Analysis of Heart Disease Using Parallel and Sequential Ensemble Methods With Feature Selection Techniques: Heart Disease Prediction

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ABSTRACT

This paper has organized a heart disease-related dataset from UCI repository. The organized dataset describes variables correlations with class-level target variables. This experiment has analyzed the variables by different machine learning algorithms. The authors have considered prediction-based previous work and finds some machine learning algorithms did not properly work or do not cover 100% classification accuracy with overfitting, underfitting, noisy data, residual errors on base level decision tree. This research has used Pearson correlation and chi-square features selection-based algorithms for heart disease attributes correlation strength. The main objective of this research to achieved highest classification accuracy with fewer errors. So, the authors have used parallel and sequential ensemble methods to reduce above drawback in prediction. The parallel and serial ensemble methods were organized by J48 algorithm, reduced error pruning, and decision stump algorithm decision tree-based algorithms. This paper has used random forest ensemble method for parallel randomly selection in prediction and various sequential ensemble methods such as AdaBoost, Gradient Boosting, and XGBoost Meta classifiers. In this paper, the experiment divides into two parts: The first part deals with J48, reduced error pruning and decision stump and generated a random forest ensemble method. This parallel ensemble method calculated high classification accuracy 100% with low error. The second part of the experiment deals with J48, reduced error pruning, and decision stump with three sequential ensemble methods, namely AdaBoostM1, XG Boost, and Gradient Boosting. The XG Boost ensemble method calculated better results or high classification accuracy and low error compare to AdaBoostM1 and Gradient Boosting ensemble methods. The XG Boost ensemble method calculated 98.05% classification accuracy, but random forest ensemble method calculated high classification accuracy 100% with low error.

KEYWORDS

AdaBoost, Chi-Square, Decision Stump Algorithm, Gradient Boosting, J48 Algorithm, Pearson Correlation, Random Forest Classifiers, Reduced Error Pruning, XGBoost
1. INTRODUCTION

Virani SS et al., (2020), introduced about heart organ importance. The heart is an important organ of human body in which various vessels support in blood flows to different parts of the body. Our heart is a complex structure consisting of muscles. It suffers from various types of diseases in the heart by more or less blood secretion. The cardiovascular is a heart diseases and the main cause of cardiovascular diseases is poor lifestyle, stress, coma, not exercising and irregular food intake. These life style leads to disability on heart and invites serious heart related diseases. So, healthy heart is very important for human life because it is necessary to keep the body healthy. If a person has been faced the problem of heart attack, then he should change his lifestyle to keep the heart healthy. Sometimes heart diseases show some of their symptoms then we should not avoid it easily.

1.1. Types of Heart Disease

1.1.1. Coronary Artery Disease

This disease is very common, which is caused due to the accumulation of arteries in the arteries and stops the flow of blood in the heart and brings the heart to a state of zero and increases the risk of stroke.

1.1.2. Hyper Tensile Heart Disease

This disease is caused by high blood flow in the arteries, as a result of which the blood vessels become heavy and the incidence related to heart disease problem.

1.1.3. Rheumatic Heart Disease

This disease arises due to damaged heart valve and the patient faced coma as heart disease which is associated with rheumatic fever. Due to this disease, the tissues connecting the brain, the joints of the brain and the skin get affected and these organs become inflamed.

1.1.4. Congenital Heart Disease

This disease is visible due to the lack of proper heart structure at birth, because it is not able to be in normal state due to bad heart condition.

1.2. The Main Causes of Heart Disease

- Increased cholesterol
- Smoking more
- Excess alcohol consumption
- Maintaining a state of constant tension
- Heredity
- Excess body fat
- High blood pressure
- Stretching with pain due to artery block in the heart and increasing the possibility of heart attack
- Excess of nausea
- Chest irritation and imbalance in digestive functions
- Excess of pain in the hands and down the left shoulder
- Excessive phlegm and white or pink color
- Excess of sweat from the body while lack of physical activity
1.3. Algorithms Description

1.3.1. J48

Gupta A et al., (2020), introduced about decision tree and their performance. C4.5 (J48) is a decision tree algorithm that was developed by Ross Quinlan. C4.5 is an extend algorithm of Quinlan’s ID3 and the decision trees generated by C4.5 can be used for prediction in data classification. The main objective of this algorithm to solve both classification and regression problems also lead to overfitting of the data (Table 1).

