different features selection methods and applied on SVM, random forest, and logistic regression machine learning algorithms. They measured receiver operating characteristic curve on bootstrapped validation cohort and find highest values (0.83) for the SVM model[10].

Yadav DC and Pal S.[2020], discussed about different medical dataset from UCI to prevent deaths from several diseases. Authors minimize error of information in diagnosis by machine learning algorithms and they used proposed new feature selection method combined with twin-bounded support vector machine. Finally TBSVM calculated accuracy (86.18%) on different medical dataset[11].

Yadav DC and Pal S [2020], discussed about lack of cardiovascular centre in rural side. In this paper authors used heart data sample from UCI repository. Authors used cluster-based DT learning at various levels for class set combination. They calculated accuracy (88.90%) by cluster Based random forest machine learning algorithm[12].

Chaurasia V et al., [2020], identified lower back pain in chronic as a muscled pain, nerves and bones. They used Genetic Algorithm (GA)-based feature selection to improve classification accuracy and used seven classification algorithms. Finally authors find k-Nearest Neighbors calculated better accuracy (85.2%) compare with other machine learning algorithms[13].

Alloghani M et al. [2020], analyzed about high-risk of cardiovascular disease and complications in kidney problem. Authors used decision tree boosted decision tree, CN2 rule, logistic regression (Ridge and Lasso), neural network, support vector machine and find support vector machine calculated highest accuracy (91.7%)[14].

Shon HS et al. [2020], discussed about kidney cancer prognosis for (1157) patients and calculated classification accuracy by machine

Table 1. Representation of previous studies by some machine learning algorithms

Authors	Methods	Classification Accuracy
Nithya A et al. [2020]	ANN and multi-kernel k-means clustering	(99.61%)
Verma AK et al. [2020],	Bagging, AdaBoost, and Gradient Boosting	(99.68%)
Harimoorthy K and Thangavelu M [2020],	SVM, RF and DT.	(98.7%)
Nazari M et al.[2020],	SVM, RF, and LR	(83%)
Lima MD et al.[2020],	TBSVM	(86.18%)
Magesh G and Swarnalatha P [2020]	Cluster-Based DT and Cluster Based RF	(88.90%)
Al Imran A et al. [2020],	Genetic Algorithm and K-NN	(85.2%)
Alloghani M et al. [2020],	DT, Ridge, Lasso, NN and SVM	(91.7%)
Shon HS et al. [2020],	RF with Lasso and Smote Sampling	(98.08%)

learning algorithms. They used Random forest with lasso method and smote sampling and find (98.08%) accuracy. Authors used different stages of prediction by various features selection methods and prediction methods for better predictions[15].

The main goal of this research is to enhanced classification accuracy by four combinations of features technique separately with Neural Network classifier approach. The neural network is analyzed for chronic kidney disease with the help of features reduction and relevant techniques.

MATERIAL AND METHODS

In this section, we experimentally define Neural Networks with features important extra tree algorithms, lasso regularization and Pearson correlation extraction methods. In this study, we conducted epoch, error rate, accuracy and their improvement from medical dataset. The medical dataset are stored from UCI with features repository and their correlative features. In this experiment, we used Python, R languages with Weka tool.

Data Description

We have analyzed 400 instances with 26 attributes of Chronic Kidney Disease to find the true and false distribution of classes by 0 and 1 as:

Classification

```
0   150
1   250
dtype: int64
```

The detailed of chronic kidney disease with attributes: Age: Represent by numeric values, bp : Measure the blood pressure, sg : represent gravity specific values, al : represents albumin values, su: sugar, rbc: count as red blood cells, pc: count pus cell, pcc: count pus cell clumps values, ba : detect bacteria, bgr : represents blood glucose random numeric values, bu : Analyzed blood urea, sc : represents serum creatinine numeric values, sod : measure sodium values in body, pot : represents potassium values, hemo : measure hemoglobin numeric values, and other attributes pcv, wc, rc, htn, dm, cad, appet, pe, classification with descriptions as packed cell, volume, white blood cell count, red blood cell count, hypertension, diabetes mellitus, coronary artery disease, appetite, pedal edema, anemia and class respectively.

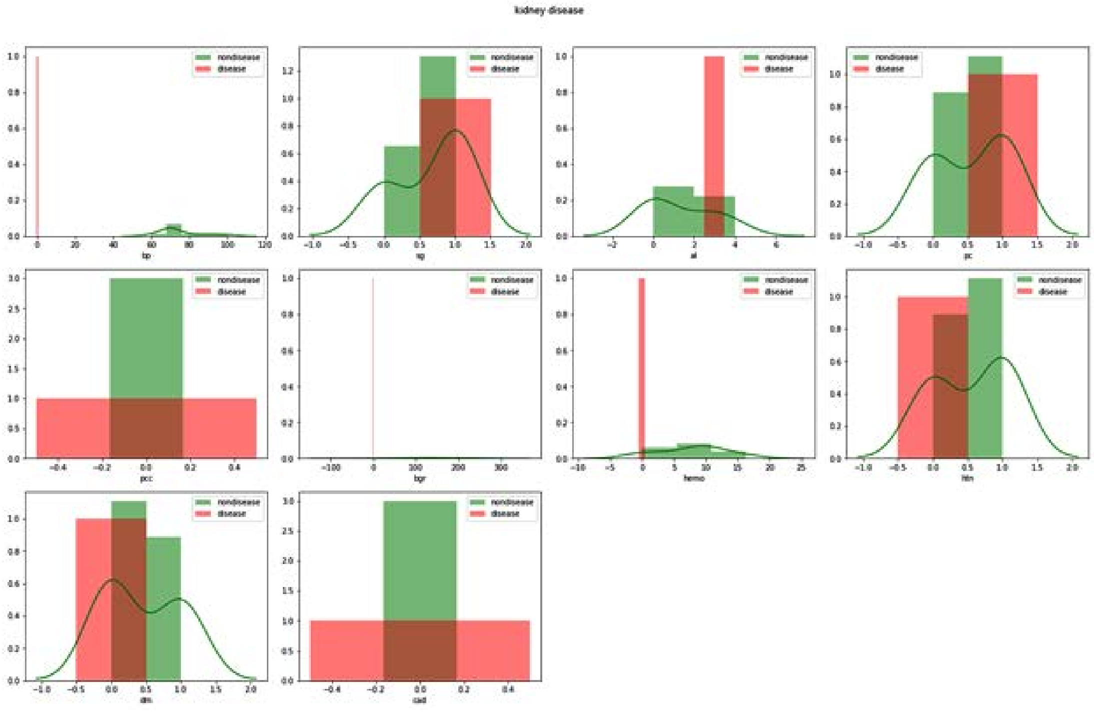

Fig. 1. Representation of density of each attributes on the basis of target variables classification

We measured the density of each attributes on the basis of target variables classification and represent as:

Epoch

In this paper, we used epoch as a number of instances passes or complete passes through chronic kidney disease training dataset[16]. In this analysis we used number of epoch from 100-600 to check the error rate and accuracy evaluated at various level.

Error Rate

In this research, we used error rate as inaccuracy of predicted output values[17]. In this experiment, we find if target values categories then the error express in the form of error rate.

Table 2. Representation of highly correlated features (cor_target>0.5) by Pearson Correlation

id	0.838528
al	0.531562
rbc	0.510667
hemo	0.569312
pcv	0.599753
rc	0.643162
htn	0.590438
dm	0.559060
classification	1.000000

Accuracy

In this experiment, we observed and examined good prediction of correct class. It makes decision in diagnosis of chronic kidney disease[18]. It is calculated as per the equation:

Accuracy=(Correctly Predicted Class)/(Total Testing Class) *100.........(1)

In the research, we have study[19-34] for accuracy and error rate on various disease and find how instances and features closely relate with each other.

Proposed Method

In this research paper, we used Neural Network as a classifier of input variables. We have used four features based algorithms: Extra Tree, Pearson Correlation, Lasso model and Chi-Square for better prediction. In this research paper, we have prepared training model on 300(75%) instances of chronic kidney disease attributes and testing on 100 (25%) instances. We calculated various prediction model of Neural Network with higher and lower classification accuracy with different error rate.