Table 1. Representation of J48 algorithm experimental performance on heart disease attributes

| cp <= 0 |
|---------|
| | ca <= 0 |
| | | thal <= 2 |
| | | | thalach <= 118: zero (8.0) |
| | | | thalach > 118 |
| | | | exang <= 0 |
| | | | | chol <= 315: one (68.0) |
| | | | | chol > 315 |
| | | | | | age <= 61: zero (4.0) |
| | | | | | | exang > 0 |
| | | | | | | | restecg <= 0: one (12.0) |
| | | | | | | | | restecg > 0 |
| | | | | | | | | | slope <= 1 |
| | | | | | | | | | | trestbps <= 115: one (3.0) |
| | | | | | | | | | | | trestbps > 115: zero (21.0) |
| | | | | | | | | | | | | age <= 65: one (3.0) |
| | | | | | | | | | | | | age > 65: zero (21.0) |
| | | | | | | | | | | | | ca > 0: zero (12.0) |
| | | | | | | | | | | | | ca > 2: one (7.0) |
| | | | | | | | | | | | | fbs > 0: one (16.0) |
| | | | | | | | | | | | | chol > 244: zero (37.0) |
| | | | | | | | | | | | | age > 68: one (22.0) |
| | | | | | | | | | | | | oldpeak > 1.9 |
| | | | | | | | | | | | | | slope <= 0: one (12.0) |
| | | | | | | | | | | | | | | slope > 0 |
| | | | | | | | | | | | | | | | ca <= 0 |
| | | | | | | | | | | | | | | | oldpeak <= 2.6: one (6.0) |
| | | | | | | | | | | | | | | | oldpeak > 2.6: zero (10.0) |
| | | | | | | | | | | | | | | | | ca > 0: zero (25.0) |
| Number of Leaves: 48 |
| Size of the tree: 95 |

1.3.2. Reduced Error Pruning

Catherine OO (2020), introduced about Clinical Diagnostic System Driven by Reduced Error. The main objective of reduced pruning tree to simplifying a decision tree by removing branches of the decision tree that is uncritical and redundant to classify instances. The advantage of reduced pruning tree is to reduce the size of decision trees by removing parts of the tree. It can not only reduce the size of the tree but also improve the classification accuracy of unseen objects (Table 2).
1.3.3. Decision Stump

Palad EB et al., (2020), introduced about decision stump machine learning classifiers in data science. It is used to generate one-level decision tree. The decision stump contains one internal node (the root) which is finally connected to the terminal nodes (its leaves). The decision stump prediction based on the value single input feature and depends upon possible several variations. This algorithm Used components weak learners or base learners in ensemble techniques parallel and sequential (Table 3).

1.3.4. Random Forest Ensemble Method

Kaandorp ML, Dwight RP., (2020), introduced about random forests algorithm work as randomly decision forests in machine learning. We can use random forest as an ensemble method for better