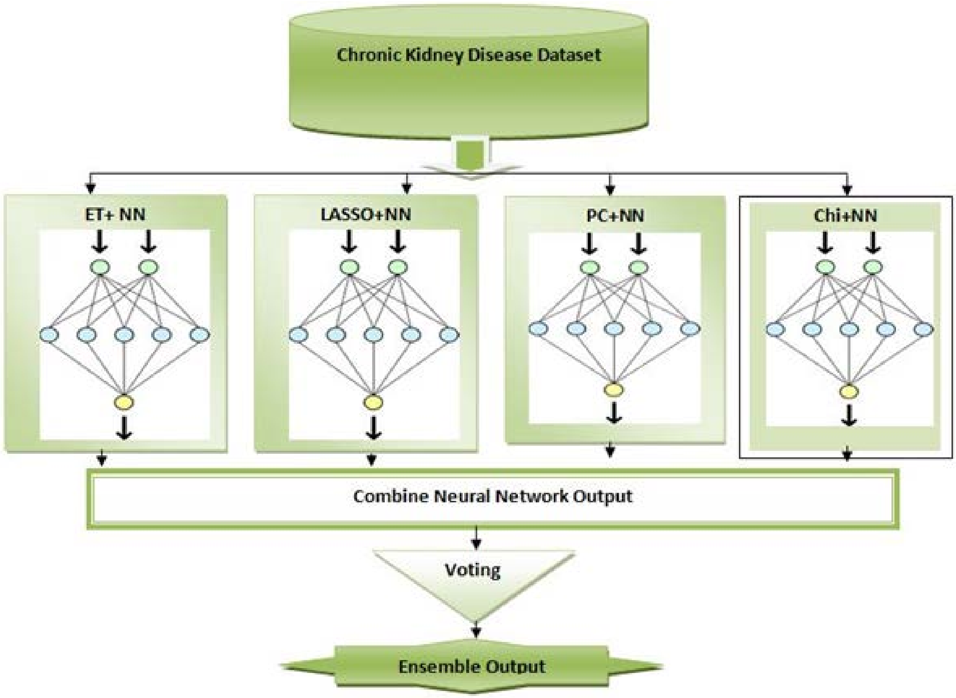

Fig. 2. The Proposed Ensemble Model of Neural Network

We have ensemble neural network with extra tree, Pearson Correlation, Chi-Square and Lasso regularization separately then find their performance improved as per experimental results. We find classification accuracy continuous increase and error rate continuous decrease with the increasing of epoch values.

RESULTS

In this section, the neural network, extra tree, lasso model, Pearson correlation and Chi-square perform the function based classification algorithms. Neural network perform as an ensemble model with lasso model. All the medical dataset are

All the Chronic Kidney features with their low and high relevant are calculated as:

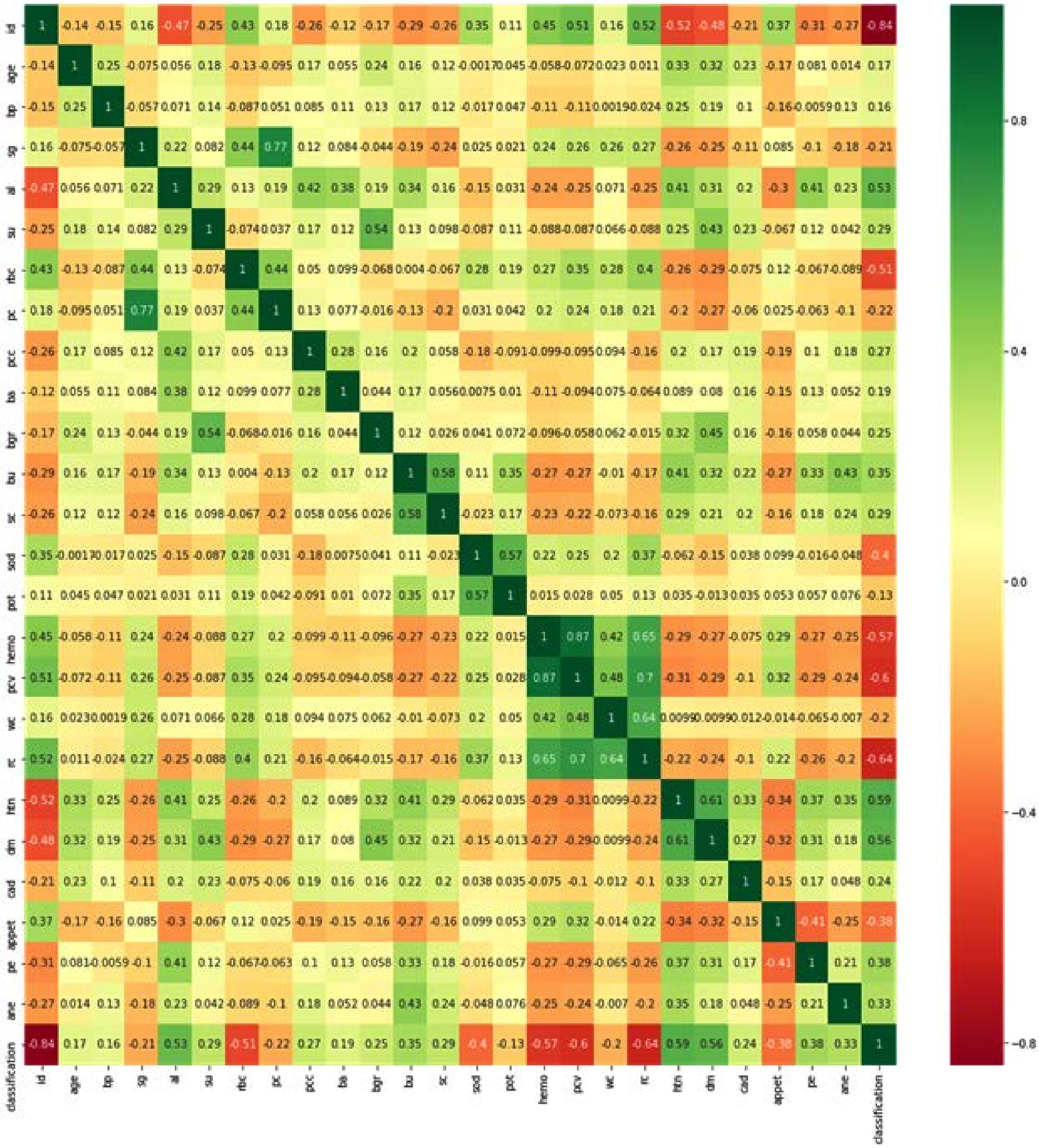

Fig. 3. Representation of Pearson Correlation with target variable classification

collected from UCI repository. All medical dataset are preprocessed and removed missing values from relative dataset and identify the important features by extra tree features algorithms. The medical dataset in these dataset have different ranges. We have used features selection techniques in whole dataset and select highly relevant attributes by Lasso model, Pearson correlation and chi-square. In each experiment the instances of kidney disease classify into two sections as like training and testing with 75% and 25% in whole instances. The results were done only by class level so we determined number of parts the input variable has to be divided.

Table 2., represents the selected highly correlated features (cor_target>0.5) because Pearson Correlation decides variables relationship between -1 to +1. The positive correlations assign both variables increase and decrease in same direction. Conversely, negative correlations assign both variables move inversely. A zero assigns no correlation between variables.

Table 3., represents the correlation matrix as square with same variables in the rows and columns. The lines 1.00 going from top left to the right bottom in diagonal form symmetrically, with the same correlation is shown in figure 3.

Table 3. Representation of correlated features in matrix format by Pearson Correlation

id	1.000000	-0.468924	0.432045	0.450748
al	-0.468924	1.000000	0.128814	-0.243399
rbc	0.432045	0.128814	1.000000	0.274146
hemo	0.450748 –	0.243399	0.274146	1.000000
pcv	0.704580	1.000000	-0.217147	-0.235200
rc	0.704580	1.000000	-0.217147	-0.235200
htn	-0.309572	-0.217147	1.000000	0.608118
dm	-0.287206	-0.235200	0.608118	1.000000

Table 4. Representation of Importance Features values by Extra tree of Chronic Kidney Disease

```
[0.0334831 0.00088889 0.00158434 0.005774340.02531112  0.03668745 0.0020202 0.00045818 0.  0.00368648
0.01682511 0.0009837  0.03013153 0.01168918 .03236054 0.02420388 0.00411614 0.05588843 0.12033901
0.15148568 0.  0.00600248 0.01873192 0.01109339 0.40625492]
```