| Table 2. Representation of REP algorithm experimental performance on heart disease attributes |
|---------------------------------------------|---------------------------------------------|
| cp < 0.5                                    |                                             |
|    | ca < 0.5                                    |
|    |    | exang < 0.5                                  |
|    |    |    | thal < 2.5                                   |
|    |    |    |    | thalach < 96.5: zero (2/0) [2/0]              |
|    |    |    |    | thalach >= 96.5: one (30/1) [25/3]           |
|    |    |    |    | thal >= 2.5                                   |
|    |    |    |    |    | restecg < 0.5: zero (11/0) [2/0]              |
|    |    |    |    |    | restecg >= 0.5                                |
|    |    |    |    |    |    | age < 41.5: zero (4/0) [4/0]                  |
|    |    |    |    |    |    | age >= 41.5: one (8/0) [1/0]                  |
|    |    |    | sex >= 0.5                                  |
|    |    |    |    | chol < 245.5                                 |
|    |    |    |    |    | oldpeak < 2.4                                |
|    |    |    |    |    |    | age < 65.5: one (21/0) [11/0]                 |
|    |    |    |    |    |    | age >= 65.5                                   |
|    |    |    |    |    |    |    | age < 68.5: zero (2/0) [2/0]                  |
|    |    |    |    |    |    |    | age >= 68.5: one (3/0) [0/0]                  |
|    |    |    |    |    |    |    | ca >= 0.5                                     |
|    |    |    |    |    |    |    | thal < 2.5: zero (10/3) [5/0]                 |
|    |    |    |    |    |    |    | thal >= 2.5: one (8/1) [6/3]                  |
|    |    |    |    |    |    |    | oldpeak >= 2.4: zero (9/0) [5/0]              |
|    |    |    |    |    |    |    | chol >= 245.5: zero (29/4) [20/2]             |
| Size of the tree: 71                        |                                             |

| Table 3. Representation of DS algorithm experimental performance on heart disease attributes |
|---------------------------------------------|---------------------------------------------|
| cp <= 0.5                                    |                                             |
|    | zero                                       | one                                        |
|    | 0.7545271629778671                         | 0.2454728370221328                        |
| cp > 0.5                                    |                                             |
|    | zero                                       | one                                        |
|    | 0.23484848484848486                       | 0.7651515151515151                      |
| cp is missing                                |                                             |
|    | zero                                       | one                                        |
|    | 0.4868292682926829                      | 0.5131707317073171                        |
classification, regression as decision tree forest model. We can use random forest as parallel ensemble method known as bagging Meta classifier algorithm. This algorithm tries to create an uncorrelated forest of trees by weak learners to strong learners and provide more accurate than that of any individual tree (Table 4).

Table 4. Representation of RF algorithm experimental performance on heart disease attributes

| cp < 0.5 | thal < 2.5 | ca < 0.5 | restecg < 0.5 | oldpeak < 0.1 | trestbps < 134 | age < 55.5: one (9/0) | age >= 55.5: zero (4/0) | age >= 46 | trestbps >= 134: one (12/0) | trestbps >= 134: zero (25/0) | age >= 56.5 | trestbps >= 171: one (14/0) | trestbps >= 171: zero (3/0) | cp < 2.5 | chol < 238.5: zero (4/0) | chol >= 238.5 | age < 66: zero (8/0) | age >= 66: one (6/0) | cp >= 2.5: zero (3/0) | oldpeak >= 2.55: zero (4/0) | Size of the tree: 135

1.3.5. AdaBoostM1 Ensemble Method
Çınar A et al., (2020), introduced about adaptive boosting is an iterative ensemble Meta classifiers algorithm. This method has organized by Yoav Freund and Robert Schapire in 1996. The main objective of this algorithm to achieved high accuracy or increase retrained the weak learners for particular data into strong learners (Table 5).

1.3.6. Gradient Boosting Ensemble Method
Ma B. et al., (2020), introduced about Meta classifier ensemble method in data science and convert organized weak learners into strong learners. Gradient boosting works as adaptive boosting algorithms but differ in optimize problems. It covers loss function and tries to optimize it to reduce error residuals (Table 6).

1.3.7. XG Boost Ensemble Method
Song S. et al., (2020), introduced about XG Boost sequential ensemble model in data science. It is part of Meta classifier in machine learning environment and it works with decision tree terminal nodes and calculates shrinking leaf nodes. This algorithm reduces high correlation between tree and work as gradient boosting but it has more speed and wide range compare to gradient boosting (Table 7).
2. RELATED WORK

Cai et al., (2020), analyzed ECG recordings of 16,557 patients for atrial fibrillation detection. They used deep learning and densely connected neural network for better prediction. Authors calculated accuracy (99.35%), sensitivity of (99.19%) and specificity (99.44%).
Buettner et al., (2020), discussed 499 patients of ECG and their recording. They used random forest, spectral analysis in machine Learning. Authors calculated (96.77%) classification accuracy for ECG medical dataset.