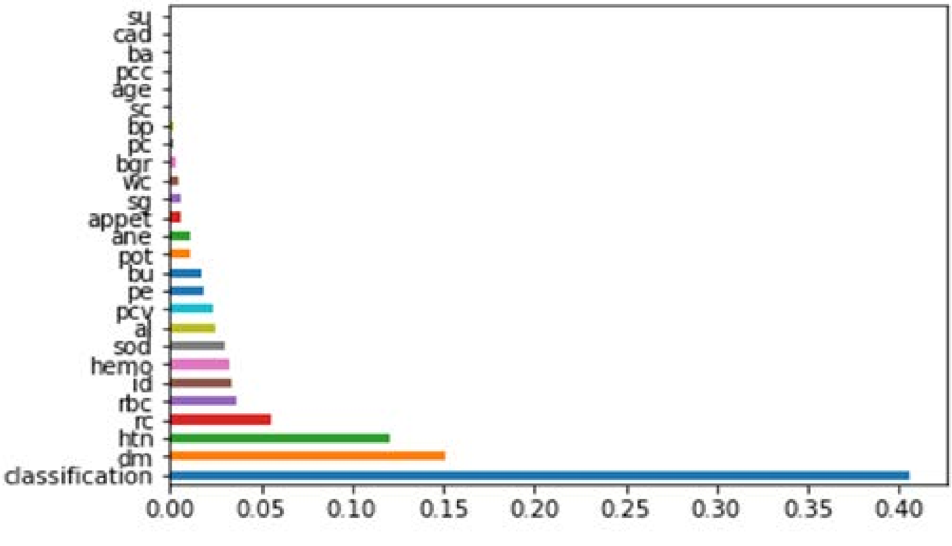

Fig. 4. Representation of Features Importance by Extra tree of Chronic Kidney Disease

Figure 3., represents selected features correlation as dark green values represents high correlation and dark red represents weak correlations. In the first row attribute ID highly correlated itself and weakly correlated with attribute Classification. In the last row Classification attribute highly correlate with itself and weakly with attributes ID.

Table 4., represents calculated important features in dataset. These calculated values plot same as in figure 4., the value (0.40625492) of attribute Classification and various attributes assigned by very less values. Figure 4., represent all attributes not assigned their less values but table 4., provide attributes decimal very less values .

Extra Tree features selection method used on whole original sample instead to reduce bias and randomly select the split point of each node to reduce variance. This features selection technique provides the results for kidney disease and calculated highest values of selected attributes: Classification, dm, htn, rc rbc, id, hemo, sod, al, pcv, pe, bu, pot and ane.