Magesh and Swarnalatha (2020), predicted 303 samples of heart patients in machine learning. Authors used random forest, cluster-based decision tree learning and calculated (89.30%) accuracy.

Harimoorthy and Thangavelu (2020), considered support vector machine with RBK and analyzed support vector machine with linear, polynomial, random forest and decision tree. Authors calculated (98.3%), (98.7%) and (89.9%) accuracy for SVM with polynomial, random forest and decision tree.

Miled et al., (2020), considered cases of heart patients and control 11,558 heart cases from 15 and 25 different institutions. They have used random forest for dementia prediction in machine learning. Authors calculated (77.43%) classification accuracy for by random forest in heart disease.

Amin, M.S., et al., (2019), discussed about hybrid technique for better prediction in heart disease medical dataset. They used naïve bayes, logistic regression, k-NN, support vector machine, neural network and vote. Authors generate a hybrid technique with naïve bayes and logistic regression and find (87.4%) classification accuracy.

Verma AK et al. (2020), analyzed 366 instances and 34 attributes of heart disease in machine learning. They have used PAC, LDA, RNC, BNB, NB, and ETC, bagging, AdaBoost, and gradient boosting algorithms and calculated (99.68%) classification accuracy.

We have considered review work (2012 -2020) and find the various accuracy near about (99%). In the work, we have compared parallel and sequential ensemble methods to reduce above drawback in prediction. The parallel and serial ensemble methods organized by J48 algorithm, Reduced Error Pruning and Decision Stump Algorithm decision tree based algorithms. In this research work, we have tried to test four ensemble methods and finally find Random Forest ensemble method provide better result (100%) accuracy.

3. METHODOLOGY

In this stage, we have organized all the experimental setup by machine learning algorithms. The data description section describes different types heart related problems with related attributes and visualized their distribution by classifier algorithms using python tool.

3.1. Data Preparation

The heart disease medical dataset consists of 1025 individuals’ instances with 14 attributes. The organized dataset collect from UCI Repository in binary and numeric format (Table 8). The target variable contain class level dependable variable in algebraic format. We calculated on the basis of class as:

| target | 0 → 499 | 1 → 526 |

3.1.1. Pairs Plot

Pérez-Enciso M et al., (2020), introduced about pair plot of attributes distribution. A pairs plot assigns the features distribution of single variables and strength between two variables. This method assigns relationship between two variables and identifies the trends for analysis (Figure 1).
3.1.2. Statistical Matrix Evaluation

In this research, we have used some computational formula for Kappa Statistic, Classification Accuracy and Errors on heart disease. Yadav DC, Pal S., (Chaurasia & Pal, 2020a; Chaurasia & Pal, 2020b; Kumar et al., 2019; Verma et al., n.d.; Yadav & Pal, 2019a; Yadav & Pal, 2019b; Yadav & Pal, 2020b).

The kappa statistic measure of how closely the instances classified using expected and observed agreement in data science environment. It is formulated as:

\[
\frac{(\text{Observed Values} - \text{Expected Values})}{(1 - \text{Expected Values})} \quad (1)
\]

The strong and weak kappa statistic values vary between (0-1). When kappa calculated values tends to 1 then it will be agree near perfection otherwise no perfection:

\[
\text{Accuracy} = \frac{(\text{correctly predicted class} / \text{total testing class}) \times 100\%} \quad (2)
\]

\[
\text{Correctly Classified} = \frac{(\text{TP} + \text{TN})}{(\text{TP} + \text{TN} + \text{FP} + \text{FN})} \quad (3)
\]

where TP = true positives, FN = false negatives, FP = false positives and TN = true negatives, respectively.

\[
\text{Mean Absolute Error (MAE)} = \frac{1}{e} \sum_{i=1}^{e} |b_{i} - b| \quad (4)
\]

where, e = number of errors and \(b_{(i)} - b\) represents errors.