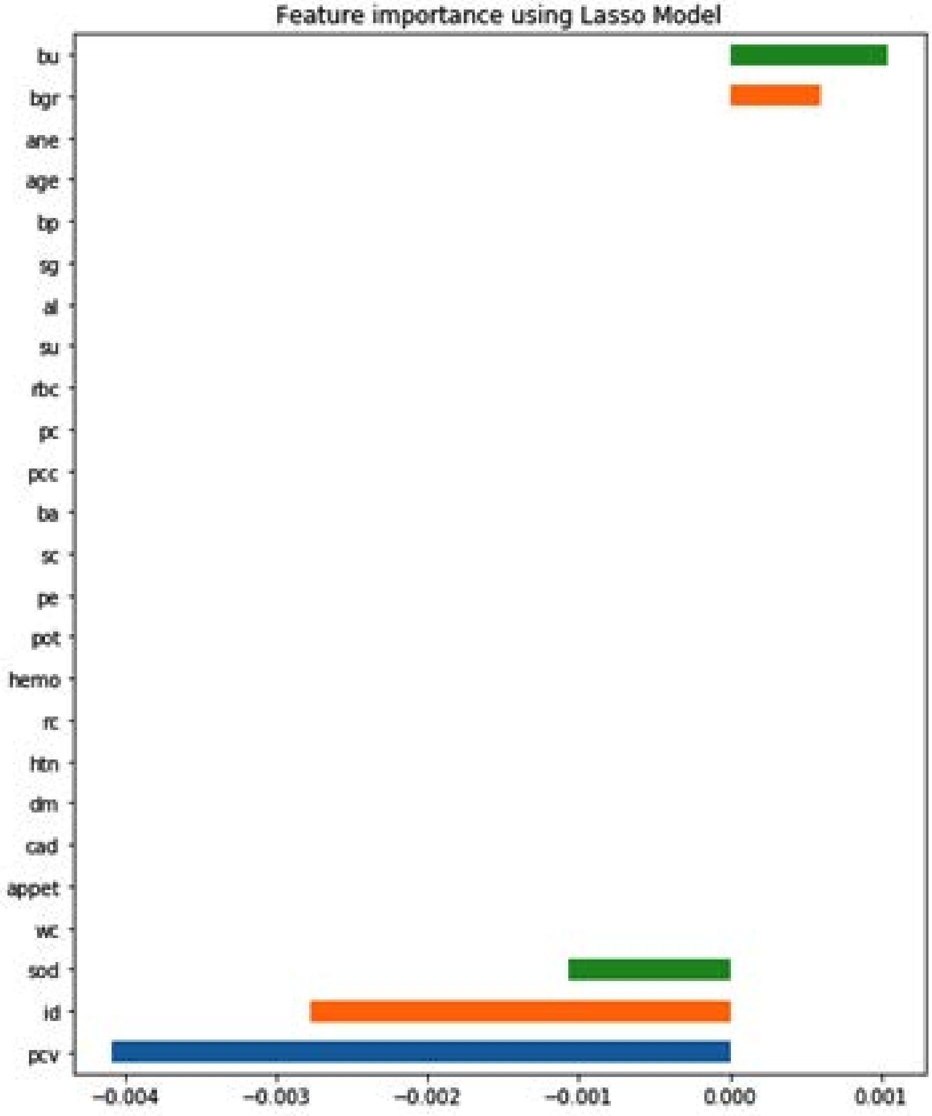

Fig. 5. Represents the result of Lasso selected attributes in CKD

Table 5. Represents the result of Chi-Square technique on CKDattributes

	Specs	Score
17	wc	52947.074533
0	id	18796.992481
11	bu	2363.959173
13	sod	1926.392920
10	bgr	1462.940044
16	pcv	1291.222184
12	sc	360.413289
15	hemo	298.668389
18	rc	291.906188
4	al	216.000000
25	classification	150.000000
5	su	94.800000
19	htn	88.200000
20	dm	82.200000
1	age	80.885458
2	bp	46.109201
23	pe	45.600000
6	rbc	39.638710
24	ane	36.000000
8	pcc	25.200000
14	pot	22.685267
21	cad	20.400000
9	ba	13.200000
22	appet	12.214721
7	pc	3.010746

The LASSO features selection method used to shrinking and removing the coefficients can reduce variance without a substantial increase of the bias. The variables that have a non-zero coefficient after the shrinking process because shrinking process penalizes the coefficients of the regression variables and regulates some of them to zero. Lasso Method represents non_ penalized variables with values range and picked 6 variables and eliminated the other 19 variables as:

Best alpha using built-in LassoCV: 0.437812

Best score using built-in LassoCV: 0.776112

Chi-Square calculated with k-fold cross validation, k=10 and explains attributes scores as:

Chi-Square used to test and compare observed with expected frequencies highly sensitive to sample size. The main objective of this features selection method to find goodness of fit variables and measures how well the observed distribution of data fits with independent variables. With the results, we find improvement in classification accuracy and reduce the error rate values by selected features mentioned in discussion section.

Table 6. Representation of training model of 300 instances of CKD attributes

Serial Epoch	NN Accuracy	ET+NN Accuracy	LASSO+NN Accuracy	PC+NN Accuracy	Chi+NN Accuracy
100	75.60	85.27	98.95	72.38	93.35
200	79.90	92.36	99.51	78.97	93.95
300	82.67	95.48	98.93	97.36	96.81
400	87.31	95.73	99.73	95.47	95.87
500	87.29	95.97	98.87	98.43	96.97
600	87.10	95.89	98.99	98.70	96.91

Table 7. Representation of testing model 100 instances of CKD attributes

Serial Epoch	NN Accuracy	ET+NN Accuracy	LASSO+NN Accuracy	PC+NN Accuracy	Chi+NN Accuracy
100	74.10	87.31	99.17	73.17	94.15
200	78.37	91.12	99.21	79.38	94.96
300	81.13	96.18	99.69	96.10	95.87
400	87.27	96.61	99.98	96.18	95.99
500	87.31	96.57	99.96	97.97	97.35
600	87.32	96.56	99.97	97.93	97.81

DISCUSSION

This section discussed all experimental setup and analyzed Chronic Kidney Disease the performance of neural network was compared with & without features selection methods: neural network with extra tree, lasso method, Pearson correlation and chi-square and predict the complex medical disease.

The table. 5 represents training model on 300 instances of CKD attributes and we find the increment in accuracy for each algorithm with the passing on different epochs. The algorithm neural network have less accuracy compare to other ensemble model but we find at a level (epoch 500 & 600) all the algorithms have minor changes. The lasso method with neural network always (epoch 100 -600) calculated high accuracy compare with other ensemble model.