### Table 8. Representation of data description of heart disease attributes

| Attributes | Description |
|------------|-------------|
| Age        | Age of the patients in years |
| Sex        | (1 = Male; 0 = Female) |
| Cp         | Categories chest pain (0: Typical Angina, 1: Atypical) |
| Trestbps   | Resting blood pressure (mm hg) |
| Chol       | Measure serum cholesterol in Mg/Dl |
| Fbs        | (Measure fasting blood sugar > 120 Mg/Dl) (1 = True; 0 = False) |
| Restecg    | Measure electrocardiographic (0: Normal; 1: Abnormality) |
| Thalach    | Measure maximum heart rate |
| Exang      | Calculated exercise induced Angina (1 = Yes; 0 = No) |
| Oldpeak    | Measure depression induced by exercise relative to rest |
| Slope      | Measure slope of peak exercise (0: Upsloping; 1: Flat; 2: Downsloping) |
| Ca         | Identify major vessels (0-3) colored by Flourosopy |
| Thal       | (1 = Normal; 2 = Fixed Defect; 3 = Reversable Defect) |
| Target     | Diagnosis of heart disease (0: Disease; 1: Nondisease) |
Relative Absolute Error (RAE) = \[ \frac{\sum_{i=1}^{e} W_i - B_i}{\sqrt{\sum_{i=1}^{e} B_i^2}} \] \tag{5}

where \( W_i \) calculate predicted value and \( B_i \) calculate actual value for \((i=1..e)\) samples:

Root Mean Square Error (RMSE) = \[ \sqrt{\frac{1}{e}\sum_{(i=1)^e} [(c)_{(i)} - (o)_{(i)}]^2} \] \tag{6}

where, \((e, c \text{ and } o)\) represents variables of sample, forecasts and observed values respectively for\((i=1..e)\).
Root Relative Square Error (RRSE) = \[
\frac{\sum_{j=1}^{e}(W_{ij} - T_{ij})^2}{\sum_{j=1}^{e}(T_{ij} - \bar{T})^2}
\] (7)

where, \(W_{ij}\) is the value predicted by the individual program \(i\) for sample case \(j\) (out of \(n\) sample cases); \(T_{ij}\) is the target value for sample case \(j\); \(\bar{T}\) represents perfect fit in sample cases:

\[
\bar{T}\sum_{j=1}^{n}(T_{ij} - \bar{T})
\] (8)

3.2. Proposed Model

In this paper, we have used Pearson Correlation and Chi-Square features selection based algorithms for heart disease attributes correlation strength. The main objective of this research is to achieve highest classification accuracy with very less error. So, we have used parallel and sequential ensemble methods to reduce the drawback in prediction. The parallel and serial ensemble methods organized by J48 algorithm, Reduced Error Pruning and Decision Stump Algorithm decision tree based algorithms. We have used Random Forest ensemble method for parallel randomly selection in prediction and various sequential ensemble methods as AdaBoost, Gradient Boosting and XGBoost Meta classifiers. After the features selection trained on (75%) dataset and the test on (25%) with tree algorithms with ensemble method. The final prediction has been measured by average voting algorithms (Figure 2).

4. RESULTS

In this research, we have used heart disease medical dataset consists of 1025 individuals’ instances with 14 attributes and Pearson Correlation and Chi-Square features selection based algorithms for heart disease attributes correlation strength.

4.1. Pearson Correlation

Fu T et al., (2020), introduced about attributes correlation by Pearson’s Correlation method. The Pearson’s Correlation method generates relationship between the continuous features and the target variables. Pearson Correlation identifies feature relations to the response variable and measures linear correlation between two variables. This method measure the results by \([-1,1]\), with -1 assign perfect
negative correlation and +1 assign perfect positive correlation. The perfect negative correlation means one variable increases, the other decreases and perfect positive correlation means no linear correlation between the two variables. We have examined and find all the attributes in this heart disease are linearly correlated with maximum number of positive correlations (Figure 3).

4.2. Chi-Square

Bahassine S et al., (2020), introduced about Chi-Square feature selection for better score values of attributes. Chi-Square is a feature selection algorithm in machine learning and test the relationship between important features in dataset. The chi-square tests the independence of two events in statistics. This algorithm provides observed count values and expected count values and measures how expected

Table 9. Representation confusion matrix for heart disease attributes prediction

|                | J48          | REP          | Decision Stump | Random Forest |
|----------------|--------------|--------------|----------------|---------------|
| a b <-- classified as | 421 78 | a b <-- classified as | a b <-- classified as | a b <-- classified as |
| a = zero       | 65 461 | a = zero     | 38 488 | a = zero |
| b = one        |       | b = one     | 122 404 | b = one |
| XG Boost       | XG Boost   | AdaboostM1   | Gradient Boosting |
| a b <-- classified as | 375 124 | a b <-- classified as | a b <-- classified as |
| a = zero       | 122 404 | a = zero     | 11 515 | a = zero |
| b = one        |       | b = one     | 486 13 | b = one |
count with observed values. In this research, we have examined and find attribute “thalach” calculated high score and attribute “fbs” calculated low value between 9 selected positive scores (Figure 4).

In the statistical analysis used methods improved the prediction in heart disease using Pearson correlation and chi-square feature selection by eliminating the misclassified instances. We compare the performance of four ensemble methods, namely Random Forest, AdaBoostM1, Gradient Boosting and XG Boosting. The prediction model evaluated all performance by confusion matrix’s true positive, false positive, true negative and false negative with class values (Table 9).

In this analysis, we examined three algorithms: J48, Reduced Error Pruning and Decision Stump and generated an ensemble method Random Forest. Random forest ensemble method calculated 100% classification accuracy, which is high compare to other three algorithms. The kappa values of random forest is high and mean absolute, root mean squared, relative absolute and root relative error values are always low of Random Forest compare to J48, Reduced Error Pruning and Decision Stump algorithms in Table 10.

In the second analysis, we compared three algorithms: J48, Reduced Error Pruning and Decision Stump with three sequential ensemble methods, namely AdaBoostM1, XG Boost and Gradient Boosting. These three ensemble methods, namely AdaBoostM1, XG Boost and Gradient Boosting generated for J48, Reduced Error Pruning and Decision Stump algorithms. In this experiment, we find XG Boost calculated 98.5% classification accuracy, which is high compare to other algorithms in this table. The kappa values of XG Boost is high and mean absolute, root mean squared, relative absolute and root relative error values are always low of XG Boost compare to other algorithms in this Table 11.

Table 10. Representation of Analysis-I by J48, REP, DS and RF algorithms

| Statistical Analysis           | J48 | Reduced Error Pruning | Decision Stump | Random Forest |
|-------------------------------|-----|-----------------------|----------------|---------------|
| Correctly Classified Instances | 86.05% | 92.88% | 76% | 100% |
| Incorrectly Classified Instances | 13.95% | 7.12% | 24.00% | 0.00% |
| Kappa statistic               | 0.7206 | 0.8575 | 0.5196 | 1 |
| Mean absolute error           | 0.216 | 0.0951 | 0.365 | 0.0174 |
| Root mean squared error       | 0.3244 | 0.2414 | 0.4275 | 0.0519 |
| Relative absolute error       | 43.24% | 19.02% | 73.05% | 3.48% |
| Root relative squared error   | 64.89% | 48.29% | 85.52% | 10.38% |