The table 7., representation the testing model on 100 instances of CKD attributes and we find the increment in accuracy for each algorithm with the passing on different epochs. The algorithm neural network have less accuracy compare to other ensemble model but we find at a level (epoch 500 & 600) all the algorithms have minor changes. The

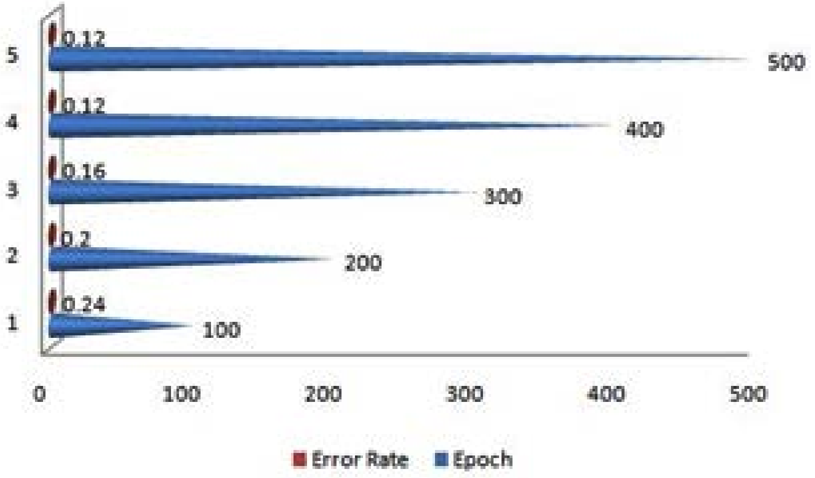

Fig. 6. Representation Neural Network Error Rate and Epoch

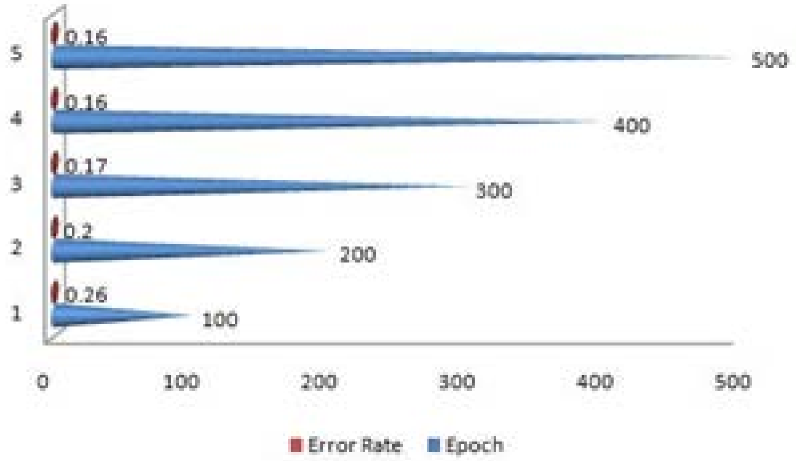

Fig. 7. Representation(ET+NN) Error Rate and Epoch

lasso method with neural network always (epoch 100 -600) calculated high accuracy compare with other ensemble model.

A figure (6-10) represent the testing model on 100 instances of CKD attributes of workflow error rate and passes epoch by neural network with features methods and generates different data prediction models. The neural network determines the nature of data and generates a train to medical data set. The experimental setup identified last score values for error rate and passes epoch. The error rate of all algorithms have major differences with the passing epoch (100-400) but after that we find minor changing (near nothing) in error rate with passing epoch (500-600). The neural network find (0.12), extra tree (0.36) and ensemble model of neural network with: extra tree (0.16), Lasso model (0.0001), Pearson correlation (0.6) and Chi-square (0.07). After the passing epochs from (100-600), we observed again from (700-1000) epochs but did not find major differences between error rate and calculated accuracy.