Table 11. Analysis-II by J48, REP, DS and AdaBoostM1, XG Boost and Gradient Boosting algorithms

| Statistical Analysis           | J48 | REP | Decision Stump | AdaBoostM1 | XG Boost | Gradient Boost |
|-------------------------------|-----|-----|----------------|------------|---------|----------------|
| Correctly Classified Instances | 86.05% | 92.88% | 76% | 84.29% | 98.05% | 97.66% |
| Incorrectly Classified Instances | 13.95% | 7.12% | 24.00% | 15.71% | 1.95% | 2.34% |
| Kappa statistic               | 0.7206 | 0.8575 | 0.5196 | 0.6857 | 0.961 | 0.9531 |
| Mean absolute error           | 0.216 | 0.0951 | 0.365 | 0.2093 | 0.02 | 0.1313 |
| Root mean squared error       | 0.3244 | 0.2414 | 0.4275 | 0.3293 | 0.1304 | 0.1938 |
| Relative absolute error       | 43.24% | 19.02% | 73.05% | 41.89% | 4.11% | 26.27% |
| Root relative squared error   | 64.89% | 48.29% | 85.52% | 65.89% | 26.10% | 38.77% |
5. DISCUSSION

We summaries experiment I and II performances for all algorithms in Figure 5 and compare their classification accuracy and error prediction results. The figure represents four different ensemble and non-ensemble machine learning algorithms.

During section, we compared experiment I and II and found Random forest ensemble method calculated 100% classification accuracy, which is high compare to other ensemble methods. The kappa values of random forest is high and mean absolute, root mean squared, relative absolute and root relative error values are always low of Random Forest compare to AdaBoostM1, XG Boost and Gradient ensemble methods (Table 12).

On the basis of some previous performance on different dataset authors: Yadav DC, Pal S, (Yadav & Pal, 2018; Yadav & Pal, 2019c; Yadav & Pal, 2020a), calculated high accuracy but not covered 100% accuracy on the basis of ensemble method with majority of voting. In various review paper, we have considered the high, Instances and the from 2012 to 2020 in Table 13.

All the mentioned authors used various instances and algorithms but did not covered 100% classification accuracy at very low error rate. In this experiment, we find Random Forest calculated 100% classification accuracy at low error rate.

6. CONCLUSION

In experiment, we have organized heart disease dataset from UCI repository and dataset contains total 14 attributes with 1025 instances. In whole analysis we found, Pearson Correlation generates fair matrix for heart disease features for prediction in machine learning. The feature selection technique

Table 12. Comparison of R F with AdaBoostM1, XG Boost and Gradient ensemble methods

| Statistical Analysis            | Random Forest | AdaBoostM1 | XG Boost | Gradient Boost |
|---------------------------------|---------------|------------|----------|----------------|
| Correctly Classified Instances  | 100%          | 84.29%     | 98.05%   | 97.66%         |
| Incorrectly Classified Instances| 0.00%         | 15.71%     | 1.95%    | 2.34%          |
| Kappa statistic                 | 1             | 0.6857     | 0.961    | 0.9531         |
| Mean absolute error             | 0.0174        | 0.2093     | 0.02     | 0.1313         |
| Root mean squared error         | 0.0519        | 0.3293     | 0.1304   | 0.1938         |
| Relative absolute error         | 3.48%         | 41.89%     | 4.11%    | 26.27%         |
| Root relative squared error     | 10.38%        | 65.89%     | 26.10%   | 38.77%         |
namely, Chi-Square generates valuable score with corresponding features. Both features selection techniques provide help in prediction for applied machine algorithms. In this paper, all experiment divides into two parts, the first part deals with J48, Reduced Error Pruning and Decision Stump and generated a Random Forest ensemble method. This parallel ensemble method calculated high classification accuracy 100% with low error. The second part of experiment deals with J48, Reduced Error Pruning and Decision Stump with three sequential ensemble methods, namely AdaBoostM1, XG Boost and Gradient Boosting. The XG Boost ensemble method calculated better results or high classification accuracy and low error compare to AdaBoostM1 and Gradient Boosting ensemble methods. The XG Boost ensemble method calculated 98.05% classification accuracy, but Random Forest ensemble method calculated high classification accuracy 100% with low error. With the results, finally we found, Random Forest performed better results compare to all other applied machine learning algorithms in this paper.

For the future work planning, we will observe other features selection method with fuzzy, artificial and Neural Network Hybrid Ensemble Method.

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