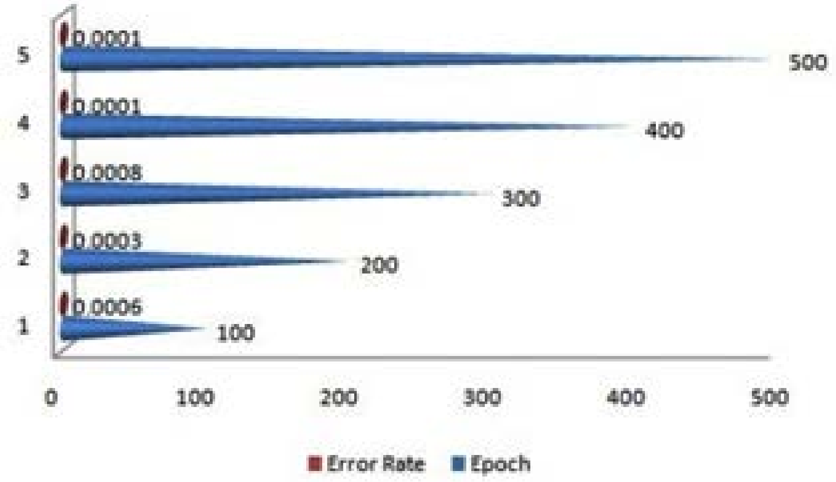

Fig. 8. Representation (Lasso+NN) Error Rate and Epoch

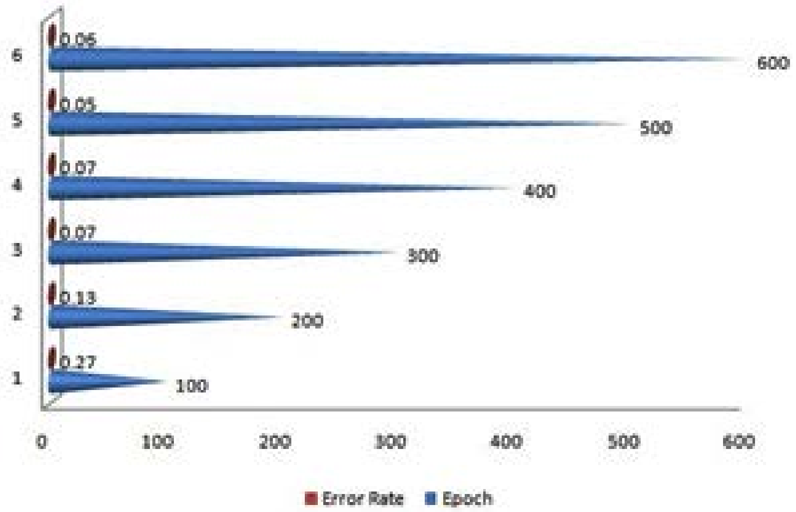

Fig. 9. Representation (PC+NN) Error Rate and Epoch

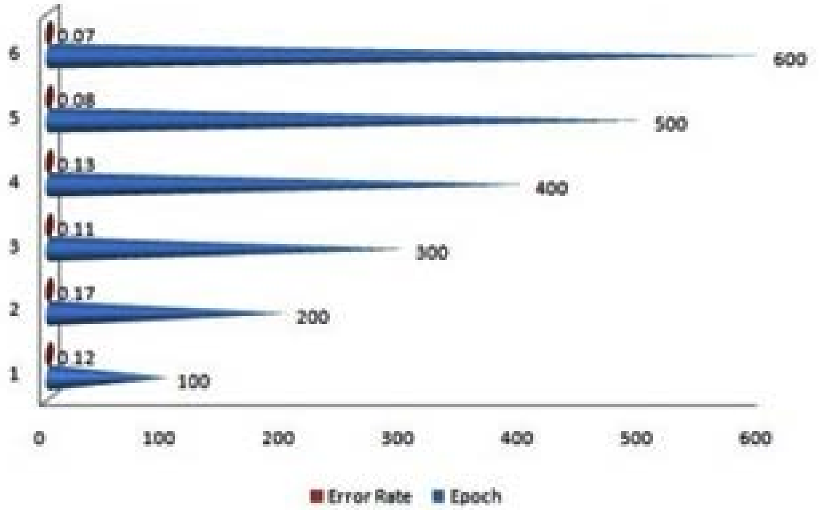

Fig. 10. Representation (Chi+NN) Error Rate and Epoch

CONCLUSION

In this research paper, we stored data from UCI Repository, 400 instances with 26 attributes of Chronic Kidney Disease. With the results, it is clear that the highest accuracy calculated (99.98%) by Neural Network ensemble with Lasso model. The Neural Network with Lasso model always calculated highest accuracy for each epoch. This ensemble model prepared minimum error rate but calculated error rate is not less compare with other algorithms. The Neural network without ensemble calculated very less error rate compare with other algorithms but calculated less accuracy compare with other algorithms. Finally we find Neural Network with Lasso Model calculated high accuracy and less error rate. The error rate of Neural Network ensemble valuable on two decimal points so we measure error rate difference were minor compare with Neural Network. So Neural Network ensemble with Lasso model performed better compare with other algorithms. For future, we will use feature extraction with feature selected as hybrid modified various applications.

Conflict of Interest

Authors have no conflict of Interest.

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